

GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:33 ; Search time 5.10277 Seconds  
(without alignments)  
928.727 Million cell updates/sec

Title: US-09-821-726a-2

Perfect score: 125  
Sequence: 1 LDTWKEKKGKPGCAPPKDLMY 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP\_TREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_virus:\*  
17: sp\_bacteriophage:\*  
17: sp\_archaea:\*

pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	59	47.2	1677	11	070373	070373 mus musculus
2	54	43.2	1194	5	09W485	09W485 drosophila
3	54	43.2	1284	5	0960F1	0960F1 drosophila
4	51.5	41.2	681	4	096P10	096P10 homo sapien
5	51.5	41.2	1308	4	060307	060307 homo sapien
6	51	40.8	153	17	057795	057795 pyrococcus
7	51	40.8	297	5	095526	095526 drosophila
8	50	40.0	224	10	08R238	08R238 oryza sativ
9	50	40.0	237	7	030097	030097 homo sapien
10	50	40.0	237	7	030098	030098 homo sapien
11	50	40.0	264	7	029970	029970 homo sapien
12	50	40.0	269	7	030155	030155 homo sapien
13	50	40.0	497	10	08S1B7	08S1B7 oryza sativ
14	50	40.0	611	5	09N893	09N893 plasmodium
15	49	39.2	191	3	074299	074299 schizophy11
16	49	39.2	266	17	09HNPF6	09HNPF6 halobacteri

17	49	39.2	331	4	016509	016509 homo sapien
18	49	39.2	333	4	09NY94	09NY94 homo sapien
19	49	39.2	331	16	093JF5	093JF5 streptomyce
20	49	39.2	1518	5	09VN58	09VN58 drosophila
21	48.5	38.8	3080	5	09VR33	09VR33 drosophila
22	48	38.4	144	16	093J11	093J11 streptomyce
23	48	38.4	145	5	09VE17	09VE17 drosophila
24	48	38.4	263	16	09RKP1	09RKP1 streptomyce
25	48	38.4	322	10	09FMD2	09FMD2 oryza sativ
26	48	38.4	1171	10	08S101	08S101 oryza sativ
27	48	38.4	1189	10	09F500	09F500 arabidopsis
28	47.5	38.0	321	16	08RG41	08RG41 fusobacteri
29	47	37.6	218	4	09NP58	09NP58 homo sapien
30	47	37.6	242	16	092KJ2	092KJ2 rhizobium m
31	47	37.6	327	11	08R1K0	08R1K0 mus musculu
32	47	37.6	363	16	08X033	08X033 ralsstonia s
33	47	37.6	371	11	08R311	08R311 mus musculu
34	47	37.6	427	12	08QNG0	08QNG0 ectocarpus
35	47	37.6	565	5	09FX29	09FX29 strongyloce
36	47	37.6	598	2	083032	083032 streptomyce
37	47	37.6	599	16	09L010	09L010 streptomyce
38	47	37.6	600	3	09C215	09C215 neurospora
39	47	37.6	715	3	08X0C4	08X0C4 neurospora
40	47	37.6	914	4	09BY10	09BY10 homo sapien
41	47	37.6	926	6	09SK63	09SK63 macaca fasc
42	47	37.6	950	4	09P2F5	09P2F5 homo sapien
43	47	37.6	4936	16	08YKJ3	08YKJ3 arabidopsi
44	46.5	37.2	921	5	09M093	09M093 drosophila
45	46.5	37.2	1240	11	070576	070576 mus musculu

## ALIGNMENTS

RESULT 1  
ID 070373 PRELIMINARY: PRT: 1677 AA.

AC 070373: 01-AUG-1998 (TREMREL. 07, Created)  
DT 01-AUG-1998 (TREMREL. 07, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE Xin.  
GN Xin.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART MUSCLE;  
RX Wang D.-Z., Hu X., Lin J.L.-C., Kitten G.T., Solursh M., Lin J.J.-C.;  
RT "Differential display of mRNAs from the atrioventricular region of  
RT developing chicken hearts at stages 15 and 21."  
RL Front. Biosci. 1:a1-a15(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART MUSCLE;  
RX MEDLINE=99146891; PubMed=10021346;  
RA Wang D.-Z., Reiter R.S., Lin J.L.-C., Wang G., Williams H.S.,  
RA Krob S.L., Schultzeiss T.M., Evans S., Lin J.J.-C.;  
RT "Regulation of a novel gene, Xin, in cardiac morphogenesis."  
RL Development 126:1281-1294(1999).  
DR EMBL: AF051945; AAC06023.1; -  
DR MGI: 1333878; Xin.  
SQ SEQUENCE 1677 AA: 182085 MW: A201CFG9A710C7FF CRC64;

Query Match 47.2%; Score 59; DB 11; Length 1677;

Best Local Similarity 64.3%; Pred. No. 3.6; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

DB 571 EEBGKGGPGAPPE 584

## RESULT 2

ID 09W485 PRELIMINARY; PRT: 1194 AA.

AC 09W485: 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)

DE CG3125 protein.

GN CG3125

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Phrygana; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephyridae; Drosophilidae; Drosophila.

NCBI\_TaxID=7227;

OX NCBI

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Aghayani A., An H.-J., Andrews-Piankoff L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Doudon K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,

RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liao X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA McKelvey G., Mitsuhashi N.V., Moberg C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

DR EMBL: AE003435; AAF46073.1;

DR FlyBase: FBgn0029797; CG3125.

DR SEQUENCE 1194 AA; 127551 MW; F0F2D3A55C7F6C59 CRC64;

Query Match 43.2%; Score 54; DB 5; Length 1194;

Best Local Similarity 64.3%; Pred. No. 15;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 VBEQKGGPGGAPP 18

DB 613 MKSPNGGPGGAPP 626

RESULT 3

ID 0960F1 PRELIMINARY; PRT: 1284 AA.

AC 0960F1: 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)

DE S004165P.

GN S004165P.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Phrygana; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephyridae; Drosophilidae; Drosophila.

NCBI\_TaxID=7227;

OX NCBI

RN [1]

RP SEQUENCE FROM N.A.

RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nuno J., Paclet J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY052093; AAK93517.1;

DR FlyBase: FBgn0029797; CG3125.

DR InterPro: IPR002035; VWF\_A.

DR SMART: SM00327; VMA: 1.

DR PROSITE: PS00234; VWF\_A.1.

SQ SEQUENCE 1284 AA; 137152 MW; E322BE35961525A1 CRC64;

Query Match 43.2%; Score 54; DB 5; Length 1284;

Best Local Similarity 64.3%; Pred. No. 16;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 VBEQKGGPGGAPP 18

DB 657 MKSPNGGPGGAPP 670

## RESULT 4

ID 09UP10 PRELIMINARY; PRT: 681 AA.

AC 09UP10: 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE KIAA0561 protein (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Lamedin J.E., McCready P.M., Skowronski E., Viswanathan V.,

RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillagen S.,

RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,

RA Dangnan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,

RA Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,

RA Duarte S., Lucas S., Bruce R., Nolan M., Trong S., Kobayashi A.,

RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

RA Olsen A.S., Carrano A.V.,

RT "Sequence analysis of a 5.7 kb region in 19p13.1."

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC007192; AAD22670.1;

DR InterPro: IPR001478; PDZ.

DR InterPro: IPR000961; PKinase\_C.

DR InterPro: IPR002965; P\_Rich\_extensn.

DR Pfam: PF00595; PDZ; 1.

DR PRINTS: PR01217; PRICHEXTNSN.

DR SMART: SM00228; PDZ; 1.

DR SMART: SM00133; S\_TR\_X.1.

DR PROSITE: PS0106; PDZ; 1.

FT NON\_TER 1

SQ SEQUENCE 681 AA; 72455 MW; 3DF3E31C24C53D2A CRC64;

Query Match 41.2%; Score 51.5; DB 4; Length 681;  
 Best Local Similarity 54.2%; Pred. No. 20;  
 Matches 13; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

OY 1 LDTWVK-----EOKGKGGGAPK 19  
 DB 155 LDTWVKFAFSSSEDEGVGGPAPK 178

## RESULT 5

060307 PRELIMINARY: PRT: 1308 AA.

AC 060307: PRELIMINARY: PRT: 1308 AA.  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
 DE KIAA0561 protein (Fragment).  
 GN KIAA0561.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=98290545; PubMed=9628581;  
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,  
 Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro."  
 RL DNA Res. 5:31-39(1998).  
 RN [2]  
 RP SEQUENCE OF 1-593 FROM N.A.  
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,  
 RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J., Liu S.,  
 RA Dangnan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Atlix C., Andeise T., Trankheim M., Amico-Keller G., Coefield J.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,  
 RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.;  
 RT "Sequence analysis of an ~600 kb region in 19p13.1 between JAK3 and  
 RT PDE4C.";  
 RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.  
 CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: AB011133; BAA25487.1;  
 DR EMBL: AC005793; AAC62830.1;  
 DR HSSP: P05132; ICTP.  
 DR Interpro: IPR000719; Euk-pkinase.  
 DR Interpro: IPR001478; PDZ.  
 DR Interpro: IPR000961; Pkinase-C.  
 DR Interpro: IPR002290; Ser\_thr\_pkinase.  
 DR Interpro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00505; PDZ\_1.  
 DR Pfam: PF00065; Pkinase\_1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR PRODOM: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00228; PDZ\_1.  
 DR SMART: SM00133; S\_TK\_X\_1.  
 DR PROSITE: PS50106; PDZ\_1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Serine/threonine-protein kinase.  
 FT NON\_TER 1 1  
 SO SEQUENCE 1308 AA; 143004 MW; 9B3A23C528EF47A6 CRC64;

OY 1 LDTWVK-----EOKGKGGGAPK 19

Query Match 41.2%; Score 51.5; DB 4; Length 1308;  
 Best Local Similarity 54.2%; Pred. No. 39;  
 Matches 13; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

DB 782 LDTWVKFAFSSSEDEGVGGPAPK 805

Query Match 40.8%; Score 51; DB 17; Length 153;  
 Best Local Similarity 60.0%; Pred. No. 5;  
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

## RESULT 6

057795 PRELIMINARY: PRT: 153 AA.

AC 057795: PRELIMINARY: PRT: 153 AA.  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
 DE Hypothetical protein PH0068.  
 GN PH0068.  
 OS Pyrococcus horikoshii.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OC NCBI\_TaxID=53953;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OT3;  
 RX MEDLINE=98344137; PubMed=9679194;  
 RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,  
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,  
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
 RA Masuchi Y., Shizuya H., Kikuchi H.;  
 RT "Complete sequence and gene organization of the genome of a hyper-  
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."  
 RL DNA Res. 5:55-76(1998).  
 DR EMBL: AP000001; BAA29137.1;  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 153 AA; 16966 MW; 9063FA1B6DA9255B CRC64;

OY 1 LDTWVKDOKGKGGK 15  
 DB 121 LDTWVKDOKGKGGK 135

## RESULT 7

095526 PRELIMINARY: PRT: 297 AA.

AC 095526: PRELIMINARY: PRT: 297 AA.  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
 DE LD33666P.  
 GN ANTP OR BG:DS07700.1 OR CG1028.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nimco J., Paclet J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Ceolner S.;  
 RT Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
 RL EMBL: AY060407; AAL25446.1;  
 DR FLYBASE: FBgn0000095; ANTP.  
 DR Interpro: IPR001827; Antennapedia.  
 DR PROSITE: PS00032; ANTENNAPEDIA; UNKNOWN\_1.  
 SO SEQUENCE 297 AA; 32845 MW; A88C5435ABD61983 CRC64;

Query Match 40.8%; Score 51; DB 5; Length 297;

Best Local Similarity 45.0%; Pred. No. 10;  
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 MYEOKGKGGAPPKDLMY 23  
DB 230 MYOQSGVPVVGAPPGMMH 249

## RESULT 8

ID Q8R238 PRELIMINARY; PRT; 224 AA.  
AC Q8R238;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DE 01159\_D09.31 (TREMBLrel. 21, Last annotation update)  
GN 01159\_D09.31.  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Eupharidiales; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=CV, NIPPONBARE;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC  
clone:01159\_D09.31";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
EMBL: AP003792; BAB89213.1, -;  
SQ SEQUENCE 224 AA; 22952 MW; 01DB382A5972633F CRC64;

Query Match  
Best Local Similarity 40.0%; Score 50; DB 10; Length 224;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEOKGKGGAPGAP 18  
DB 103 KKKKGRKGGLP 115

## RESULT 9

ID Q30097 PRELIMINARY; PRT; 237 AA.  
AC Q30097;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
GN HLA-DQB1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yasunaga S.;  
RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
EMBL: LA0180; AAA92331.1, -;  
DR HSSP: P13760; 2SEB.  
DR InterPro: IPR003597; Ig\_C1.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR000353; MHC\_II\_beta.  
DR Pfam: PF00047; Ig\_1.  
DR Pfam: PF00969; MHC\_II\_beta.  
DR Prodom: PD000328; MHC\_II\_beta; 1.  
DR SMART: SM00407; IG\_C1; 1.  
DR PROSITE: PS00290; IG\_MHC; 1.  
DR Glycoprotein; MHC II; Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 237 AA; 27038 MW; 460B53ABCATBC8EA CRC64;

Best Local Similarity 34.8%; Pred. No. 11;  
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMYEOKGKGGAPPKDLMY 23  
DB 215 LGLIRGSRKRGQPPAGLLH 237

## RESULT 10

ID Q30098 PRELIMINARY; PRT; 237 AA.  
AC Q30098;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
GN HLA-DQB1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yasunaga S.;  
RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
EMBL: LA0181; AAA92332.1, -;  
DR HSSP: P13760; 2SEB.  
DR InterPro: IPR003597; Ig\_C1.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR000353; MHC\_II\_beta.  
DR Pfam: PF00047; Ig\_1.  
DR Pfam: PF00969; MHC\_II\_beta.  
DR Prodom: PD000328; MHC\_II\_beta; 1.  
DR SMART: SM00407; IG\_C1; 1.  
DR PROSITE: PS00290; IG\_MHC; 1.  
DR Glycoprotein; MHC II; Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 237 AA; 27179 MW; 75C1B91440C0D5DF CRC64;

Query Match  
Best Local Similarity 40.0%; Score 50; DB 7; Length 237;  
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMYEOKGKGGAPPKDLMY 23  
DB 215 LGLIRGSRKRGQPPAGLLH 237

## RESULT 11

ID Q29970 PRELIMINARY; PRT; 264 AA.  
AC Q29970;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
GN Cell surface glycoprotein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-88226367; PubMed-3371836;  
RA Yasunami M.;  
RT "Structural analysis of human major histocompatibility complex class  
II genes";  
RT Fukuda Igaku Zasshi 79:153-167(1988).  
DR EMBL: M57649; AAA63217.1, -;  
DR HSSP: P13760; 2SEB.  
DR InterPro: IPR003597; Ig\_C1.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR000353; MHC\_II\_beta.



DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00969; MHC\_II\_beta; 1.  
 DR ProDom; PD000328; MHC\_II\_beta; 1.  
 DR SMART; SM00407; IGL1; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Glycoprotein; MHC II; Transmembrane.  
 FT NON\_TER  
 SQ SEQUENCE 264 AA: 29871 MW: BB6AA9054F3CB75 CRC64:

Query Match 40.0%; Score 50; DB 7; Length 264;  
 Best Local Similarity 34.8%; Pred. No. 13;  
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 IDTMYEKGKGGGAPPKDLMY 23  
 : : : : :  
 DB 242 LGIIIRORSQKGGPGPPAGLILH 264

## RESULT 12

ID Q30155 PRELIMINARY; PRT; 269 AA.  
 AC Q30155;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE HLA-DRB2 protein.  
 GN HLA-DRB2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-87192945; PubMed-3494674;  
 RA Tsunamoto K., Yasunami M., Kimura A., Inoko H., Ando A., Hirose T.,  
 RA Inayama S., Sasazuki T.;  
 RT "Dc41 beta gene from HLA-DR2-Dw12 consists of six exons and expresses  
 multiple Dc41 beta polypeptides through alternative splicing.";  
 RL Immunogenetics 25:343-346(1987).  
 DR EMBL; M16276; AAA59823.1; -.  
 DR HSSP; P13760; 2SEB.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR000353; MHC\_II\_beta.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00969; MHC\_II\_beta; 1.  
 DR ProDom; PD000328; MHC\_II\_beta; 1.  
 DR SMART; SM00407; IGL1; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Glycoprotein; MHC II; Transmembrane.  
 SQ SEQUENCE 269 AA: 30532 MW: 4F81EG5AD92A6EA CRC64:

Query Match 40.0%; Score 50; DB 7; Length 269;  
 Best Local Similarity 34.8%; Pred. No. 13;  
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 LDTMYEKGKGGGAPPKDLMY 23  
 : : : : :  
 DB 247 LGIIIRORSQKGGPGPPAGLILH 269

## RESULT 13

ID Q8S1B7 PRELIMINARY; PRT; 497 AA.  
 AC Q8S1B7;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE B114B07.4 protein.  
 GN B114B07.4.  
 OS Oryza sativa (Japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Eupharitidae; Oryzae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC  
 clone:B114B07.";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP003334; BAB8995.1; -.  
 DR EMBL; AP003334; BAB8995.1; -.  
 SQ SEQUENCE 497 AA: 55128 MW: B0B9AD8400F94C4 CRC64:

Query Match 40.0%; Score 50; DB 10; Length 497;  
 Best Local Similarity 61.5%; Pred. No. 24;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 KEQKGGGPGAPP 18  
 : : : : :  
 DB 378 KKKKGGGPGAPP 390

## RESULT 14

ID Q9N893 PRELIMINARY; PRT; 611 AA.  
 AC Q9N893;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE Vir12 protein.  
 GN Vir12.  
 OS Plasmodium vivax.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5855;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Oliver K., Bowman S., Hall N., Quail M., Rajandream M.A., Harris D.,  
 RA del Portillo H.A., Lanzer M., Barrell B.G.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL360354; CAB96702.1; -.  
 SQ SEQUENCE 611 AA: 68442 MW: A642D1893D7D8F4 CRC64:

Query Match 40.0%; Score 50; DB 5; Length 611;  
 Best Local Similarity 56.2%; Pred. No. 30;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 MYEKGKGGGAPPK 19  
 : : : : :  
 DB 366 ITRKGGVSPAGSPSK 381

## RESULT 15

ID Q74299 PRELIMINARY; PRT; 191 AA.  
 AC Q74299;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE ORP15 protein precursor.  
 OS Schizophyllum commune (Bracket fungus).  
 OC Eukaryota; Fungi; Basidiomycota; Hymenozetes; Homobasidiomycetes;  
 OC Agaricales; Schizophyllaceae; Schizophyllum.  
 OX NCBI\_TaxID=5334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=4-40;  
 RA Lugones L.G.;  
 RL Thesis (1998), University of Groningen.  
 DR EMBL; AJ007503; CA007544.1; -.  
 KW Signal.  
 FT SIGNAL  
 SQ SEQUENCE 191 AA: 19973 MW: 778518F0D830179 CRC64:

Query Match 39.2%; Score 49; DB 3; Length 191;

Best Local Similarity 60.0%; Pred. No. 13;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 VKEQKRGKPGGAPPK 19  
::| | | | | | | |  
Db 90 IEEIKGKRPAGGHPPK 104

Search completed: April 11, 2003, 16:14:15  
Job time : 8.10277 secs

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 ; Search time 1.35073 Seconds  
(without alignments)  
706.250 Million cell updates/sec

Title: US-09-821-726a-2

Perfect score: 125  
Sequence: 1 LDTMYKQKGGKGGAPKDLMY 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	184	1 CILP_MOUSE	Q9cr36 mus musculu
2	90	72.0	199	1 CILP_HUMAN	Q9cr37 mus sapien
3	51	40.8	378	1 HMAN_DROME	P02833 drosophila
4	49	39.2	142	1 VPUB_KLEPN	P20775 klebsiella
5	49	39.2	331	1 TAL_HUMAN	P17542 homo sapien
6	47	37.6	233	1 HB2A_RAT	P06341 ratius norv
7	47	37.6	263	1 HB2B_RAT	P29826 ratius norv
8	46	36.8	267	1 TRUA_CHLMU	Q9p10 chlamydia m
9	46	36.8	267	1 TRUA_CHLTR	O84469 chlamydia t
10	46	36.8	268	1 HB2X_HUMAN	P05338 homo sapien
11	46	36.8	398	1 ACOC_BACSU	O31550 bacillus su
12	46	36.8	423	1 VAR_MOUSE	O62463 mus musculu
13	46	36.8	697	1 GONL_PYRAE	O82277 pyrobaculum
14	45.5	36.4	402	1 GONL_HUMAN	P56680 humicola in
15	45	36.0	137	1 LSM4_MOUSE	O9qxa5 mus musculu
16	45	36.0	139	1 LSM4_HUMAN	O9y420 homo sapien
17	45	36.0	160	1 PFMD_SCEOB	P19586 sceneemus
18	45	36.0	263	1 HB2K_MOUSE	P06343 mus musculu
19	45	36.0	263	1 HB2S_MOUSE	P06344 mus musculu
20	45	36.0	263	1 HB2U_MOUSE	P14883 mus musculu
21	45	36.0	265	1 HB2V_MOUSE	P14884 mus musculu
22	45	36.0	265	1 HB2W_MOUSE	P01921 mus musculu
23	45	36.0	265	1 HB2Z_MOUSE	P06342 mus musculu
24	45	36.0	302	1 CCDC_CAEEL	P17657 caenorhabdi
25	45	36.0	863	1 AKX1_MOUSE	O35625 mus musculu
26	45	36.0	863	1 AKX1_MOUSE	O35625 mus musculu
27	45	36.0	3414	1 POLG_TBVEV	O01299 t genome po
28	44.5	35.6	264	1 COLI_MACNE	P14336 t genome po
29	44.5	35.6	267	1 COLI_MACNE	P14336 t genome po
30	44.5	35.6	267	1 COLI_MACNE	P14336 t genome po
31	44.5	35.6	311	1 MRAM_CAUCR	O9tqj6 caulicotr
32	44	35.2	172	1 CH18_DROME	P07184 drosophila
33	44	35.2	231	1 DEOC_THETN	O8rb49 thermocaneer

34	44	35.2	275	1 CAB4_HUMAN	P57796 homo sapien
35	44	35.2	375	1 SOX3_MOUSE	P53784 mus musculu
36	44	35.2	471	1 S61A_YARLI	P78979 yarrowia li
37	44	35.2	479	1 PGRC_LEIME	O27685 leishmania
38	44	35.2	506	1 CP4B_RABIT	P15128 onychocyst
39	44	35.2	540	1 CH61_SYNY3	O05972 syncrocyct
40	44	35.2	546	1 RUB1_BRANA	P21239 brassica na
41	44	35.2	550	1 GPC1_CHICK	P50593 gallus gall
42	44	35.2	783	1 CAP5_MOUSE	P55284 mus musculu
43	43.5	34.8	212	1 COLI_SHEEP	P01191 o corticotr
44	43.5	34.8	265	1 COLI_BOVIN	P01190 b corticotr
45	43.5	34.8	431	1 HXB3_HUMAN	P14651 homo sapien

## ALIGNMENTS

RESULT 1  
CILP\_MOUSE STANDARD: PRT: 184 AA.  
ID CILP\_MOUSE  
AC O9CR36: O9D7K7: O9CT25:  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE CILP protein homolog.  
GN CILP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID:10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SRRAIN-C57BL/6J; TISSUE=Stomach, and Tongue;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,  
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fieleschman W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirral L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Mashio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guncioncin S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,  
RA Hayashizaki Y.;  
RL "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
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DR EMBL; AK008990; BAB26010.1;  
DR EMBL; AK008622; BAB25784.1;  
DR EMBL; AK008641; BAB25801.1;  
DR EMBL; AK008647; BAB25805.1;  
DR EMBL; AK008722; BAB25856.1;  
DR EMBL; AK008745; BAB25872.1;  
DR EMBL; AK008933; BAB25975.1;  
DR EMBL; AK008956; BAB25988.1;  
DR EMBL; AK009145; BAB26103.1;  
DR EMBL; AK019050; BAB31525.1;



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DR EMBL; M20705; AAA70216.1; -
DR EMBL; M12009; AAA79241.1; -
DR PIR; A03318; A03318
DR PIR; A25399; A25399
DR PIR; A23450; A23450
DR PIR; C24780; C24780
DR PIR; A25400; A25400
DR PDB; 1HOW; 31-OCT-93
DR PDB; 2HOW; 31-OCT-93
DR PDB; 1AHD; 31-OCT-93
DR PDB; 1SAN; 30-APR-94
DR PDB; 9ANT; 18-NOV-98
DR TRANSFAC; T00026; -
DR Flybase; Fgn0000095; Antp
DR InterPro; IPR001827; Antennapedia
DR InterPro; IPR001356; Homeobox
DR Pfam; PF00046; homeobox_1
DR PRINTS; PR00025; ANTENNAPEIDIA
DR PRINTS; PR00024; HOMEBOX
DR Pfdom; PD000010; Homeobox; 1
DR SMART; SM00389; HOX; 1
DR PROSITE; PS00027; HOMEBOX_1; 1
DR PROSITE; PS00032; ANTENNAPEIDIA; 1
DR PROSITE; PS50071; HOMEBOX_2; 1
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Homeobox; 3D-structure.
KW 3D-structure.
FT DOMAIN 76 81 GLN-RICH (OPA-REPEAT)
FT DOMAIN 110 155 GLN-RICH (OPA-REPEAT)
FT DOMAIN 283 288 ANT-YPE HEXAPEPTIDE
FT DNA_BIND 297 356 HOMEBOX
FT CONFLICT 300 300 G -> E (IN REF. 7)
FT HELIX 306 318
FT HELIX 324 334
FT HELIX 335 335
FT TURN 335 350
FT HELIX 339 355
FT TURN 351 355
FT TURN 358 359
FT TURN 359 359
SQ SEQUENCE 378 AA; 42761 MW; D653232A8622D055 CRC64;

OY 4 MYKDGKGGKPGAPPKDLMY 23
1::11111111::11
DB 230 MYOQSGVPVGAPPGGMH 249

Query Match 40.8%; Score 51; DB 1; Length 378;
Best Local Similarity 45.0%; Pred. No. 5.5; Mismatches 6; Indels 0; Gaps 0;
Matches 9; Conservative 5;

RESULT 4
YPUB_KLEPN STANDARD; PRT; 142 AA.
ID YPUB_KLEPN
AC P20775;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT Hypothetical protein in PULS 3' region (Fragment).
DE Klebsiella pneumoniae.
OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OC NCBI_TaxID=573;
OX
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69291709; PubMed=2661532;
RA "Klebsiella pneumoniae puls gene encodes an outer membrane
RT lipoprotein required for pullulanase secretion."
RT J. Bacteriol. 171:3673-3679(1985).
RC -----
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DR EMBL; M29097; AAA61979.1; -  
DR PIR; D32880; D32880  
KW Hypothetical protein  
FT NON\_TER 142  
SQ SEQUENCE 142 AA; 16447 MW; 03ED03FBF63242D0 CRC64;

Query Match  
Best local Similarity 39.2%; Score 49; DB 1; Length 142;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 QKSGPGGAPK 19  
Db 49 RKGKGGKPPR 60

## RESULT 5

TAL\_HUMAN  
ID TAL\_HUMAN STANDARD; PRT; 331 AA.  
AC P17342;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DE T-cell acute lymphocytic leukemia-1 protein (TAL-1 protein) (STEM cell protein) (T-cell leukemia/lymphoma-5 protein).  
GN TAL1 OR SCL OR TC15.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid:9606;  
RN (1)  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RA MEDLINE=91061750; PubMed=2247063;  
RA Apian P.D., Begley C.G., Bertness V., Nussmeier M., Ezquerria A., Coligan J., Kirsch I.R.;  
RT "The SCL gene is formed from a transcriptionally complex locus."  
RL Mol. Cell. Biol. 10:6426-6435(1990).  
RP SEQUENCE FROM N.A.  
RA Grafham D.;  
RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE OF 118-331 FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=9009309; PubMed=2602361;  
RA Begley C.G., Apian P.D., Denning S.M., Haynes B.F., Waldmann T.A., Kirsch I.R.;  
RT "The gene SCL is expressed during early hematopoiesis and encodes a protein involved in T-cell development."  
RL Proc. Natl. Acad. Sci. U.S.A. 86:10128-10132(1989).  
RP SEQUENCE OF 181-331 FROM N.A.  
RA MEDLINE=90151616; PubMed=2303035;  
RA Chen Q., Cheng J.-T., Tsai L.H., Schneider N., Buchanan G., Carroll A., Crist W., Ozanne B., Siciliano M.J., Baer R.;  
RT "The tal gene undergoes chromosome translocation in T cell leukemia and potentially encodes a helix-loop-helix protein."  
RL EMBO J. 9:415-424(1990).  
RP SEQUENCE OF 106-148 FROM N.A.  
RX MEDLINE=91037802; PubMed=2230650;  
RA Chen Q., Yang C.Y.C., Tsan J.T., Xia Y., Ragab A.H., Peiper S.C., Carroll A., Baer R.;  
RT "Coding sequences of the tal-1 gene are disrupted by chromosome translocation in human T cell leukemia."  
RL J. Exp. Med. 172:1403-1408(1990).  
RP FUNCTION;  
RX MEDLINE=93011002; PubMed=1396592;  
RA Apian P.D., Nakahara K., Orkin S.H., Kirsch I.R.;  
RT "The SCL gene product: a positive regulator of erythroid

RT differentiation."  
RL EMBL J. 11:4073-4081(1992).

RA MEDLINE=93173511; PubMed=8437851;  
RX Cheng J.-T., Hsu H.-L., Hwang L.-Y., Baer R.;  
RT "Products of the TAL1 oncogene: basic helix-loop-helix proteins phosphorylated at serine residues."  
RL Oncogene 8:677-683(1993).

CC -1 FUNCTION: IMPLICATED IN THE GENESIS OF HEMOPHOETIC MALIGNANCIES.  
CC IT MAY PLAY AN IMPORTANT ROLE IN HEMOPHOETIC DIFFERENTIATION.  
CC SERVES AS A POSITIVE REGULATOR OF ERYTHROID DIFFERENTIATION.  
CC TO THE LIM DOMAIN CONTAINING PROTEIN RHOMBOTIN-2.  
CC BHLH PROTEIN. FORMS HETERODIMERS WITH E12 AND E47. BINDS TO DRG1.  
CC PP39-TAL1 AND PP22-TAL1; ARE PRODUCED BY ALTERNATIVE SPLICING. THE  
CC SPLICING PATTERN IS CELL-LINEAGE DEPENDENT.  
CC -1 TISSUE SPECIFICITY: LEUKEMIC STEM CELL.  
CC -1 DOMAIN: THE HELIX-LOOP-HELIX DOMAIN IS NECESSARY AND SUFFICIENT  
CC FOR THE INTERACTION WITH DRG1.  
CC -1 DISEASE: SOME T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) (A FORM  
CC OF STEM-CELL LEUKEMIA) ARE CHARACTERIZED BY A CHROMOSOMAL  
CC TRANSLOCATION T(1;14)(p32;q11) WHICH INVOLVES TAL1 AND T-CELL  
CC RECEPTOR ALPHA CHAIN (TCRA) GENES.  
CC -1 SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
CC TRANSCRIPTION FACTORS.

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DR EMBL; M61108; AAA36600.1;  
DR EMBL; M61103; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; M61104; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; M61105; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; M63572; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; AL135960; CAB72103.1;  
DR EMBL; M63589; AAA36599.1;  
DR EMBL; M63576; AAA36599.1; JOINED.  
DR EMBL; M29038; AAA36598.1;  
DR EMBL; X58621; CAA1476.1;  
DR EMBL; X58622; CAA1477.1;  
DR PIR; A34519; A34519.  
DR PIR; A36358; A36358.  
DR TRANSFAC; T00790;  
DR Genew; HGNC:11556; TAL1.  
DR MIM; 187040;  
DR InterPro; IPR001092; HLH\_basic.  
DR Pfam; PF00010; HLH\_1.  
DR SMART; SM00353; HLH\_1.  
DR PROSITE; PS00038; HLH\_1.  
DR PROSITE; PS50888; HLH\_2; 1.  
KW DNA-binding; Transcription regulation; Differentiation;  
KW Proto-oncogene; Chromosomal translocation; Alternative splicing;  
KW Phosphorylation.  
FT DOMAIN 89 132 PRO-RICH.  
FT DNA\_BIND 187 199 BASIC DOMAIN.  
FT DOMAIN 200 240 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
FT DOMAIN 263 274 POLY-GLY.  
FT VARSPIC 1 25 MISSING (IN ISOFORM PP39-TAL1).  
FT VARSPIC 1 175 MISSING (IN ISOFORM PP22-TAL1).  
SQ SEQUENCE 331 AA; 34270 MW; 33BBE31589DBB7C7 CRC64;

Query Match  
Best local Similarity 39.2%; Score 49; DB 1; Length 331;  
Matches 69.2%; Pred. No. 9.2;

```

Query Match          37.6%;   Score 47;   DB 1;   Length 263;
Best local Similarity 36.4%;   Pred. No. 14;
Matches      8;   Conservative      5;   Mismatches      9;   Indels      0;   Gaps
Oy      1   LDITWKEQKCGKGCAPPKDL 22
          | : : : | | | :
Db      241  LGLFIRKRGKGPFGPPAGL 262

RESULT 8
TRUA_CHLMU
ID      TRUA_CHLMU      STANDARD;      PRT;      267 AA.
AC      O9PPT0:
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DEF     tRNA pseudouridine synthase A (EC 4.2.1.70) (pseudouridylate synthase
DE      1) (pseudouridine synthase I) (uracil hydrolyase).
DE      GN
TRUA OR TC074B.

```

OS Chlamydia muridarum.  
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 CC NCBI\_TaxID=83560;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MOPN / Ni99;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Gwin M., Nelson W., DeBoy R., Kolony J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RT "Genome sequences of Chlamydia trachomatis MOPN and Chlamydia  
 pneumoniae AR39";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 CC -1- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITIONS 38, 39 AND 40 IN  
 CC THE ANTICODON STEM AND LOOP OF TRANSFER RNAs (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine  
 CC 5-phosphate + H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE TRUA FAMILY OF PSEUDOURIDINE SYNTHASES.  
 CC -----  
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 CC -----  
 CC EMBL: AE002343; AAF39555.1;  
 DR InterPro: IPR001406; Pseudou\_synth\_1.  
 DR Pfam: PF01416; Pseudou\_synth\_1.  
 DR TIGRfams: TIGR00071; hist\_trua; 1.  
 KW Lyase; trna processing; Complete proteome.  
 FT ACT\_SITE 52 BY SIMILARITY.  
 SQ SEQUENCE 267 AA; 30413 MW; CEBDB356B8EDBA7 CRC64;  
 Query Match 36.8%; Score 46; DB 1; Length 267;  
 Best Local Similarity 42.9%; Pred. No. 20;  
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 LDTWKEQKGGCGGAPPKDL 21  
 DB 221 LEMLEKRRKGGPSPAPPYGL 241  
 RESULT 9  
 TRUA\_CHLTR STANDARD: PRT; 267 AA.  
 AC 084469;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE trna pseudouridine synthase A (EC 4.2.1.70) (Pseudouridylylate synthase  
 DE I) (Pseudouridine synthase I) (Uracil hydrolase).  
 GN TRUA OR CT463.  
 OS Chlamydia trachomatis.  
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 CC NCBI\_TaxID=813;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-D/UM-3/CX;  
 RX MEDLINE=99000809; PubMed=9784136;  
 RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,  
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,  
 RA Davis R.W.;  
 RT "Genome sequence of an obligate intracellular pathogen of humans:  
 RT Chlamydia trachomatis";  
 RL Science 282:754-759(1998).  
 CC -1- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITIONS 38, 39 AND 40 IN  
 CC THE ANTICODON STEM AND LOOP OF TRANSFER RNAs (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine

CC 5'-phosphate + H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE TRUA FAMILY OF PSEUDOURIDINE SYNTHASES.  
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 CC -----  
 CC EMBL: AE001320; AAC68063.1;  
 DR InterPro: IPR001406; Pseudou\_synth\_1.  
 DR Pfam: PF01416; Pseudou\_synth\_1.  
 DR TIGRfams: TIGR00071; hist\_trua; 1.  
 KW Lyase; trna processing; Complete proteome.  
 FT ACT\_SITE 53 BY SIMILARITY.  
 SQ SEQUENCE 267 AA; 30427 MW; 917EX49E394B3CB3 CRC64;  
 Query Match 36.8%; Score 46; DB 1; Length 267;  
 Best Local Similarity 42.9%; Pred. No. 20;  
 Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 LDTWKEQKGGCGGAPPKDL 21  
 DB 221 LDMLATRRKGGPSPAPPYGL 241  
 RESULT 10  
 HB2X\_HUMAN STANDARD: PRT; 268 AA.  
 ID HB2X\_HUMAN  
 AC P05538;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE HLA class II histocompatibility antigen, DR beta chain precursor.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=87250501; PubMed=3036828;  
 RA Jonsson A.K., Hyldig-Nielsen J.J., Serenius B., Larhammar D.,  
 RA Andersson G., Joergensen F., Peterson P.A., Rask L.;  
 RT "Class II genes of the human major histocompatibility complex.  
 RT Comparisons of the DQ and DX alpha and beta genes";  
 RL J. Biol. Chem. 262:8767-8777(1987).  
 GN [2]  
 OS SEQUENCE OF 38-125 FROM N.A.  
 CC MEDLINE=85216510; PubMed=3858830;  
 RA Okada K., Boss J.M., Prentice H., Spies T., Mengler R., Auffray C.,  
 RA Lillie J.W., Grossberger D., Strominger J.L.;  
 RT "Gene organization of DC and DX subregions of the human major  
 RT histocompatibility complex";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3410-3414(1985).  
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 CC -----  
 CC EMBL: M29614; -; NOT ANNOTATED CDS.  
 DR EMBL: M29615; -; NOT ANNOTATED CDS.  
 DR EMBL: M11136; -; NOT ANNOTATED CDS.  
 DR PIR: D29312; D29312.  
 DR HSSP: P13760; 2SER.  
 DR Genew: HGNC:4945; HLA-DQB2.  
 DR InterPro: IPR003006; I9\_MHC.  
 DR InterPro: IPR003597; I9\_c1.



DR InterPro: IPR000353; MHC\_II\_beta.  
 DR Pfam: PF00047; Ig\_1.  
 DR Pfam: PF00969; MHC\_II\_beta; 1.  
 DR ProDom: PD000328; MHC\_II\_beta; 1.  
 DR SMART: SM00407; IgC1; 1.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 DR MHC II; Transmembrane; Glycoprotein; Signal.  
 KW MHC II; 32  
 FT SIGNAL 1  
 FT CHAIN 33 268  
 FT DOMAIN 33 126  
 FT DOMAIN 127 229  
 FT TRANSMEM 230 250  
 FT DOMAIN 251 268  
 FT DOMAIN 47 110  
 FT DISULFID 148 204  
 FT CARBOHYD 51 51  
 SO SEQUENCE 268 AA; 30386 MW; 2746ED6CC5D44AE2 CRC64;

Query Match 36.8%; Score 46; DB 1; Length 268;  
 Best Local Similarity 34.8%; Pred. No. 20;  
 Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 1 LDTWKEQKGGKGGAPGPKDLMY 23  
 DB 246 LGLIRHNGOKRGRPPAGLH 268

## RESULT 11

ACOC\_BACSU STANDARD; PRT; 398 AA.  
 AC 031550;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dihydroilpoamide acetyltransferase component of acetoin cleaving  
 DE system (EC 2.3.1.12) (Acetoin dehydrogenase E2 component).  
 GN ACOC.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 ON NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AC327;  
 RC MEDLINE=97124190; PubMed=8969503;  
 RA Yamamoto H., Uchiyama S., Sekiguchi J.;  
 RT Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76  
 RT degrees region of the Bacillus subtilis chromosome containing genes  
 RT for trehalose metabolism and acetoin utilization.";  
 RL Microbiology 142:3057-3065(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RC MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Carter N.M.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano N.J., Daniel R.A.,  
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Emmerson P.T.,  
 RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,  
 RA Enlian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galletton N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly J., Grandi G.,  
 RA Giuseppe G., Guy B.J., Haga K., Hatesch J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Ilaya M., Jones L.,  
 RA Joris B., Katamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Konungstein G., Krogh S., Kumano M.,  
 RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel S.C., Medigue C.,  
 RA Medina N., Melhado R.P., Mizuno M., Mostl D., Nakai S., Nodack M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Pujic P., Putnelle B., Rapoport G., Rey M., Reynolds S.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takachi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
 RA Totsu Y., Uchiyama S., Vandenbol M., Vannier F., Vassatoli A.,  
 RA Viart A., Wambut R., Medler E., Yamane K., Yasumoto K., Yata K.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yoshikawa H., Danchin A.,  
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,  
 RA "The complete genome sequence of the Gram-positive bacterium Bacillus  
 RT subtilis.";  
 RT Nature 390:249-256(1997).  
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + dihydroilpoamide = CoA + S-  
 CC -1- acetyl-dihydroilpoamide  
 CC -1- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL  
 CC -1- COFACTOR (PROBABLY).  
 CC -1- PATHWAY: Acetoin catabolism.  
 CC -1- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.  
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 CC -----

CC EMBL: D78509; BAA24294.1; -;  
 CC EMBL: Z99108; CAB12637.1; -;  
 CC HSSP: P07016; 1BBL.  
 CC Subtilist; BG12560; acoc.  
 CC InterPro: IPR001078; 2oxoacid.dh.  
 CC InterPro: IPR000089; Biotin\_lipoyl.  
 CC InterPro: IPR004167; E3 binding.  
 CC InterPro: IPR003016; lipoyl.  
 CC InterPro: IPR00198; 2-oxoacid.dh; 1.  
 CC Pfam: PF00198; 2-oxoacid.dh; 1.  
 CC Pfam: PF02817; e3-binding; 1.  
 CC Pfam: PF00364; biotin\_lipoyl; 1.  
 CC ProDom: PD001115; 2oxoacid.dh; 1.  
 CC PROSITE: PS00189; LIPOYL; FALSE-NEG.  
 CC TRANSFERASE; Acyltransferase; Lipoyl; Complete proteome.  
 KW DOMAIN 1 76  
 FT BINDING 43 43  
 FT ACT\_SITE 371 371  
 FT ACT\_SITE 375 375  
 FT ACT\_SITE 375 375  
 SO SEQUENCE 398 AA; 42885 MW; 559564C27C1C64F6 CRC64;

Query Match 36.8%; Score 46; DB 1; Length 398;  
 Best Local Similarity 56.2%; Pred. No. 29;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 5 VKEQKGGKGGAPGPKD 20  
 DB 134 LKOLKGTGCGRIVKD 149

## RESULT 12

VIAR\_MOUSE STANDARD; PRT; 423 AA.  
 ID VIAR\_MOUSE  
 AC 062463; 062464; 090YH2;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Vasopressin Via receptor (VIAR) (Vascular/hepatic-type arginine  
 DE vasopressin receptor) (Antidiuretic hormone receptor 1a) (AVPR 1la).  
 GN AVPR1A.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Onodera Y., Maekawa K., Arai Y.;  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Svt;  
 RX MEDLINE=20132529; PubMed=10669045;  
 RA Kikuchi S., Tanoue A., Goda N., Matsuo N., Teujimoto G.;  
 RT Structure and sequence of the mouse V1a and V1b vasopressin receptor  
 genes.";  
 RL Jpn. J. Pharmacol. 81:388-392(1999).  
 CC -1- FUNCTION: RECEPTOR FOR ARGININE VASOPRESSIN. THE ACTIVITY OF THIS  
 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A PHOSPHATIDYL-  
 INOSITOL-CALCIUM SECOND MESSENGER SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC  
 DR EMBL: D49729; BAA08566.1; -;  
 DR EMBL: D49730; BAA08567.1; -;  
 DR EMBL: AB030013; BAA89050.1; -;  
 DR MGD: MGI:1859216; Avpr1a.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm1; 1.  
 DR PRINTS: PR00237; GPCR\_Rhodopsn.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 52  
 FT TRANSSEM 53 76  
 FT DOMAIN 77 88  
 FT TRANSSEM 89 110  
 FT DOMAIN 111 125  
 FT TRANSSEM 126 147  
 FT DOMAIN 148 168  
 FT TRANSSEM 169 190  
 FT DOMAIN 191 220  
 FT TRANSSEM 221 241  
 FT DOMAIN 242 298  
 FT TRANSSEM 299 318  
 FT DOMAIN 319 335  
 FT TRANSSEM 337 356  
 FT DOMAIN 357 423  
 FT CARBOHYD 27 27  
 FT CARBOHYD 198 198  
 FT DISULFID 124 205  
 FT VARIANT 41 42  
 FT VARIANT 55 55  
 SQ SEQUENCE 423 AA; 47181 MW; C75AF1D0A0820C6 CRC64;  
 Query Match 36.8%; Score 46; DB 1; Length 423;  
 Best Local Similarity 50.0%; Pred. No. 31;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 Oy 6 KEQKRGKPGAPPKDL 21  
 Db 30 REAAGIGEGSGPGDV 45  
 RESULT 13  
 ID PURL\_PYRAE STANDARD; PRT; 697 AA.  
 AC 08237;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Phosphoribosylformylglycinamide synthase II (EC 6.3.5.3) (FGAM

DE synthase II).  
 GN PURL OR PAE0225.  
 OS Pyrobaculum aerophilum.  
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
 OC Thermoproteaceae; Pyrobaculum.  
 OX NCBI\_TaxID=13773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;  
 RX PubMed=11792869;  
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stettler K.O., Simon M.I.,  
 RT Miller J.H.;  
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum  
 aerophilum".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).  
 CC -1- CATALYTIC ACTIVITY: ATP + 5'-phosphoribosylformylglycinamide + L-  
 glutamine + H(2)O = ADP + phosphate + 5'-glutamate.  
 CC -1- PHOSPHORYLFORMYLGLYCINAMIDE + L-GLUTAMATE.  
 CC -1- PATHWAY: De novo purine biosynthesis; fourth step.  
 CC -1- SUBUNIT: Heterodimer of two subunits, purQ and purL.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE FGAMS FAMILY.  
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 CC  
 DR EMBL: AE00957; AAU62642.1; -;  
 DR InterPro: IPR00728; AIRS-related.  
 DR Pfam: PF00586; AIRS; 2.  
 DR Pfam: PF02769; AIRS\_C; 2.  
 KW Purine biosynthesis; Ligase; ATP-binding; Complete proteome.  
 FT NP\_BIND 91 102  
 SQ SEQUENCE 697 AA; 74373 MW; 94219332A19B8558 CRC64;  
 Query Match 36.8%; Score 46; DB 1; Length 697;  
 Best Local Similarity 50.0%; Pred. No. 51;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 Oy 5 VKRQKRGKPGAPPKLM 22  
 Db 173 IVEKDGVPKGAEPGLI 190  
 RESULT 14  
 ID GUNL\_HUMIN STANDARD; PRT; 402 AA.  
 AC P56680;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Endoglucanase I (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase).  
 GN Cel7B.  
 OS Humicola insolens.  
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.  
 OX NCBI\_TaxID=34413;  
 RN [1]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT S37W/P39W.  
 RX MEDLINE=97475713; PubMed=9335168;  
 RA Davies G.J., Ducros V., Lewis R.J., Borchert T.V., Schlein M.;  
 RT "Oligosaccharide specificity of a family 7 endoglucanase: Insertion  
 of potential sugar-binding subsites.";  
 RL J. Biotechnol. 57:91-100(1997).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MUTAGENESIS.  
 RX MEDLINE=98437137; PubMed=9761741;  
 RA Mackenzie L.F., Sulzenbacher G., Divine C., Jones T.A., Woeldike H.F.,  
 RT Schuelein M., Withers S.G., Davies G.J.;  
 RT "Crystal structure of the family 7 endoglucanase I (Cel7B) from

```

RT Humicola insolens at 2.2 A resolution and identification of the
RT catalytic nucleophile by trapping of the covalent glycosyl-enzyme
intermediate."
RL Biochem. J. 335:409-416(1998).
CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
CC (1) EXOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
CC (2) EXOCELLULOHYDROLASES THAT CUT THE DISACCHARIDE CELLULOSE
CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLULOSE AND OTHER
CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY C (FAMILY 7 OF GLYCOSYL
CC HYDROLASES).
DR PDB: 1A39; 02-MAR-99.
DR PDB: 2A39; 16-FEB-99.
DR InterPro: IPR001722; GH_7.
DR Pfam: PF00840; Glyco_hydro_7. 1.
DR ProDom: PD186135; GH_7; 1.
DR Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein;
KW 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 197 197 NUCLEOPHILE.
FT ACT_SITE 202 202 PROTON DONOR.
FT DISULFID 18 24
FT DISULFID 51 73
FT DISULFID 63 69
FT DISULFID 140 365
FT DISULFID 172 195
FT DISULFID 176 194
FT DISULFID 215 234
FT DISULFID 223 228
FT DISULFID 239 315
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 402 AA; 44577 MW; E0C6D31375D1635F CRC64;

Query Match 36.4%; Score 45.5; DB 1; Length 402;
Best Local Similarity 36.7%; Pred. No. 35;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKQKGGKPGGA-----PPKDL 21
   |||::: :|||::: |||:::
DB 33 LDSLSHPIHRAEGLGPGCGDMGNPPKDV 62

RESULT 15
LSM4_MOUSE
ID LSM4_MOUSE STANDARD: PRT; 137 AA.
AC O90XA5:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE U6 snRNA-associated Sm-like protein Lsm4.
GN LSM4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20094984; PubMed=10629062;
RA Hirsch E., Ohashi T., Ahmad M., Stamm S., Faessler R.;
RT Peri-implantation lethality in mice lacking the Sm motif-containing
RT protein Lsm4."
RL Mol. Cell. Biol. 20:1055-1062(2000).
CC -1- FUNCTION: BINDS SPECIFICALLY TO THE 3'-TERMINAL U-TRACT OF U6
CC snRNA (BY SIMILARITY).
CC -1- SUBUNIT: LSM SUBUNITS FORM A HETEROMER WITH A DOUGNOT SHAPE.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).

```

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CC -1- SIMILARITY: BELONGS TO THE SNRNP SM PROTEINS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ249439; CAB65729.1; -.
DR HSSP: P43331; ID3B.
DR MCD: MGI:1354692; Lsm4.
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam: PF01423; Sm; 1.
DR Nucleolar protein; Ribonucleoprotein; mRNA splicing; mRNA processing;
KW RNA-binding.
SQ SEQUENCE 137 AA; 15076 MW; A917E16E61467940 CRC64;

Query Match 36.0%; Score 45; DB 1; Length 137;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KEQKGGKPGGA 16
   |||::: |||
DB 95 KQKGRGKGGA 105

Search completed: April 11, 2003, 16:11:50
Job time : 2.5174 secs

```



GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:53 ; Search time 2.47635 Seconds  
(without alignments)  
892.885 Million cell updates/sec

Title: US-09-821-726A-2

Perfect score: 125  
Sequence: 1 LDTMKRQKKGKGGAPKDLMY 23

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR73:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	59	47.2	1677	2	T14267	Xin protein, stage
2	51	40.8	153	2	B71226	hypothetical prote
3	51	40.8	298	2	A49630	ubiquitin conjugat
4	51	40.8	378	2	A25399	homeotic protein A
5	50	40.0	269	2	I54432	MHC class II histo
6	49	39.2	142	2	D32880	hypothetical prote
7	49	39.2	266	2	B84351	pseudouridylylate sy
8	49	39.2	331	2	T50596	T-cell acute lymph
9	48	38.4	218	2	T51887	probable oxidoredu
10	47	37.6	233	1	HLRTAB	hypothetical prote
11	47	37.6	263	1	HLRTAB	R11 class II histo
12	47	37.6	298	2	T42070	class II histocomp
13	47	37.6	739	2	T49456	protein serine/thr
14	47	37.6	4936	2	A42515	hypothetical prote
15	46	37.2	1240	2	T30834	hypothetical prote
16	46	36.8	267	2	D81659	nuclear protein SA
17	46	36.8	267	2	C71511	tRNA pseudouridine
18	46	36.8	268	2	D29312	probable pseudouri
19	46	36.8	268	2	T29525	MHC class II histo
20	46	36.8	315	2	F69581	hypothetical prote
21	46	36.8	511	2	S24345	acetoin dehydrogen
22	46	36.8	709	2	T34706	Balbani ring 1 pr
23	46	36.8	886	2	S07132	fatty acid oxidati
24	46	36.8	886	2	T48818	hypothetical prote
25	46	36.8	2022	2	T03455	glucan 1,4-alpha-g
26	46	36.8	4957	2	T03455	ALR protein - huma
27	46	36.8	5262	2	T03454	ALR protein - huma
28	45.5	36.4	376	2	A12339	dihydroxylate oxi
29	45.5	36.4	579	2	D72092	conserved hypothet

30	45.5	36.4	579	2	C86532	CT082 hypothetical
31	45	36.0	160	1	S05340	plastoquinol-plast
32	45	36.0	233	2	I59495	major histocompati
33	45	36.0	238	2	A53278	MHC class II histo
34	45	36.0	263	1	HLMSBK	MHC class II histo
35	45	36.0	263	1	HLMSBU	MHC class II histo
36	45	36.0	263	1	HLMSBS	MHC class II histo
37	45	36.0	263	2	A61389	MHC class II histo
38	45	36.0	263	2	A25911	MHC class II histo
39	45	36.0	265	1	HLMSAB	MHC class II histo
40	45	36.0	265	1	HLMSQB	MHC class II histo
41	45	36.0	265	2	I48656	histocompatibility
42	45	36.0	302	2	A31921	collagen dpy-13 pr
43	45	36.0	394	2	S26492	homeotic protein A
44	45	36.0	472	2	T03169	probable glycoprot
45	45	36.0	596	2	T52331	pectinesterase (EC

## ALIGNMENTS

RESULT 1  
T14267  
Xin protein, stage early embryo - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: T14267  
R:Wang, D.Z.; Lin, J.J.C.  
Submitted to the EMBL Data Library, March 1998  
A:Description: Involvement of a novel gene, Xin, in cardiac looping.  
A:Reference number: Z17948  
A:Accession: T14267  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1677 <MAN>  
A:Cross-references: EMBL:AF051945; NID:q2970645; PID:q2970646; PIDN:AAC06023.1  
A:Experimental source: cardiac muscle; stage early embryo

Query Match  
Best Local Similarity 47.2%; Score 59; DB 2; Length 1677;  
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 6 KEOKGKGGAPK 19  
DB 571 EBERKGGPPPE 584

RESULT 2  
B71226  
hypothetical protein PH0068 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000  
C:Accession: B71226  
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Ogu  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A:Reference number: A71000; MUID:98344137; PMID:9679194  
A:Accession: B71226  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-153 <KAW>  
A:Cross-references: GB:AP000001; NID:q3236128; PIDN:BAA29137.1; PID:q3256454  
A:Experimental source: strain OT3  
A:Note: this accession replaces an interim accession for a sequence replaced by Genba  
C:Genetics:  
A:Gene: PH0068  
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0068  
Query Match  
Best Local Similarity 40.8%; Score 51; DB 2; Length 153;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LDTWKEQKGGPGG 15  
 Db 121 LDTIIEEEMKGVGG 135

## RESULT 3

ubiquitin conjugating enzyme - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 05-Nov-1999  
 C:Accession: A49630  
 R:Plon, S.E.; Lepply, K.A.; Do, H.N.; Groudine, M.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 10484-10488, 1993  
 A:Title: Cloning of the human homolog of the CDC34 cell cycle gene by complementation in  
 A:Reference number: A49630; MUID:94068425; PMID:8248134  
 A:Accession: A49630  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Cross-references: GB:L22005; NID:9388308; PIDN:AA037534.1; PID:9388309  
 C:Superfamily: human ubiquitin-protein ligase E2

Query Match 40.8%; Score 51; DB 2; Length 298;  
 Best Local Similarity 61.5%; Pred. No. 12;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 6 KEQKGGPGGAP 18  
 Db 21 EEAGGGGSGSP 33

## RESULT 4

homeotic protein Antennapedia - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 09-Jun-2000  
 C:Accession: A23450; A25400; A25399; A03318; C24780; S02593  
 R:Schmueder, S.; Kuroiwa, A.; Baumgartner, P.; Gehring, W.J.  
 EMBO J. 5, 733-739, 1986  
 A:Title: Structural organization and sequence of the homeotic gene Antennapedia of Drosophila  
 A:Reference number: A23450; MUID:99334708; PMID:10408949  
 A:Accession: A23450  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-378 <SCB>  
 A:Cross-references: GB:X03790; NID:97593; PIDN:CAA27417.1; PID:9293776; PID:91805742  
 R:Laughon, A.; Boulet, A.M.; Bermingham Jr., J.R.; Laymon, R.A.; Scott, M.P.  
 Mol. Cell. Biol. 6, 4676-4689, 1986  
 A:Title: Structure of transcripts from the homeotic antennapedia gene of Drosophila melanogaster  
 A:Reference number: A25400; MUID:87089829; PMID:2879223  
 A:Accession: A25400  
 A:Molecule type: DNA  
 A:Residues: 1-378 <LAU>  
 A:Cross-references: GB:M4496; GB:K01950; NID:9156945; PIDN:AAA28376.1; PID:9156947  
 R:Strother, V.L.; Jorgensen, E.M.; Garber, R.L.  
 Mol. Cell. Biol. 6, 4667-4675, 1986  
 A:Title: Multiple transcripts from the antennapedia gene of Drosophila melanogaster.  
 A:Accession: A25399; MUID:87089828; PMID:2879222  
 A:Accession: A25399  
 A:Molecule type: mRNA  
 A:Residues: 1-378 <STR>  
 A:Cross-references: GB:M20704; GB:M4699; GB:M4701; NID:9156948; PIDN:AAA70214.1; PID:9156949  
 R:McGinnis, W.; Garber, R.L.; Wirtz, J.; Kuroiwa, A.; Gehring, W.J.  
 Cell 37, 403-408, 1984  
 A:Title: A homologous protein-coding sequence in Drosophila homeotic genes and its conse  
 A:Reference number: A90847; MUID:84205674; PMID:6327065  
 A:Accession: A03318  
 A:Molecule type: DNA  
 A:Residues: 296-362, 'D' <MCG>  
 A:Cross-references: GB:K01948; NID:9156931; PIDN:AAA28373.1; PID:9156934  
 R:Regulski, M.; Harding, K.; Kostriken, R.; Karch, F.; Levine, M.; McGinnis, W.  
 Cell 43, 71-80, 1985  
 A:Title: Homeo box genes of the Antennapedia and Bithorax complexes of Drosophila.

A:Reference number: A90874; MUID:86079516; PMID:2416463  
 A:Accession: C24780

A:Molecule type: DNA  
 A:Residues: 297-299, 'E', 301-357 <REG>  
 A:Cross-references: GB:M12009; NID:9156939; PIDN:AAA72241.1; PID:9156940  
 R:Bermingham Jr., J.R.; Scott, M.P.  
 EMBO J. 7, 3211-3222, 1988  
 A:Title: Developmentally regulated alternative splicing of transcripts from the Drosophila

A:Reference number: S02593; MUID:89030617; PMID:2903048  
 A:Contents: annotation; alternative splicing  
 C:Comment: This homeotic protein controls development of cells in the mesothorax segm  
 C:Genetics:  
 A:Gene: FlyBase:Antp  
 A:Cross-references: FlyBase:Fgn0000095  
 A:Map position: 3A47.8; 84B1-2  
 A:Introns: 207/3; 220/3; 296/1  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regul  
 F:298-354/Domain: homeobox homology <HGX>

Query Match 40.8%; Score 51; DB 2; Length 378;  
 Best Local Similarity 45.0%; Pred. No. 15;  
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 Qy 4 MYEQKGGPGGAPKDLWY 23  
 Db 230 MYQOQSGVPVCGAPQGMH 249

## RESULT 5

MHC class II histocompatibility antigen DQ $\beta$ -beta chain precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 05-May-2000  
 C:Accession: I54432; I67725; I68723; I59623  
 R:Tsukamoto, K.; Yasunami, M.; Kimura, A.; Inoko, H.; Ando, A.; Hirose, T.; Inayama, A.  
 Immunogenetics 25, 343-346, 1987  
 A:Title: DQ $\beta$  beta gene from HLA-DR2-DW12 consists of six exons and expresses multiple  
 A:Reference number: I54432; MUID:87192945; PMID:3494674  
 A:Accession: I54432  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-269 <TSU>  
 A:Cross-references: GB:M6276; NID:9188397; PIDN:AAA59823.1; PID:9307272  
 R:Fukunaka Igaku Zaishi 79, 153-167, 1988  
 A:Title: Structural analysis of human major histocompatibility complex class II gene  
 A:Reference number: I53630; MUID:88226367; PMID:3371836  
 A:Accession: I67725  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 6-269 <FKU>  
 A:Cross-references: GB:M57649; NID:9187852; PIDN:AAA63217.1; PID:9187853  
 R:Lee, B.S.; Bell, J.I.; Rust, N.A.; McDevitt, H.O.  
 Immunogenetics 26, 85-91, 1987  
 A:Title: Structural and functional variability among DQ beta alleles of DR2 subtypes.  
 A:Reference number: I54440; MUID:87278366; PMID:2886427  
 A:Accession: I68723  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 33-83, 'P', 85-122 <LEE>  
 A:Cross-references: GB:M17204; NID:9187906; PIDN:AAA59698.1; PID:9187907  
 R:Singal, D.P.; Qiu, X.; Sood, S.K.  
 Tissue Antigens 40, 104-107, 1992  
 A:Title: Molecular analysis of novel HLA-DR2-DQ $\beta$  haplotypes in Asian Indians.  
 A:Reference number: I59623; MUID:93031783; PMID:1412415  
 A:Accession: I59623  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 45-83, 'P', 85-112 <SIN>  
 A:Cross-references: GB:M6740; NID:9188221; PIDN:AAA5778.1; PID:9188222

C:Genetics:  
A:Gene: GDB:HLA-DQB1; HLA-DW12  
A:Cross-references: GDB:120517; OMIM:142857  
A:Map position: 6p21.3-6p21.3  
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology  
C:Keywords: glycoprotein  
F:142-207/Domain: immunoglobulin homology <IM>

Query Match 40.0%; Score 50; DB 2; Length 269;  
Best Local Similarity 34.8%; Pred. No. 15;  
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 LDTMVEKQKGGPGAPKDLMY 23  
DB 247 LGLLIKRSQKPGCPGAPGLIH 269

RESULT 6  
D32880  
hypothetical protein (puls 3' region) - Klebsiella pneumoniae (fragment)

C:Species: Klebsiella pneumoniae  
C:Date: 08-Dec-1989 #sequence\_revision 08-Dec-1989 #text\_change 30-Sep-1993  
C:Accession: D32880  
R:ID:Entrez: C.; Pugsley, A.P.  
J. Bacteriol. 171, 3673-3679, 1989  
A:Title: Klebsiella pneumoniae puls gene encodes an outer membrane lipoprotein required  
A:Reference number: A32880; MUID:89291709; PMID:2661532  
A:Accession: D32880  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-142 <DEN>  
A:Cross-references: GB:M29097  
C:Superfamily: penicillin-binding protein 1B

Query Match 39.2%; Score 49; DB 2; Length 142;  
Best Local Similarity 66.7%; Pred. No. 11;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 8 OKGKPGGAPPK 19  
DB 49 RKGGKGGKPPR 60

RESULT 7  
B84351  
pseudouridylate synthase I [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 24-May-2001  
C:Accession: B84351  
R:ID:W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Jasky, S.; Leihauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jaido  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li  
A:Title: Genome sequence of Halobacterium species NRC-1.  
A:Reference number: A84160; MUID:20504483; PMID:11016950  
A:Accession: B84351  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-266 <STO>  
A:Cross-references: GB:AE004437; NID:910581435; P1DN:AA620174.1; GSPDB:GN00138  
C:Genetics:  
A:Gene: trna  
C:Superfamily: trna-pseudouridine synthase I

Query Match 39.2%; Score 49; DB 2; Length 266;  
Best Local Similarity 40.0%; Pred. No. 20;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 LDTMVEKQKGGPGAPKDL 20  
DB 197 IDTVLGDPEVAGPDGVFPAD 216

RESULT 8  
A36358  
T-cell acute lymphocytic leukemia 1 protein - human

C:Species: Homo sapiens (man)  
C:Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 17-Nov-2000  
C:Accession: A36358; A34519; S55280; I38254; S12374  
R:Appl. P.D.; Begley, C.G.; Bettress, V.; Nussmeier, M.; Ezquerro, A.; Colligan, J.;  
Mol. Cell. Biol. 10, 6426-6435, 1990  
A:Title: The SCL gene is formed from a transcriptionally complex locus.  
A:Reference number: A36358; MUID:91061750; PMID:2247063  
A:Accession: A36358  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-331 <APL>  
A:Cross-references: GB:M61108; NID:9469058; P1DN:AAA36600.1; PID:9337970  
R:Appl. P.D.; Deming, S.M.; Haynes, B.F.; Waldmann, T.A.; Kirsch, I.R.  
Proc. Natl. Acad. Sci. U.S.A. 86, 10128-10132, 1989  
A:Title: The gene SCL is expressed during early hematopoiesis and encodes a different  
A:Reference number: A34519; MUID:90099309; PMID:2602361  
A:Accession: A34519  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 118-331 <BE>  
A:Cross-references: GB:M29038; NID:9337958; P1DN:AAA36588.1; PID:9337959  
R:Bernard, O.; Lecointe, N.; Jonveaux, P.; Souyfi, M.; Mauchauffe, M.; Berger, R.; La  
Oncogene 6, 1477-1488, 1991  
A:Title: Two site-specific deletions, and t(1;14) translocation restricted to human T-  
A:Reference number: S55280; MUID:91360285; PMID:1886719  
A:Accession: S55280  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-292, 294-331 <BE>  
A:Cross-references: EMBL:S53245; NID:9234755; P1DN:AB19683.1; PID:9234756  
R:Chen, Q.; Yang, C.Y.; Tsai, L.H.; Schneider, N.; Buchanan, G.; Carroll, A.;  
J. Exp. Med. 172, 1403-1408, 1990  
A:Title: Coding sequences of the tal-1 gene are disrupted by chromosome translocation  
A:Reference number: I38253; MUID:91037802; PMID:2230650  
A:Accession: I38254  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 106-148 <RES>  
A:Cross-references: EMBL:X58622; NID:936685; P1DN:CAA41477.1; PID:936686  
R:Chen, Q.; Cheng, J.T.; Tsai, L.H.; Schneider, N.; Buchanan, G.; Carroll, A.; Crist,  
EMBO J. 9, 415-424, 1990  
A:Title: The tal gene undergoes chromosome translocation in T cell leukemia and poten  
A:Reference number: S12374; MUID:90151616; PMID:2303035  
A:Accession: S12374  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: R.157-331 <CHE>  
A:Cross-references: EMBL:X51990  
C:Genetics:  
A:Gene: GDB:TAL1; SCL; TGL5  
A:Cross-references: GDB:I120759; OMIM:187040  
A:Map position: 1p32-1p32  
A:Introns: 180/73  
C:Superfamily: lyl-1 protein  
C:Keywords: DNA binding; transcription regulation

Query Match 39.2%; Score 49; DB 2; Length 331;  
Best Local Similarity 69.2%; Pred. No. 25;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 10 GKGPGGAPPKDL 22  
DB 269 GGGGCGAPPPDDL 281

RESULT 9  
J50596  
probable oxidoreductase [imported] - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor

Query Match	Score	DB	Length
Best Local Similarity	43.58	2	263
Matches	10; Conservative	27;	

QY	1	LPTMVEKQKGRGAPPKDLMY	23	Indels	Gaps
Db	93	LDLFFNNAGTFCGSGVPEEDLPY	115		

Query Match	37.6%	Score 47	DB 2	Length 218
Best local Similarity	66.7%	Pred. No. 31		
Matches	8	Conservative	1	Mismatches
			3	Indels
			0	Gaps
QY	6	KQCKGKGGPGAP	17	
	11	1111111		
DBb	9	KESPEKGGPGAP	20	

F:81-184/Domain: beta 2<RET>  
F:106-171/Domain: immunoglobulin homology<IM>  
F:195-217/Domain: transmembrane #status predicted<TM>  
F:216-233/Domain: intracellular #status predicted<IN>  
F:10-74,113-169/disulfide bonds: #status predicted<NB>  
F:14/Binding site: carboxylate #status predicted<NB>

Query Match	37.68;	Score 47;	DB 1;	Length 233;
Best Local Similarity	36.48;	Pred. No. 33;		
Matches	8;	Conservative		

QY	1	LDIMVKEOKGKPGCAPPKDLM	22
		:::: 111 11 1	
Db	211	LGLEFIRHKRQGRQSPRPAGLL	232

## RESULT 12

A;Residues: 1-263 <SYH>

C/superfamily: class II histocompatibility antigen; PID:CA339934.1; PID:g57153  
C/Keywords: glycoprotein, heterodimer; transmembrane protein  
F1-27//Domain: signal sequence #status predicted <STG>  
F1-28-263//Product: class II histocompatibility antigen RT1-B-1 beta chain #status pred  
F1-28-120//Domain: extracellular #status predicted <EXT>  
F1-28-120//Domain: beta 1 <RFT1>

F:121-224/Domain:	beta_2<BERT2>
F:136-201/Domain:	immunoglobulin
F:225-245/Domain:	transmembrane
F:246-263/Domain:	intracellular
F:42-104,143-199/Dissulfide bonds:	#status predicted <TMM> #status predicted <INT>
F:46/Binding site:	carbohydrate (#status predicted)

	Score	DB 1	Length
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Best Local Similarity	47;	1;	263;
Matches	36.48;		
	Pred NO	37.	

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Db	241	LDGFIHNRKRGSRPPAGSL	262						

RESULT 1.3  
T42070

protein serine/threonine kinase - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision  
C:Accession: T42070  
R:Ogawara, H.  
submitted to the EMBL Data Library, August 1998  
A:Reference number: Z22055  
A:Accession: T42070  
A:Status: preliminary; translated from GR/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-598 <OGA>  
A:Cross-references: EMBL:AB016932; PDB:BAAB32455.1  
C:Genetics:  
C:Gene: pkan

Query Match	37.68;	Score 47;	DB 2;	Length 598;
Best Local Similarity	72.7%;	Pred. No. 85;		
Matches	8;	Conservative	1;	Mismatches
			2;	Indels
				0;
				Gaps
				0;



OY 10 GKGGGAPPKD 20  
 |||||: 1  
 Db 433 GKGGGVPAD 443

RESULT 14

T49456  
 hypothetical protein B14D6.80 [imported] - Neurospora crassa  
 C:Species: Neurospora crassa  
 C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
 C:Accession: T49456  
 R:Schulte, U.; Aign, V.; Hohnsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
 submitted to the Protein Sequence Database, May 2000  
 A:Reference number: Z25022  
 A:Accession: T49456  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-739 <SCH>  
 A:Cross-references: EMRL:A1356173; GSPDB:GN00116; NCSP:B14D6.80  
 A:Experimental source: BAC clone B14D6; strain OR74A  
 C:Genetics:  
 A:Gene: NCSP:B14D6.80  
 A:Map position: 6

Query Match 37.6%; Score 47; DB 2; Length 739;  
 Best Local Similarity 61.5%; Pred. No. 1e+02;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 OY 6 KEQKGGGAPPKD 18  
 :|||||: 1  
 Db 217 REQKGGGAPSTTP 229

RESULT 15

AH2515  
 hypothetical protein alr7304 [imported] - Nostoc sp. (strain PCC 7120) plasmid PCC7120a1  
 C:Species: Nostoc sp.  
 A:Mole: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
 C:Accession: AH2515  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi,  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AH2515  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-4936 <RUR>  
 A:Cross-references: GB:BA000020; PIDN:BA878388.1; PID:917135842; GSPDB:GN00180  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: alr7304  
 A:Genome: plasmid

Query Match 37.6%; Score 47; DB 2; Length 4936;  
 Best Local Similarity 40.0%; Pred. No. 6.9e+02;  
 Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 OY 1 LDTWVKEQKGGGAPPKD 20  
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 Db 2312 VDDGIEONGRPNPDPKD 2331

Search completed: April 11, 2003, 16:15:26  
 Job time : 4.47635 secs



Mon Apr 14 14:02:26 2003

us-09-821-726a-2.rapb

Page 1

GenCore version 5.1.4-P5-4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:11:18 : Search time 2.28874 Seconds  
(without alignments)  
614.367 Million cell updates/sec

Title: US-09-821-726a-2

Perfect score: 125  
Sequence: 1 LDTWKEQKGGKPGGAPPKDLMY 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
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pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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2	90	72.0	185	US-09-992-598-211	Sequence 211, App
3	90	72.0	185	US-09-989-293A-211	Sequence 211, App
4	90	72.0	185	US-09-989-735-211	Sequence 211, App
5	90	72.0	185	US-09-980-444-211	Sequence 211, App
6	90	72.0	185	US-10-001-054-14	Sequence 14, App
7	90	72.0	185	US-09-989-730-211	Sequence 211, App
8	90	72.0	185	US-09-990-436-211	Sequence 211, App
9	90	72.0	185	US-09-991-181-211	Sequence 211, App
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11	90	72.0	185	US-09-989-734-211	Sequence 211, App
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14	90	72.0	185	US-09-990-438-211	Sequence 211, App
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16	90	72.0	185	US-09-997-428-211	Sequence 211, App
17	90	72.0	185	US-09-997-666-211	Sequence 211, App
18	90	72.0	185	US-10-227-884-148	Sequence 148, App
19	90	72.0	185	US-09-990-711-211	Sequence 211, App

20	90	72.0	185	US-10-230-163-148	Sequence 148, App
21	90	72.0	185	US-09-989-726-211	Sequence 211, App
22	90	72.0	185	US-09-746-783-146	Sequence 146, App
23	90	72.0	185	US-09-930-437-211	Sequence 211, App
24	90	72.0	185	US-09-998-156-211	Sequence 211, App
25	90	72.0	185	US-10-218-631-148	Sequence 148, App
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28	90	72.0	185	US-09-991-172-211	Sequence 211, App
29	90	72.0	185	US-09-997-514-211	Sequence 105, App
30	90	72.0	185	US-09-997-573-211	Sequence 148, App
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34	90	72.0	185	US-09-990-726-211	Sequence 211, App
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43	90	72.0	185	US-09-989-723-211	Sequence 211, App
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# ALIGNMENTS

RESULT 1  
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Sequence 212, Application US/10050704  
Publication No. US20030050442A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
FILE REFERENCE: P2039P1  
TITLE OF INVENTION: 62 Human Secreted Proteins  
CURRENT APPLICATION NUMBER: US/10/050,704  
CURRENT FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: 09/684,524  
PRIOR FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: PCT/US00/08979  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/128,693  
PRIOR FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: 60/130,991  
PRIOR FILING DATE: 1999-04-26  
NUMBER OF SEQ ID NOS: 344  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 212  
LENGTH: 182  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-050-704-212  
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Db 97 LDTWKEQKKGKPGGAPPKDLMY 121  
RESULT 2  
US-09-992-598-211  
Sequence 211, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
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 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C20  
 CURRENT APPLICATION NUMBER: US/09/992,598  
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 PRIOR FILING DATE: 1997-06-16  
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Query Match 72.0%; Score 90; DB 9; Length 185;
Best Local Similarity 72.0%; Pred. No. 3; Mismatches 3; Indels 2; Gaps 1;
Matches 18; Conservative 2;

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QY 1 LDTWVKEOK--GKGGGAPKDLMT 23
11:11111111111111111111
DB 97 IDALVKEKKLOGKGGGPPKGLMT 121

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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
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 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 72.0% Score 90; DB 9; Length 185;  
 Best Local Similarity 72.0%; Pred. No. 3, 6e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVEQK--GKPGGAPPKDLMY 23  
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RESULT 4  
 US-09-989-735-211

; Sequence 211, Application US/09989735  
 ; Publication No. US20020193299A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Bolstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gottard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James

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us-09-821-726a-2.rapb

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhaog, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C61  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: US/09/989,735  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062250  
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Query Match 72.0%; Score 90; DB 9; Length 185;  
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Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVEKQ--GKPGGAPPKDLMY 23  
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RESULT 5

US-09-990-444-211  
 Sequence 211, Application US/09990444  
 Publication No. US20020193300A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Bolstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gunney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2730PIC19  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 72.0%; Score 90; DB 9; Length 185;  
Best Local Similarity 72.0%; Pred. No. 3; 6e-05;  
Matches 18; Conservative 3; Indels 2; Gaps 1;  
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DB 97 LDTWKEOKGKPGCAPPKDLMY 121

RESULT 6  
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Sequence 14, Application US/10001054  
Publication No. US20020192209A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Baker, Kevin  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin  
APPLICANT: Hebert, Carolyn  
APPLICANT: Henzler, William  
APPLICANT: Kabakoff, Rhona  
APPLICANT: Shelton, David  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
CELL GROWTH  
FILE REFERENCE: P3034R1PCT  
CURRENT FILING DATE: 2001-11-30  
PRIOR FILING DATE: 1997-09-17  
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PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02

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 PRIOR FILING DATE: 2001-07-09  
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 PRIOR FILING DATE: 2001-08-29  
 NUMBER OF SEQ ID NOS: 91  
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 LENGTH: 185  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-10-001-054-14

Query Match 72.0%; Score 90; DB 9; Length 185;  
 Best Local Similarity 72.0%; Pred. No. 3,6e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

OY 1 LDTWKEOK--GKGFGAPPKDLMY 23  
 DB 97 LDALVKEKKLOGKGGPPKGLMY 121

RESULT 7  
 US-09-989-730-211  
 Sequence 211, Application US/09989730  
 Publication No. US20020197674A1

GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Bostein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gottlieb, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C69  
 CURRENT APPLICATION NUMBER: US/09/989,730  
 PRIOR FILING DATE: 2001-11-20  
 PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match Best Local Similarity 72.0%; Score 90; DB 9; Length 185;  
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDVWKEOK--GKGGGAPPKDMY 23  
Db 97 LDALYKKEKLOGKGPPPKGLMY 121

RESULT 8  
US-09-990-436-211

;; Sequence 211, Application US/09990436  
;; Publication No. US20020198148A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gertlisen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Goddard, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kijavio, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zhenlin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C14  
;; CURRENT APPLICATION NUMBER: US/09/990.436  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
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;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07



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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match  
Best Local Similarity 72.0%; Score 90; DB 9; Length 185;  
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

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DB 97 LQALVKEKKLQCKGCGPPKGLMY 121

# RESULT 9

US-09-991-181-211  
Sequence 211, Application US/09991181  
Publication No. US20020197615A1  
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: F2730P1C53  
CURRENT APPLICATION NUMBER: US/09/991,181

PRIOR FILING DATE: 2001-11-16  
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 PRIOR FILING DATE: 1998-07-09

Query Match 72.0%; Score 90; DB 9; Length 185;  
 Best Local Similarity 72.0%; Pred. No. 3.6e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDMVKEOK--GKSGAPPKDLMY 23  
 Db 97 LDMVKEOKLQKSGKPGPKGLMY 121



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RESULT 11  
US-09-989-734-211  
Sequence 211, Application US/09989734  
Publication No. US2003000531A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desmoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivat J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC64  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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Query Match 72.08; Score 90; DB 9; Length 185;  
Best Local Similarity 72.08; Pred. No. 3.6e-05;  
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

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Db 97 LDALVKKKKLQGGKPGGPPPKGLMY 121

RESULT 12  
US-09-997-653-211

; Sequence 211, Application US/09997653  
; Publication No. US20030008297A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
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APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kjaavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC38  
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PRIOR FILING DATE: 1998-07-09

Query Match 72.08; Score 90; DB 9; Length 185;  
Best Local Similarity 72.08; Pred. No. 3 6e-05; 3; Indels 2; Gaps 1;  
Matches 18; Conservative

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DB 97 LDALVEKKLQCKGPGCPPKGLMY 121

RESULT 13  
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Sequence 211, Application US/09993667  
Publication No. US20030022187A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C4  
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 PRIOR FILING DATE: 1998-07-09

Query Match 72.0% Score 90: DB 9: Length 185:  
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 Publication No. US20030027985A1

GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerlitsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Matanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C18  
 CURRENT APPLICATION NUMBER: 2001-11-14  
 CURRENT FILING DATE: 2001-11-14  
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Query Match 72.0%; Score 90; DB 9; Length 185;

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Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

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Job time : 4.28874 secs



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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:08:13 ; Search time 2.32626 Seconds  
(Without alignments)  
290.907 Million cell updates/sec

Title: US-09-821-726A-2  
Perfect score: 125  
Sequence: 1 LDTMYKEOKGKPGCAPPKDLMY 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AI: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/Backfill1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	40.8	298	3	US-08-767-942A-25
2	51	40.8	298	4	US-09-177-165A-23
3	46	36.8	467	4	US-09-002-361-3
4	46	36.8	496	4	US-09-002-361-2
5	45.5	36.4	402	3	US-08-709-974A-1
6	45.5	36.4	402	3	US-08-709-974A-5
7	45.5	36.4	415	2	US-08-833-642A-5
8	45.5	36.4	415	3	US-08-709-974A-4
9	45.5	36.4	415	4	US-09-069-632-1
10	45.5	36.4	435	1	US-08-479-939-27
11	45.5	36.4	435	1	US-08-483-432-27
12	45.5	36.4	435	1	US-08-483-432-27
13	45.5	36.4	435	1	US-09-069-632-3
14	45.5	36.4	435	1	US-08-484-905-119
15	45.5	36.4	435	1	US-08-481-985B-119
16	45.5	36.4	435	1	US-08-370-476-119
17	45.5	36.4	435	1	US-08-207-481-39
18	45.5	36.4	435	1	PCT-US95-02689-41
19	45.5	36.4	435	1	US-08-890-865A-1
20	44.5	35.6	92	4	US-09-217-228-13
21	44.5	35.6	92	4	US-09-217-228-8
22	44.5	35.6	91	4	US-09-217-228-2
23	44.5	35.6	114	4	US-09-217-228-5
24	44.5	35.6	331	4	US-09-217-228-6
25	44.5	35.6	422	4	US-09-217-228-7
26	44.5	35.6	422	4	US-08-709-979A-3
27	44.5	35.6	9	2	US-08-460-890A-57

28	43	34.4	9	3	US-08-167-641C-57	Sequence 57, Appl
29	43	34.4	9	4	US-08-460-971A-57	Sequence 57, Appl
30	43	34.4	9	4	US-08-462-040-57	Sequence 26, Appl
31	43	34.4	321	3	US-08-362-670B-26	Sequence 26, Appl
32	43	34.4	321	3	US-08-333-576C-26	Sequence 26, Appl
33	43	34.4	321	5	US-08-808-324-26	Sequence 26, Appl
34	43	34.4	321	5	PCT-US94-14030A-26	Sequence 11, Appl
35	43	34.4	456	3	US-08-709-979A-11	Sequence 6, Appl
36	43	34.4	456	3	US-08-378-255-6	Sequence 4, Appl
37	43	34.4	880	4	US-09-141-212-2	Sequence 4, Appl
38	43	34.4	880	4	US-09-141-212-4	Sequence 4, Appl
39	43	34.4	880	4	US-09-552-351-4	Sequence 6, Appl
40	43	34.4	880	4	US-09-251-372-6	Sequence 2, Appl
41	43	34.4	880	4	US-09-561-138-2	Sequence 4, Appl
42	43	34.4	880	4	US-09-561-138-6	Sequence 6, Appl
43	43	34.4	880	4	US-09-715-336-6	Sequence 6, Appl
44	43	34.4	880	4	US-09-811-241-6	Sequence 6, Appl
45	43	34.4	880	4	US-09-811-241-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-08-767-942A-25  
Sequence 25, Application US/08767942A  
Patent No. 6068982

GENERAL INFORMATION:  
APPLICANT: Rolfe, Mark  
APPLICANT: Chiu, M. Isabel  
APPLICANT: Berlin, Vivian  
APPLICANT: Damaguer, Veronique  
APPLICANT: Draetta, Giulio  
APPLICANT: Guillaume, Cottarel  
TITLE OF INVENTION: UNDOUBTIN CONJUGATING ENZYMES  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/767,942A  
FILING DATE: 17-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-029, 04  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-1000

INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-767-942A-25

Query Match  
Best Local Similarity 61.5%  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 KEOKGKPGCAP 18  
DB 21 EEPAGGPGGSP 33



```

Patent No. 6117664
GENERAL INFORMATION:
APPLICANT: Sch Jain, Martin
APPLICANT: Rosholm, Peter
APPLICANT: Nielsen, Jack Bech
APPLICANT: Hansen, Svend Aage
APPLICANT: von der Osten, Claus
APPLICANT: NO. 6117664el Alkaline Cellulases
TITLE OF INVENTION: 11
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6117664 No. 6117664disk of No. 6117664th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,974A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta 35,127Y
REGISTRATION NUMBER: 4160.414-US
REFERENCE/DOCKET NUMBER: 4160.414-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-1

Query Match 36.4% Score 45.5; DB 3; Length 402;
Best Local Similarity 36.7%; Pred. No. 48;
Matches 11; Conservative 5; Mismatches 62

OY 1 1DTM---VKQKKGKPGGA-----PPKDL 21
11: : : 11111 11111
DB 33 LDLSHPHRAEGIDPGCGCDMGNPPKDV 62

RESULT 6
US-08-709-974A-5
Sequence 5, Application US/08709974A
GENERAL INFORMATION:
APPLICANT: Sch Jain, Martin
APPLICANT: Rosholm, Peter
APPLICANT: Nielsen, Jack Bech
APPLICANT: Hansen, Svend Aage
APPLICANT: von der Osten, Claus
APPLICANT: NO. 6117664el Alkaline Cellulases
TITLE OF INVENTION: 11
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6117664 No. 6117664disk of No. 6117664th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,974A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127Y
REFERENCE/DOCKET NUMBER: 4160.414-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-5

Query Match 36.4% Score 45.5; DB 3; Length 402;
Best Local Similarity 36.7%; Pred. No. 48;
Matches 11; Conservative 5; Mismatches 62

OY 1 1DTM---VKQKKGKPGGA-----PPKDL 21
11: : : 11111 11111
DB 33 LDLSHPHRAEGIDPGCGCDMGNPPKDV 62

RESULT 7
US-08-833-642A-5
Sequence 5, Application US/08833642A
GENERAL INFORMATION:
APPLICANT: Ivan M. A. J. Herbols et al.
TITLE OF INVENTION: Liquid Detergent Compositions
Containing Cellulase and Amine
TITLE OF INVENTION: 5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Jackline Ann Zurcher
STREET: 255 E. Fifth Street
STREET: 1900 Chemed Center
CITY: Cincinnati
STATE: Ohio
COUNTRY: USA
ZIP: 45202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,642A
FILING DATE: April 8, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Zurcher, J. A.
REGISTRATION NUMBER: P42,251
REFERENCE/DOCKET NUMBER: CM551C
TELEPHONE: (513) 977-8377
TELEFAX: (513) 977-8141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-642A-5

Query Match 36.4% Score 45.5; DB 2; Length 415;
Best Local Similarity 36.7%; Pred. No. 49;

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Page 4

Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;  
QY 1 LDTM---VKROKRGPGGA-----PPKDL 21  
Db 33 LDSLSPHRAEGLGPGCGGMGNPPKDV 62

RESULT 8  
US-08-709-974A-4  
Sequence 4, Application US/08709974A  
Patent No. 6117664  
GENERAL INFORMATION:  
APPLICANT: Sch lein, Martin  
APPLICANT: Rosholt, Peter  
APPLICANT: Nielsen, Jack Bech  
APPLICANT: Hansen, Svend Aage  
TITLE OF INVENTION: No. 6117664el Alkaline Cellulases  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESS: No. 6117664 No. 6117664disk of No. 6117664th America, Inc.  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,974A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valeta  
REGISTRATION NUMBER: 35,127Y  
TELECOMMUNICATION INFORMATION: 4160,414-US  
TELEPHONE: 212-867-0123  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 415 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-709-974A-4

Query Match  
Best Local Similarity 36.4%; Score 45.5; DB 3; Length 415;  
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;  
QY 1 LDTM---VKROKRGPGGA-----PPKDL 21  
Db 33 LDSLSPHRAEGLGPGCGGMGNPPKDV 62

RESULT 9  
US-09-069-632-1  
Sequence 1, Application US/09069632  
Patent No. 6261828  
GENERAL INFORMATION:  
APPLICANT: Lund, Henrik  
TITLE OF INVENTION: A Process For Combined Desizing  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESSES:  
ADDRESS: No. 62618280 No. 6261828disk of No. 6261828th America, Inc.  
CITY: New York

STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/069,632  
FILING DATE: 29-APR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK96/00469  
FILING DATE: 15-NOV-1996  
APPLICATION NUMBER: 1278/95  
FILING DATE: 15-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valeta  
REGISTRATION NUMBER: 35,127  
TELECOMMUNICATION INFORMATION: 4588,204-US  
TELEPHONE: 212-867-0123  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 415 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-069-632-1

Query Match  
Best Local Similarity 36.4%; Score 45.5; DB 4; Length 415;  
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;  
QY 1 LDTM---VKROKRGPGGA-----PPKDL 21  
Db 33 LDSLSPHRAEGLGPGCGGMGNPPKDV 62

RESULT 10  
US-08-361-920-27  
Sequence 27, Application US/08361920  
Patent No. 5457046  
GENERAL INFORMATION:  
APPLICANT: Woeldike, Heile F.  
APPLICANT: Hagen, Frederick  
APPLICANT: Hjort, Carsten M.  
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESSES:  
ADDRESS: No. 54570460 No. 5457046disk of No. 5457046th America, Inc.  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,920  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/940,860  
FILING DATE: 28-OCT-1992

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APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA: PCT/DK91/00124
APPLICATION NUMBER: 3435.204-US
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-361-920-27

Query Match      36.4%  Score 45.5;  DB 1;  Length 435;
Best Local Similarity 36.7%;  Pred. No. 52;
Matches 11;  Conservative 5;  Mismatches 5;  Indels 9;  Gaps 2;
OY      1  LDPM---VKQKGGKPGGA-----PPKDL 21
        11::  : 1 1111 1111:
Db      53  LDLSHPHRAEGLPGCGGDMGNPPKDV 82

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RESULT 11
US-08-479-939-27
Sequence 27, Application US/08479939
Patent No. 5686593
GENERAL INFORMATION:
APPLICANT: Woelldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hasstrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESS: No. 56865930 No. 5686593disk of No. 5686593th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-in Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/479,939
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US/08/361,920
FILING DATE: 22-DEC-1994
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA: PCT/DK91/00124
APPLICATION NUMBER:
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-432-27
Query Match      36.4%  Score 45.5;  DB 1;  Length 435;
Best Local Similarity 36.7%;  Pred. No. 52;
Matches 11;  Conservative 5;  Mismatches 5;  Indels 9;  Gaps 2;
OY      1  LDPM---VKQKGGKPGGA-----PPKDL 21
        11::  : 1 1111 1111:
Db      53  LDLSHPHRAEGLPGCGGDMGNPPKDV 82

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TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-939-27

Query Match      36.4%  Score 45.5;  DB 1;  Length 435;
Best Local Similarity 36.7%;  Pred. No. 52;
Matches 11;  Conservative 5;  Mismatches 5;  Indels 9;  Gaps 2;
OY      1  LDPM---VKQKGGKPGGA-----PPKDL 21
        11::  : 1 1111 1111:
Db      53  LDLSHPHRAEGLPGCGGDMGNPPKDV 82

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RESULT 12
US-08-483-432-27
Sequence 27, Application US/08483432
Patent No. 5763254
GENERAL INFORMATION:
APPLICANT: Woelldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hasstrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESS: No. 57632540 No. 5763254disk of No. 5763254th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-in Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/483,432
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA: PCT/DK91/00124
APPLICATION NUMBER:
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-432-27
Query Match      36.4%  Score 45.5;  DB 1;  Length 435;
Best Local Similarity 36.7%;  Pred. No. 52;
Matches 11;  Conservative 5;  Mismatches 5;  Indels 9;  Gaps 2;
OY      1  LDPM---VKQKGGKPGGA-----PPKDL 21
        11::  : 1 1111 1111:
Db      53  LDLSHPHRAEGLPGCGGDMGNPPKDV 82

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Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;  
QY 1 LDTM---VKRQKGGGGA-----PPKDL 21  
DB 53 LDTSLPHIRAEGLGPGCGDMGNPPKDV 82

## RESULT 13

US-09-069-632-3  
Sequence 3, Application US/09069632  
Patent No. 6261828  
GENERAL INFORMATION:  
APPLICANT: Lund, Henrik  
TITLE OF INVENTION: A Process For Combined Desizing  
NUMBER OF SEQUENCES: And Stone-Washing of Dyed Denim  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 62618280 No. 6261828disk of No. 6261828th America, Inc.  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/069,632  
FILING DATE: 29-APR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK96/00469  
FILING DATE: 15-NOV-1996  
APPLICATION NUMBER: 1278/95  
FILING DATE: 15-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valeta  
REGISTRATION NUMBER: 35,127  
REFERENCE/DOCKET NUMBER: 4588, 204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 435 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-069-632-3

## Query Match

Best Local Similarity 36.4%; Score 45.5; DB 4; Length 435;  
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKRQKGGGGA-----PPKDL 21  
DB 53 LDTSLPHIRAEGLGPGCGDMGNPPKDV 82

## RESULT 14

US-08-484-905-119  
Sequence 119, Application US/08484905  
Patent No. 5976551  
GENERAL INFORMATION:  
APPLICANT: Motiez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: An Altered Major Histocompatibility  
Complex(MHC) Determinant and Methods for Using the  
TITLE OF INVENTION: Determinant

## NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,905  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 03495, 0106-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 119:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-905-119

## Query Match

Best Local Similarity 36.0%; Score 45; DB 2; Length 265;  
Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 LDTMVKRQKGGGGA-----PPKDL 22  
DB 243 LGLFIRHSOKGPGPPAGL 264

## RESULT 15

US-08-481-985B-119  
Sequence 119, Application US/08481985B  
Patent No. 6011146  
GENERAL INFORMATION:  
APPLICANT: Motiez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: Altered Major Histocompatibility Complex  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,985B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/801,818  
 FILING DATE: 05-DEC-1991  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/792,473  
 FILING DATE: 15-NOV-1991  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03495.0106-04000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 119:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 265 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-481-985B-119

Query Match 36.0%; Score 45; DB 3; Length 265;  
 Best Local Similarity 36.4%; Pred. No. 36;  
 Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 LDTMVKEQKGGPGGAPPKDLM 22  
 Db 243 LGLFIRHRSSQKGGPGPPAGLL 264

Search completed: April 11, 2003, 16:16:33  
 Job time: 3.32626 secs





Mon Apr 14 14:02:38 2003

us-09-821-726a-3.ra1

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model  
Run on: April 11, 2003, 16:08:13 ; Search time 1.41599 Seconds  
(without alignments)  
290.907 Million cell updates/sec

Title: US-09-821-726A-3  
Perfect score: 81  
Sequence: 1 KXIOGKGGGPPK 14

Scoring table: BLAST62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues  
Total number of hits satisfying chosen parameters: 262574  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents-AA\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	61.7	673	4	US-09-078-347A-2
2	49	60.5	855	4	US-09-813-819-2
3	49	60.5	855	4	US-09-920-048-2
4	45	55.6	402	2	US-08-709-979A-3
5	45	55.6	402	3	US-08-709-974A-1
6	45	55.6	415	2	US-08-833-642A-5
7	45	55.6	415	3	US-08-709-974A-4
8	45	55.6	415	4	US-09-069-632-1
9	45	55.6	415	4	US-08-361-920-27
10	45	55.6	435	1	US-08-479-939-27
11	45	55.6	435	1	US-08-483-432-27
12	45	55.6	435	1	US-09-069-632-3
13	45	55.6	435	1	US-09-817-180-2
14	45	55.6	435	1	US-09-817-180-2
15	45	55.6	435	1	US-09-817-180-2
16	45	55.6	435	1	US-09-817-180-2
17	45	55.6	435	1	US-09-817-180-2
18	45	55.6	435	1	US-09-817-180-2
19	45	55.6	435	1	US-09-817-180-2
20	45	55.6	435	1	US-09-817-180-2
21	45	55.6	435	1	US-09-817-180-2
22	45	55.6	435	1	US-09-817-180-2
23	45	55.6	435	1	US-09-817-180-2
24	45	55.6	435	1	US-09-817-180-2
25	45	55.6	435	1	US-09-817-180-2
26	45	55.6	435	1	US-09-817-180-2
27	45	55.6	435	1	US-09-817-180-2

28	43	53.1	298	5	PCT-US95-02689-41	Sequence 41, Appl
29	43	53.1	311	2	US-08-318-837-9	Sequence 9, Appl
30	43	53.1	118	1	US-08-393-985-14	Sequence 25, Appl
31	42	51.9	298	3	US-08-767-942A-25	Sequence 23, Appl
32	42	51.9	298	4	US-09-177-165A-23	Sequence 26, Appl
33	42	51.9	494	4	US-09-126-420A-26	Sequence 9, Appl
34	41.5	51.2	1461	4	US-08-585-887-9	Sequence 9, Appl
35	41.5	51.2	1461	4	US-08-289-578-9	Sequence 19, Appl
36	41	50.6	107	3	US-08-478-097A-19	Sequence 11, Appl
37	41	50.6	124	4	US-08-455-559-11	Sequence 11, Appl
38	41	50.6	124	4	US-09-145-060-11	Sequence 11, Appl
39	41	50.6	147	5	PCT-US94-00657-11	Sequence 10, Appl
40	41	50.6	437	2	US-09-347-833-10	Sequence 8, Appl
41	41	50.6	629	3	US-08-935-450-8	Sequence 6, Appl
42	41	50.6	629	3	US-08-464-258B-6	Sequence 6, Appl
43	41	50.6	3025	6	5223423-3	Patent No. 5223423
44	40	49.4	112	2	US-08-301-915-3	Sequence 3, Appl
45	40	49.4	112	3	US-08-524-694A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-09-078-347A-2  
Sequence 2, Application US/09078347A  
Patent No. 6132968  
GENERAL INFORMATION:  
APPLICANT: Le, Xiao-Chun  
APPLICANT: Weinfield, Michael  
TITLE OF INVENTION: Methods for Quantitating Low Level  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESS: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/078,347A  
FILING DATE: 13-MAY-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Peter G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: UALB-03283  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 397-8338  
TELEFAX: (415) 705-8410  
INFORMATION FOR SPO. ID NO.: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-078-347A-2  
Query Match 61.7%; Score 50; DB 4; Length 673;  
Best Local Similarity 72.7%; Pred. No. 34;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 3 LOGKGGGPPK 13  
DB 313 LSGRGGGPPK 323



TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 402 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-709-974A-1

Query Match 55.6%; Score 45; DB 3; Length 402;  
Best Local Similarity 47.4%; Pred. No. 93;  
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 KLOGKPGG-----PPPK 14  
: : | | | | | | | | | |  
DB 42 RAEGIGPGCGDGNPPPK 60

RESULT 6  
US-08-709-974A-5  
; Sequence 5, Application US/08709974A  
; Patent No. 6117664  
; GENERAL INFORMATION:  
; APPLICANT: Sch Jain, Martin  
; APPLICANT: Rosholm, Peter  
; APPLICANT: Nielsen, Jack Bech  
; APPLICANT: Hansen, Svend Aage  
; APPLICANT: von der Osten/Claus  
; TITLE OF INVENTION: No. 6117664e1 Alkaline Cellulases  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/709,974A  
; FILING DATE: 09-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gregg, Valeta  
; REGISTRATION NUMBER: 35,127Y  
; REFERENCE/DOCKET NUMBER: 4160.414-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 402 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-709-974A-5

Query Match 55.6%; Score 45; DB 3; Length 402;  
Best Local Similarity 47.4%; Pred. No. 93;  
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 KLOGKPGG-----PPPK 14  
: : | | | | | | | | | |  
DB 42 RAEGIGPGCGDGNPPPK 60

RESULT 7

US-08-833-642A-5  
; Sequence 5, Application US/08833642A  
; Patent No. 5883066  
; GENERAL INFORMATION:  
; APPLICANT: Ivan M. A. J. Herbots et al.  
; TITLE OF INVENTION: Liquid Detergent Compositions  
; TITLE OF INVENTION: Containing Cellulase and Amine  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jackie Ann Zurcher  
; ADDRESSEE: Dinsmore & Shohl LLP  
; STREET: 255 E. Fifth Street  
; STREET: 1900 Chemed Center  
; CITY: Cincinnati  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 45202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/833,642A  
; FILING DATE: April 8, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zurcher, J. A.  
; REGISTRATION NUMBER: P42,251  
; REFERENCE/DOCKET NUMBER: CM551C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (513) 977-8377  
; TELEFAX: (513) 977-8141  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 415 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-833-642A-5

Query Match 55.6%; Score 45; DB 2; Length 415;  
Best Local Similarity 47.4%; Pred. No. 96;  
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 KLOGKPGG-----PPPK 14  
: : | | | | | | | | | |  
DB 42 RAEGIGPGCGDGNPPPK 60

RESULT 8  
US-08-709-974A-4  
; Sequence 4, Application US/08709974A  
; Patent No. 6117664  
; GENERAL INFORMATION:  
; APPLICANT: Sch Jain, Martin  
; APPLICANT: Rosholm, Peter  
; APPLICANT: Nielsen, Jack Bech  
; APPLICANT: Hansen, Svend Aage  
; APPLICANT: von der Osten/Claus  
; TITLE OF INVENTION: No. 6117664e1 Alkaline Cellulases  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,974A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valeta  
REGISTRATION NUMBER: 35,127Y  
REFERENCE/DOCKET NUMBER: 4160,414-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 415 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-709-974A-4

Query Match  
Best Local Similarity 55.6%; Score 45; DB 3; Length 415;  
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 KLOGKGPBG-----PPPK 14  
: : | | | | | | | | | |  
Db 42 RAEGLGPGCGCDMGNGNPPK 60

RESULT 9  
US-09-069-632-1  
Sequence 1, Application US/09069632  
Patent No. 6261828  
GENERAL INFORMATION:  
APPLICANT: Lund, Henrik  
TITLE OF INVENTION: A Process For Combined Desizing  
TITLE OF INVENTION: And Stone-Washing of Dyed Denim  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 62618280 No. 6261828disk of No. 6261828th America, Inc.  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/069,632  
FILING DATE: 29-APR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK96/00469  
FILING DATE: 15-NOV-1996  
APPLICATION NUMBER: 1278/95  
FILING DATE: 15-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valeta  
REGISTRATION NUMBER: 35,127  
REFERENCE/DOCKET NUMBER: 4588,204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 415 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-09-069-632-1

Query Match  
Best Local Similarity 55.6%; Score 45; DB 4; Length 415;  
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 KLOGKGPBG-----PPPK 14  
: : | | | | | | | | | |  
Db 42 RAEGLGPGCGCDMGNGNPPK 60

RESULT 10

US-08-361-920-27  
Sequence 27, Application US/08361920  
Patent No. 5457046

GENERAL INFORMATION:

APPLICANT: Woeldike, Helle F.

APPLICANT: Hagen, Frederick

APPLICANT: Hjort, Carsten M.

APPLICANT: Sven, Hasstrup

TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 54570460 No. 5457046disk of No. 5457046th America, Inc.

STREET: 405 Lexington Avenue, 62nd Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/361,920

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/940,860

FILING DATE: 28-OCT-1992

APPLICATION NUMBER: DK 1158/90

FILING DATE: 09-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK91/00124

FILING DATE: 08-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 3435,204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-867-0298

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 435 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-361-920-27

Query Match  
Best Local Similarity 55.6%; Score 45; DB 1; Length 435;  
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 KLOGKGPBG-----PPPK 14  
: : | | | | | | | | | |  
Db 62 RAEGLGPGCGCDMGNGNPPK 80

RESULT 11  
US-08-479-939-27

; Sequence 27, Application US/08479939  
; Patent No. 5686593  
; GENERAL INFORMATION:  
; APPLICANT: Woeldike, Helle F.  
; APPLICANT: Hagen, Frederick  
; APPLICANT: Hjort, Carsten M.  
; APPLICANT: Sven, Hasstrup  
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose  
; TITLE OF INVENTION: or Hemicellulose  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 56865930 No. 5686593disk of No. 5686593th America, Inc.  
; STREET: 405 Lexington Avenue, 62nd Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-6201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479, 939  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/361, 920  
; FILING DATE: 22-DEC-1994  
; APPLICATION NUMBER: US 07/940, 860  
; FILING DATE: 28-OCT-1992  
; APPLICATION NUMBER: DK 1158/90  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/DK91/00124  
; FILING DATE: 08-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lambiris, Elias J.  
; REGISTRATION NUMBER: 33,728  
; REFERENCE/DOCKET NUMBER: 3435,204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-867-0298  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 435 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-479-939-27

Query Match 55.6%; Score 45; DB 1; Length 435;  
Best Local Similarity 47.4%; Pred. No. 1e+02;  
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14  
; : : | | | | | | | | | |  
Db 62 RAEGLGPGCGGDMGNPPK 80

RESULT 12  
US-08-483-432-27  
; Sequence 27, Application US/08483432  
; Patent No. 5763254  
; GENERAL INFORMATION:  
; APPLICANT: Woeldike, Helle F.  
; APPLICANT: Hagen, Frederick  
; APPLICANT: Hjort, Carsten M.  
; APPLICANT: Sven, Hasstrup  
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose  
; TITLE OF INVENTION: or Hemicellulose  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 57632540 No. 5763254disk of No. 5763254th America, Inc.  
; STREET: 405 Lexington Avenue, 62nd Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-6201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,432  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/361, 920  
; FILING DATE:  
; APPLICATION NUMBER: US 07/940, 860  
; FILING DATE: 28-OCT-1992  
; APPLICATION NUMBER: DK 1158/90  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/DK91/00124  
; FILING DATE: 08-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lambiris, Elias J.  
; REGISTRATION NUMBER: 33,728  
; REFERENCE/DOCKET NUMBER: 3435,204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-867-0298  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 435 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-483-432-27

Query Match 55.6%; Score 45; DB 1; Length 435;  
Best Local Similarity 47.4%; Pred. No. 1e+02;  
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14  
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Db 62 RAEGLGPGCGGDMGNPPK 80

RESULT 13  
US-09-069-632-3  
; Sequence 3, Application US/09069632  
; Patent No. 6261828  
; GENERAL INFORMATION:  
; APPLICANT: Lund, Henrik  
; TITLE OF INVENTION: A Process For Combined Desizing  
; TITLE OF INVENTION: And Stone-Washing of Dyed Denim  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 62618280 No. 6261828disk of No. 6261828th America, Inc.  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/069, 632  
; FILING DATE: 29-APR-1998

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK96/00469
; FILING DATE: 15-NOV-1996
; APPLICATION NUMBER: 1278/95
; FILING DATE: 15-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Greg9, Valeta
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4588.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-069-632-3

Query Match          55.6%; Score 45; DB 4; Length 435;
Best Local Similarity 47.4%; Pred. No. 1e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY      2 KLQKGPGRGPP 14
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Db      62 RAEGLGPGCGCGDMGNPPK 80

RESULT 14
US-09-817-180-2
; Sequence 2, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Human
; US-09-817-180-2

Query Match          55.6%; Score 45; DB 4; Length 752;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 KLQKGPGRGPP 13
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Db      387 KLEHLGPGEPP 398

RESULT 15
US-09-817-180-4
; Sequence 4, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Human
; US-09-817-180-4

Query Match          55.6%; Score 45; DB 4; Length 822;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 KLQKGPGRGPP 13
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Db      387 KLEHLGPGEPP 398

Search completed: April 11, 2003, 16:16:35
Job time : 3.41599 secs
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(without alignments)  
614.367 Million cell updates/sec

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Perfect score:	81
Sequence:	1 KKLQKGKPGPPK 14

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Gapop 10.0 , Gapext 0.5

Searched: 248812  
bits satisfying chosen parameters: 248812

Minimum	DB seq	length:	0
Maximum	DB seq	length:	2000000000

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post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing First 45 summaries

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12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*

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## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	81	100.0	185	9	US-09-992-598-211	Sequence 211, App
3	81	100.0	185	9	US-09-989-293A-211	Sequence 211, App
4	81	100.0	185	9	US-09-989-735-211	Sequence 211, App
5	81	100.0	185	9	US-09-990-444-211	Sequence 211, App
6	81	100.0	185	9	US-10-001-050-14	Sequence 14, App
7	81	100.0	185	9	US-09-989-730-211	Sequence 211, App
8	81	100.0	185	9	US-09-990-436-211	Sequence 211, App
9	81	100.0	185	9	US-09-991-181-211	Sequence 211, App
10	81	100.0	185	9	US-09-993-687-211	Sequence 211, App
11	81	100.0	185	9	US-09-989-734-211	Sequence 211, App
12	81	100.0	185	9	US-09-997-653-211	Sequence 211, App
13	81	100.0	185	9	US-09-993-667-211	Sequence 211, App
14	81	100.0	185	9	US-09-990-438-211	Sequence 211, App
15	81	100.0	185	9	US-09-990-562-211	Sequence 211, App
16	81	100.0	185	9	US-09-997-468-211	Sequence 211, App
17	81	100.0	185	9	US-09-997-666-211	Sequence 148, App
18	81	100.0	185	9	US-10-227-864-148	Sequence 211, App
19	81	100.0	185	9	US-09-990-711-211	Sequence 211, App

[illegible]

## ALIGNMENTS

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RESULT 1
US-10-050-704-212
; Sequence 212, Application US/10050704
; Publication No. US20030050442A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: P2039P1
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 09/684,524
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: PCT/US00/08979
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,693
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/130,991
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 212
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens
US-10-050-704-212
Query Match
Best local Similarity 100.0%; Score 81; DB 9; Length 182;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 KRLGGKPGGPPK 14
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Db 104 KRLGGKPGGPPK 117

RESULT 2
US-09-992-598-211
; Sequence 211, Application US/09992598
; Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.

```

APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Baton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C20  
 CURRENT APPLICATION NUMBER: US/09/992,598  
 PRIOR FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787  
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Query Match          100.0%; Score 81; DB 9; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.001; 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY      1 KKLCKGCGGPPK 14
DB      104 KKLCKGCGGPPK 117

RESULT 3
US-09-989-293A-211
Sequence 211, Application US/09989293A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerbier, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C66
CURRENT FILING DATE: 2001-11-20
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 0.001;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KKLGGKGGGPPK 14  
 Db 104 KKLGGKGGGPPK 117

RESULT 4  
 US-09-989-735-211  
 Sequence 211, Application US/09989735  
 Publication No. US20020193299A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Baton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerlitsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C61  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;

Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLGGKGGGPPK 14  
 Db 104 KKLGGKGGGPPK 117

RESULT 5

US-09-990-444-211

Sequence 211, Application US/09990444

Publication No. US20020193300A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerltzen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C19  
 CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLGGKGGGPPK 14  
Db 104 KKLGGKGGGPPK 117

RESULT 6  
US-10-001-054-14  
Sequence 14, Application US/10001054  
Publication No. US20020192209A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Baker, Kevin  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin  
APPLICANT: Hebert, Carolyn  
APPLICANT: Henzel, William  
APPLICANT: Kabakoff, Rhona  
APPLICANT: Shelton, David  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
FILE REFERENCE: P3034R1PCT  
CURRENT APPLICATION NUMBER: US/10/001,054  
CURRENT FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 60/059114  
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 US-10-001-054-14

Query Match 100.0%; Score 81; DB 9; Length 185;  
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QY 1 KKLGGKGGGPPK 14  
 Db 104 KKLGGKGGGPPK 117

RESULT 7

US-09-989-730-211  
 ; Sequence 211, Application US/09989730  
 ; Publication No. US20020197674A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerlitsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730PIC69  
 ; CURRENT APPLICATION NUMBER: US/09/989,730  
 ; PRIOR FILING DATE: 2001-11-20  
 ; PRIOR APPLICATION NUMBER: 60/049787  
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 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;  
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 Db 104 KLOGKGPGGPPK 117

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 Publication No. US20020198148A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
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 APPLICANT: Goddard, Audrey  
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 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 0.001;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 KKLGGKGGGPPK 14  
 DB 104 KKLGGKGGGPPK 117

RESULT 9  
 US-09-991-181-211  
 Sequence 211, Application us/09991181  
 Publication No. US20020197615A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
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 APPLICANT: Gerber, Hanspeter  
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 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730PTC53  
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Best local similarity 100.0%; Pred. No. 0.001;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 104 KKGKGGGPPK 117  
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; Sequence 211, Application US/09993687  
; Publication No. US2002019814941  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey J.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paonli, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumasi, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C11  
; CURRENT APPLICATION NUMBER: US/09/993,687  
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Query Match 100.0%; Score 81; DB 9; Length 185;  
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 DB 104 KKLGGKGGGPPK 117

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US-09-989-734-211  
Sequence 211, Application US/09989734  
Publication No. US20030003531A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Gerltsen, Mary E.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC64  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;  
Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLGGKGGGPPK 14  
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Db 104 KKLGGKGGGPPK 117

RESULT 12  
US-09-997-653-211

; Sequence 211, Application US/09997653  
; Publication No. US2003008297A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301C38  
CURRENT APPLICATION NUMBER: US/09/997,653  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;  
Best local Similarity 100.0%; Pred. No. 0.001;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPK 14  
Db 104 KKLQKGPGGPPK 117

RESULT 13  
US-09-993-667-211  
; Sequence 211, Application US/09993667  
; Publication No. US20030022187A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C4  
 CURRENT APPLICATION NUMBER: US/09/993,667  
 PRIOR FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
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 PRIOR APPLICATION NUMBER: 60/090445  
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 PRIOR FILING DATE: 1998-06-24



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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;  
Best Local Similarity 100.0%; Pred No. 0.001;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLQKGGGPPK 14  
Db 104 KKLQKGGGPPK 117

RESULT 14  
US-09-990-438-211  
Sequence 211, Application US/09990438  
Publication No. US2003002754A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC3  
CURRENT APPLICATION NUMBER: US/09/990,438  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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Query Match 100.0%; Score 81; DB 9; Length 185;  
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QY 1 KKLGGKGGGPPK 14  
 DB 104 KKLGGKGGGPPK 117

RESULT 15  
 US-09-990-562-211  
 Sequence 211, Application US/09990562  
 Publication No. US20030027965A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Geritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Guiney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC18  
CURRENT APPLICATION NUMBER: US/09/990,562  
CURRENT FILING DATE: 2001-11-14  
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 0.001;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKKGPGPPK 14  
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 DB 104 KKLQKKGPGPPK 117

Search completed: April 11, 2003, 16:17:42  
 Job time : 2.39315 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:53 ; Search time 1.50734 Seconds  
(without alignments)  
892.885 Million cell updates/sec

Title: US-09-821-726a-3  
Perfect score: 81  
Sequence: 1 KKLCKGPGGPPPK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR.73:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	74.1	1677	T14267	Xin protein, stage
2	50	61.7	673	BVECB	excinuclease ABC C
3	50	61.7	673	A99736	excision nuclease
4	50	61.7	673	B85586	DNA repair, excisi
5	50	61.7	673	AD0597	excision nuclease
6	47	58.0	22	C42856	hypothetical prote
7	47	58.0	669	D82739	excinuclease ABC s
8	46	56.8	377	E87022	probable conserved
9	46	56.8	426	A39695	transforming prote
10	46	56.8	551	S57447	HPR11-7 protein -
11	46	56.8	830	T16148	hypothetical prote
12	46	56.8	1105	S40243	hypothetical prote
13	46	56.8	1215	T32734	DNA-directed DNA p
14	46	56.8	1357	T29265	myosin-IA - Acanth
15	46	56.8	1357	T29265	hypothetical prote
16	45.5	56.2	579	D72092	conserved hypotet
17	45.5	56.2	579	C86532	CT082 hypothetical
18	45	55.6	477	H96833	hypothetical prote
19	45	55.6	609	TVMVCS	protein-tyrosine k
20	45	55.6	609	TVMVCS	protein-tyrosine k
21	45	55.6	820	TVMVCF	protein-tyrosine k
22	45	55.6	822	TVMVCF	protein-tyrosine k
23	45	55.6	2715	T13049	eyelid - fruit fly
24	44	54.3	142	D32880	hypothetical prote
25	44	54.3	149	T31446	phastocinonol-plas
26	44	54.3	182	B86462	hypothetical prote
27	44	54.3	216	TVMHRR	transforming prote
28	44	54.3	230	T56979	nitric-oxide synth
29	44	54.3	347	E97487	hypothetical prote

30	44	54.3	347	AE2705	ABC transporter, s
31	44	54.3	558	B81711	conserved hypotet
32	44	54.3	560	D71560	hypothetical prote
33	44	54.3	593	D74323	cell division cycl
34	44	54.3	670	A83255	excinuclease ABC s
35	44	54.3	706	D97303	ABC-type multidrug
36	44	54.3	996	A71080	hypothetical prote
37	44	54.3	1202	A71424	nitric-oxide synth
38	44	54.3	1203	A47501	nitric-oxide synth
39	44	54.3	1205	A38943	nitric-oxide synth
40	44	54.3	1464	S59856	collagen alpha 1(I
41	43.5	53.7	1049	CG8075	collagen alpha 1(I
42	43	53.1	140	S46351	vpx protein - simi
43	43	53.1	189	A86369	hypothetical prote
44	43	53.1	221	G72665	hypothetical prote
45	43	53.1	224	B72710	hypothetical prote

## ALIGNMENTS

RESULT 1  
T14267  
Xin protein, stage early embryo - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Sep-1999 #sequence\_revistion 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: T14267  
R:Wang, D.Z.; Lin, J.J.C.  
A:Submitted to the EMBL Data Library, March 1998  
A:Description: Involvement of a novel gene, Xin, in cardiac looping.  
A:Reference number: Z17948  
A:Accession: T14267  
A:Stature: preliminary; translated from GB/EMBL/DBD1  
A:Molecule type: mRNA  
A:Residues: 1-1677 <NAN>  
A:Cross-references: EMBL:AF051945; NID:92970645; PID:92970646; PIDN:AAC06023.1  
A:Experimental source: cardiac muscle; stage early embryo

Query Match  
Best local similarity 81.8%; Pred. No. 1.9;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 QGKPGGPPPK 14  
DB 574 ECKGPGGPPPE 584

RESULT 2  
BVECB  
excinuclease ABC chain B - Escherichia coli (strain K-12)  
N:Alternate names: uvrB protein  
C:Contents: excision endonuclease ABC (EC 3.1.-.-) chain B  
C:Species: Escherichia coli  
C:Date: 31-Mar-1988 #sequence\_revistion 31-Mar-1988 #text\_change 01-Mar-2002  
C:Accession: A93613; A93612; A23765; A24939  
R:Backendorf, C.; Spatnik, H.; Barbeiro, A.P.; van de Putte, P.  
A:Nucleic Acids Res. 14, 2877-2890, 1986  
A:Title: Structure of the uvrB gene of Escherichia coli. Homology with other DNA repa  
A:Reference number: A93613; MUID:86176773; PMID:3008099  
A:Accession: A93613  
A:Molecule type: DNA  
A:Residues: 1-673 <BAC>  
A:Cross-references: GB:X03722; NID:943285; PIDN:CAA27357.1; PID:943286  
R:Arlikar, E.; Kulkarni, M.S.; Thomas, D.C.; Sancar, A.  
Nucleic Acids Res. 14, 2637-2650, 1986  
A:Title: Sequences of the E. coli uvrB gene and protein.  
A:Reference number: A93612; MUID:86176755; PMID:3515321  
A:Accession: A93612  
A:Molecule type: DNA  
A:Residues: 1-476, 'R', 478-673 <ARI>  
A:Cross-references: GB:X03678; GB:J01722; GB:J01723; GB:M24329; GB:V00374; GB:V00375;  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Bernal, N.T.; Burland, V.; Riley, M.;  
A.: Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of *Escherichia coli* K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: C64814  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-673 <BLAT>  
A:Cross-references: GB:AE000180; GB:U00096; NID:q1786988; PIDN:AC73866.1; PID:q1786996;  
C:Comment: Source: strain K-12, substrain MG1655  
C:Genetics: uvrA, uvrB, and uvrC function together as excision nuclease.  
A:Gene: uvrB  
A:Map position: 18 min  
C:Function:  
A:Description: stimulates the ATPase activity of uvrA protein in the presence of UV-irradiation  
C:Superfamily: excinuclease ABC chain B  
C:Keywords: ATP; DNA repair; hydrolase; nucleotide binding; P-loop  
E:338-339/Region: nucleotide-binding motif A (P-loop)  
E:338-341/Region: DEXH motif

Query Match  
Best Local Similarity 61.7%; Score 50; DB 1; Length 673;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 LOGKPGGPP 13  
DB 313 LSGRPGGPP 323

RESULT 3  
A99736  
excision nuclease subunit B [Imported] - *Escherichia coli* (strain O157:H7, substrain RIM)  
C:Species: *Escherichia coli*  
C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
C:Accession: A99736  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;  
gasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: A99736  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-673 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA34280.1; PID:q13360316; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509552  
C:Genetics:  
A:Gene: ECG0857  
C:Superfamily: excinuclease ABC chain B

Query Match  
Best Local Similarity 61.7%; Score 50; DB 2; Length 673;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 LOGKPGGPP 13  
DB 313 LSGRPGGPP 323

RESULT 4  
B85586  
DNA repair, excision nuclease subunit B [Imported] - *Escherichia coli* (strain O157:H7, S)  
C:Species: *Escherichia coli*  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: B85586  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: B85586  
A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-673 <STO>  
A:Cross-references: GB:AE005174; NID:q12513768; PIDN:AG55150.1; GSPDB:GN00145; UMG:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: uvrB  
C:Superfamily: excinuclease ABC chain B

Query Match  
Best Local Similarity 61.7%; Score 50; DB 2; Length 673;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 LOGKPGGPP 13  
DB 313 LSGRPGGPP 323

RESULT 5  
AD0597  
excision nuclease ABC chain B STY0831 [Imported] - *Salmonella enterica* subsp. enteric  
C:Species: *Salmonella enterica* subsp. enterica serovar Typh  
A:Note: this species has also been called *Salmonella typhi*  
C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AD0597  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Church  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,  
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se  
A:Reference number: AB0502; PMID:11677608  
A:Accession: AD0597  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-673 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CA005246.1; PID:q16502016; GSPDB:GN00176  
A:Genes: STY0831  
C:Superfamily: excinuclease ABC chain B

Query Match  
Best Local Similarity 61.7%; Score 50; DB 2; Length 673;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 LOGKPGGPP 13  
DB 313 LSGRPGGPP 323

RESULT 6  
C42856  
hypothetical protein 3 EPF-region [Imported] - human (fragment)  
C:Species: *Homo sapiens* (man)  
C>Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
C:Accession: C42856  
R:Liu, Z.; Diaz, L.A.; Haas, A.L.; Giudice, G.J.  
J. Biol. Chem. 267, 15829-15835, 1992  
A:Title: cDNA cloning of a novel human ubiquitin carrier protein. An antigenic domain  
this human epidermal transcript.  
A:Reference number: A42856; MUID:92348449; PMID:1379239  
A:Accession: C42856  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-22 <LIU>  
A:Experimental source: keratinocyte  
A:Note: sequence extracted from NCBI backbone (NCBI:109895, NCBI:109899)

Query Match  
Best Local Similarity 58.0%; Score 47; DB 2; Length 22;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 LOGKPGGPP 13  
DB 313 LSGRPGGPP 323

Mon Apr 14 14:02:42 2003

us-09-821-726a-3.rpt

Db 6 KNACRGPGCPP 17

RESULT 7

D82739

exonuclease ABC subunit B XF0967 [Imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000

C:Accession: D82739

R:Accession: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences

R:Accession: 151-157, 2000

R:Accession: 151-157, 2000

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R:Accession: 151-157, 2000

R:Accession: 151-157, 2000

R:Accession: 151-157, 2000

Db 254 GPGCPP 260

RESULT 9

A39695

transferring protein (N-myc) - common canary

C:Species: Serinus canaria (common canary)

C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 28-Feb-1997

C:Accession: A39695

R:Accession: A39695

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R:Accession: A39695

R:Accession: A39695

R:Taich, A.  
 submitted to the EMBL Data Library, March 1995  
 A:Description: The sequence of C. elegans cosmid F25B5.  
 A:Reference number: Z18468  
 A:Accession: T16148  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-561 <TAIR>  
 A:Cross-references: EMBL:U23172; NID:g726388; PID:g726394; PIDN:AAC46528.1; CESP:F25B5.7  
 A:Experimental source: strain Bristol N2  
 A:Gene: CESP:F25B5.7  
 A:Introns: 39/2; 157/3; 258/2; 290/2; 356/1; 531/1

Query Match  
 Best Local Similarity 56.8%; Score 46; DB 2; Length 561;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7 GPGGPP 13  
 Db 409 GPGGPP 415

RESULT 12  
 T18860  
 hypothetical protein CO2C6.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
 C:Accession: T18860  
 R:Swindburn, J.  
 submitted to the EMBL Data Library, August 1996  
 A:Reference number: Z19032  
 A:Accession: T18860  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-830 <WIL>  
 A:Cross-references: EMBL:Z79596; PIDN:CAB01857.1; GSPDB:GN00028; CESP:CO2C6.1  
 C:Genetics:  
 A:Gene: CESP:CO2C6.1  
 A:Map position: X  
 A:Introns: 56/2; 131/1; 333/2; 501/2; 593/2; 686/3; 815/2  
 C:Superfamily: human dynamin II; pleckstrin repeat homology

Query Match  
 Best Local Similarity 56.8%; Score 46; DB 2; Length 830;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7 GPGGPP 13  
 Db 818 GPGGPP 824

RESULT 13  
 S40243  
 DNA-directed DNA polymerase (EC 2.7.7.7) delta chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S40243; J70670  
 R:Cullmann, G.; Hindges, R.; Berchtold, M.W.; Huebscher, U.  
 submitted to the EMBL Data Library, March 1993  
 A:Reference number: S40243  
 A:Accession: S40243  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1105 <CUIL>  
 A:Cross-references: EMBL:Z21848; NID:g438133; PIDN:CAA7895.1; PID:g438134  
 Gene 134, 191-200, 1993  
 A:Title: Cloning of a mouse cDNA encoding DNA polymerase delta: refinement of the homology  
 A:Reference number: J70670; MUID:94085777; PMID:8262377  
 A:Molecule type: DNA  
 A:Residues: 1-111, 'G', 113, 'P', 115-1034, 'Y', 1036-1105 <U2>

A:Cross-references: EMBL:Z21848  
 A:Note: the sequence translated from Z21848 is inconsistent with that from this sequence  
 C:Comment: Three DNA polymerases alpha, delta and epsilon chains are essential. This  
 C:Genetics:  
 A:Gene: poldelta  
 C:Superfamily: herpesvirus DNA-directed DNA polymerase  
 C:Keywords: DNA replication; heterodimer; nucleotidyltransferase

Query Match  
 Best Local Similarity 56.8%; Score 46; DB 1; Length 1105;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 KIKGKGPGGPP 14  
 Db 4 KRKGPGGVPK 17

RESULT 14  
 T32734  
 myosin-IA - Acanthamoeba castellanii  
 C:Species: Acanthamoeba castellanii  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 08-Sep-2000  
 C:Accession: T32734  
 R:Lee, W.L.; Ostap, E.M.; Zol, H.G.; Pollard, T.D.  
 submitted to the EMBL Data Library, August 1998  
 A:Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-IA G  
 A:Reference number: Z21216  
 A:Accession: T32734  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1215 <LEP>  
 A:Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAC35357.1  
 C:Genetics:  
 A:Gene: MYA  
 A:Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 5  
 C:Superfamily: protozoan myosin heavy chain IIB; myosin motor domain homology; SH3 hom  
 F:14-674/Domain: myosin motor domain homology <MMO>

Query Match  
 Best Local Similarity 56.8%; Score 46; DB 2; Length 1215;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7 GPGGPP 13  
 Db 1075 GPGGPP 1081

RESULT 15  
 T29265  
 hypothetical protein C01G8.7 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T29265  
 R:Du, Z.; Gatlung, S.  
 submitted to the EMBL Data Library, November 1996  
 A:Description: The sequence of C. elegans cosmid C01G8.  
 A:Reference number: Z20597  
 A:Accession: T29265  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1357 <D02>  
 A:Cross-references: EMBL:U80439; PIDN:AAB37645.1; GSPDB:GN00019; CESP:C01G8.7  
 A:Experimental source: strain Bristol N2; clone C01G8  
 A:Gene: CESP:C01G8.7  
 A:Map position: 1  
 A:Introns: 89/1; 488/1; 701/3; 1056/2; 1159/3; 1197/1; 1312/3

Query Match  
 Best Local Similarity 56.8%; Score 46; DB 2; Length 1357;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Oy 7 GPGPPP 13  
| | | | |  
Db 153 GPGPPP 159

Search completed: April 11, 2003, 16:15:28  
Job time : 3.50734 secs



Mon Apr 14 14:02:52 2003

us-09-821-726a-3.ispt

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:33 ; Search time 3.10604 Seconds  
(without alignments)  
928.727 Million cell updates/sec

Title: US-09-821-726A-3  
Perfect score: 1 KKLQKPGGPPPK 14  
Sequence:

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPREMBL\_21:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mmc:\*

8: sp\_organelle:\*

9: sp-phage:\*

10: sp-plant:\*

11: sp-rodent:\*

12: sp-virus:\*

13: sp-vertebrate:\*

14: sp-unclassified:\*

15: sp-rvivirus:\*

16: sp\_bacteriophage:\*

17: sp-archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	74.1	1677	11 070373	070373 mus musculus
2	52	64.2	467	1 09H9F1	09H9F1 homo sapien
3	50	61.7	333	2 09APQ3	09APQ3 uncultured
4	49	60.5	212	2 09APJ1	09APJ1 methylolact
5	48	59.3	409	16 08XRJ2	08XRJ2 ralslonia s
6	48	59.3	547	11 097472	097472 mus musculu
7	48	59.3	547	11 091XC0	091XC0 mus musculu
8	48	59.3	774	5 09V620	09V620 drosophila
9	48	59.3	813	5 095MY2	095MY2 drosophila
10	48	59.3	1289	10 099FI07	099FI07 aradidopsis
11	48	59.3	1292	3 096WLO	096WLO ustiliago ma
12	48	59.3	2061	3 09VU09	09VU09 drosophila
13	47	58.0	104	6 08WNT3	08WNT3 procyon lot
14	47	58.0	262	12 09DMB2	09DMB2 rat clyomeg
15	47	58.0	420	4 08WYU4	08WYU4 homo sapien
16	47	58.0	494	6 08S068	08S068 sus scrofa

17	47	58.0	673	2 09RBK2	09RBK2 xanthomonas
18	47	58.0	1963	5 09VSK5	09VSK5 drosophila
19	47	58.0	1966	5 09NHX6	09NHX6 drosophila
20	47	58.0	1985	5 08T9N4	08T9N4 oryza sativ
21	46	56.8	172	10 08S0G1	08S0G1 homo sapien
22	46	56.8	241	4 095542	095542 homo sapien
23	46	56.8	250	4 075894	075894 homo sapien
24	46	56.8	281	4 095010	095010 caenorhabdi
25	46	56.8	322	13 095010	095010 caenorhabdi
26	46	56.8	377	16 069559	069559 mycobacteri
27	46	56.8	495	5 095YB0	095YB0 caenorhabdi
28	46	56.8	549	5 09BIB7	09BIB7 caenorhabdi
29	46	56.8	551	4 016630	016630 homo sapien
30	46	56.8	561	4 009542	009542 caenorhabdi
31	46	56.8	588	4 09BM18	09BM18 homo sapien
32	46	56.8	1105	11 091V70	091V70 mus musculu
33	46	56.8	1194	5 09M485	09M485 drosophila
34	46	56.8	1215	5 077202	077202 acanthamoeb
35	46	56.8	1256	5 095YV9	095YV9 caenorhabdi
36	46	56.8	1284	5 0960F1	0960F1 drosophila
37	46	56.8	1724	5 091019	091019 caenorhabdi
38	45.5	56.2	579	16 0928K7	0928K7 chlamydia p
39	45	55.0	153	11 09CTM4	09CTM4 mus musculu
40	45	55.0	171	10 09SSB8	09SSB8 arabidopsis
41	45	55.6	224	10 08R238	08R238 oryza sativ
42	45	55.6	316	15 099857	099857 chimpanzee
43	45	55.6	497	10 08S1B7	08S1B7 oryza sativ
44	45	55.6	585	4 08TE04	08TE04 homo sapien
45	45	55.6	976	6 09M2T1	09M2T1 canis famli

## ALIGNMENTS

## RESULT 1

070373 PRELIMINARY: PRT: 1677 AA.

AC 070373: 070373: 07, Created)  
 DT 01-AUG-1998 (TREMURel. 07, last sequence update)  
 DT 01-AUG-1998 (TREMURel. 07, last sequence update)  
 DT 01-DEC-2001 (TREMURel. 19, last annotation update)  
 DE Xin.  
 GN Xin.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_TaxID=10090;  
 OX 11)  
 RN 11)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEART MUSCLE;  
 RX PubMed=9159189;  
 RA Wang D.-Z., Hu X., Lin J.L.-C., Kitten G.T., Solursh M., Lin J.J.-C.;  
 RT "Differential display of mRNAs from the atrioventricular region of  
 RT developing chicken hearts at stages 15 and 21.";  
 RL Front. Biosci. 1:al-a15(1996).  
 RN 12)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEART MUSCLE;  
 RX MEDLINE=9146891; PubMed=10021346;  
 RA Wang D.-Z., Reiter R.S., Lin J.L.-C., Wang Q., Williams H.S.,  
 RA Krob S.L., Schulteis T.M., Evans S., Lin J.J.-C.;  
 RT "Requirement of a novel gene, Xin, in cardiac morphogenesis.";  
 RT Development 126:1281-1294(1999).  
 DR EMBL: AF01945; AAC06023.1; -;  
 DR MGI: MGI:133878; Xin.  
 SQ SEQUENCE 1677 AA; 182085 MW; A201CFGA710CTFE CRC64;

Query Match 74.1% Score 60; DB 11; Length 1677;  
 Best local Similarity 81.8%; Pred. NO. 2.2;  
 Matches 9; Conservative 0; Indels 0; Gaps 0;

4 QGKPGGPPPK 14  
 :|||||:

Db 574 ECKGPGGPPPE 584

## RESULT 2

Q9H9F1 PRELIMINARY; PRT; 467 AA.  
 ID Q9H9F1  
 AC Q9H9F1  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE CDNA FLJ12800 fis, clone NT2RP2002079, weakly similar to histone H1, gonadal.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN NCBI\_Taxid=9606;  
 RP SEQUENCE FROM N.A.  
 RA Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y., Oshima A., "NEDO human cDNA sequencing project."  
 RT Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.  
 RL EMBL: AK022862; BAB14278.1;  
 DR InterPro: IPR000637; AT\_hook.  
 DR SMART: SM00384; AT\_hook.  
 SO SEQUENCE 467 AA; 49648 MW; 287B1BF4CF30B1A1 CRC64;

Query Match  
 Best Local Similarity 64.2%; Score 52; DB 4; Length 467;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KRIKGGGPGGPPK 14  
 Db 213 KRSSGKGPENPPK 226

## RESULT 3

Q9APQ3 PRELIMINARY; PRT; 333 AA.  
 ID Q9APQ3  
 AC Q9APQ3  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 GN Excision nuclease subunit B (Fragment).  
 OS unclutered bacterium pCOSH1.  
 OC Bacteria; environmental samples.  
 OX NCBI\_Taxid=143796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20575196; PubMed=11133432;  
 RA Entcheva P., Liebl W., Johann A., Hartisch T., Streif W.R.;  
 RT "Direct cloning from enrichment cultures a reliable strategy for  
 RT isolation of complete operons and genes from microbial consortia."  
 RL Appl. Environ. Microbiol. 67:89-99(2001).  
 DR EMBL: AF530772; AAC60567.1;  
 DR HSBP; P56981; ID9X.  
 DR InterPro: IPR001410; DEAD.  
 FT NON\_TER  
 FT NON\_TER  
 FT NON\_TER  
 SO SEQUENCE 333 AA; 38155 MW; E6401C01A8A46DEF CRC64;

Query Match  
 Best Local Similarity 61.7%; Score 50; DB 2; Length 333;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPGPP 13  
 Db 135 LSGRGPGGPP 145

## RESULT 4

Q9APJ1 PRELIMINARY; PRT; 212 AA.  
 ID Q9APJ1  
 AC Q9APJ1  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE putative regulator for granula-associated protein.  
 OS Methylobacterium extorquens.  
 OC Bacteria; Proteobacteria; alpha subphylum; Rhizobiaceae group;  
 OC NCBI\_Taxid=408;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AMI;  
 RX MEDLINE=21142531; PubMed=11208803;  
 RA Korotkova N., Lidstrom M.E.;  
 RT "Connection between Poly-beta-Hydroxybutyrate Biosynthesis and Growth  
 RT on C1 and C2 Compounds in the Methylobacterium Methylobacterium extorquens  
 RL J. Bacteriol. 183:1038-1046(2001).  
 DR EMBL: AF287907; AAK11535.1;  
 SO SEQUENCE 212 AA; 23141 MW; 4121BD0E8A3FBAC3 CRC64;

Query Match  
 Best Local Similarity 60.5%; Score 49; DB 2; Length 212;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GKGPGGPP 13  
 Db 162 GFGPGGPP 170

## RESULT 5

Q8XRL2 PRELIMINARY; PRT; 409 AA.  
 ID Q8XRL2  
 AC Q8XRL2  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DE Probable drug efflux lipoprotein.  
 GN KSP0819 OR RS01888.  
 OS Ralstonia solanacearum (Pseudomonas solanacearum).  
 OC Bacteria; Proteobacteria; beta subphylum; Ralstonia group;  
 OX Ralstonia.  
 OX NCBI\_Taxid=305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GMT1000;  
 RX MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brothier P., Camus J.C., Cartolico L.,  
 RA Chandler M., Choinse N., Claudel-Renard C., Cunac S., Demange N.,  
 RA Gaspin C., Lavy M., Molan A., Robert C., Saurin W., Schlex T.,  
 RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,  
 RA Weissenbach J., Boucher C.A.;  
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum."  
 RL Nature 415:497-502(2002).  
 DR EMBL: AL646081; CAD17970.1;  
 DR InterPro: IPR002215; HlyD.  
 DR Pfam: PF00529; HlyD.  
 KW Plasmid; Complete proteome.  
 SO SEQUENCE 409 AA; 42873 MW; 97003B2B7F95401B CRC64;

Query Match  
 Best Local Similarity 60.5%; Score 49; DB 16; Length 409;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GKGPGGPP 13  
 Db 25 GKGPGGPP 33

RESULT 6  
 ID P97472 PRELIMINARY; PRT: 547 AA.  
 AC P97472:  
 DT 01-MAY-1997 (TReMBLrel. 03, Created)  
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Ajuba.  
 GN JUB OR AJUBA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NC NCBL\_Taxid=10090;  
 RX MEDLINE-99263009; PubMed-10330178;  
 RP SEQUENCE FROM N.A.  
 RA Goyal R.K., Lin P., Kanungo J., Payne A.S., Muslin A.J.,  
 RA Longmore G.D.;  
 RA "Ajuba, a novel LIM protein, interacts with Grb2, augments mitogen-  
 RT activated protein kinase activity in fibroblasts, and promotes meiotic  
 RT maturation of Xenopus oocytes in a Grb2- and Ras-dependent manner."  
 RL Mol. Cell. Biol. 19:4379-4389(1999).  
 CC -1- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC  
 CC IONS.  
 DR EMBL: U79776; AAB38287.1; -;  
 DR HSSP: Q05158; 10LI.  
 DR MGD: MGI:1341886; JUB.  
 DR InterPro: IPR001781; LIM.  
 DR Pfam: PF00412; LIM; 3.  
 DR ProDom: PD000094; LIM; 3.  
 DR SMART: SM00132; LIM; 3.  
 DR PROSITE: PS00478; LIM\_DOMAIN\_1; 2.  
 DR PROSITE: PS50023; LIM\_DOMAIN\_2; 3.  
 DR LIM domain: Metal-binding; Zinc.  
 KW SEQUENCE 547 AA; 57901 MW; C326772AC1C441B2 CRC64;  
 SQ

Query Match 59.3%; Score 48; DB 11; Length 547;  
 Best Local Similarity 53.8%; Pred. No. 42;  
 Matches 7; Conservative 3; Mismatches 0; Gaps 0;

OY 1 KKLQKGP GCGPP 13  
 DB 93 QREGSGFPGCPP 105

RESULT 7  
 ID Q91XC0 PRELIMINARY; PRT: 547 AA.  
 AC Q91XC0:  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Similar to ajuba.  
 GN JUB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NC NCBL\_Taxid=10090;  
 RX MEDLINE-10090;  
 RP SEQUENCE FROM N.A.  
 RA Straussberg R.;  
 RA TISSUE-SALIVARY GLAND;  
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC  
 CC IONS.  
 DR EMBL: BC011035; AAH11035.1; -;  
 DR MGD: MGI:1341886; JUB.  
 DR InterPro: IPR001781; LIM.  
 DR Pfam: PF00412; LIM; 3.  
 DR ProDom: PD000094; LIM; 3.  
 DR PROSITE: PS00478; LIM\_DOMAIN\_1; UNKNOWN\_2.  
 DR PROSITE: PS00478; LIM\_DOMAIN\_2.

DR PROSITE: PS50023; LIM\_DOMAIN\_2; 3.  
 KW LIM domain: Metal-binding; Zinc.  
 SQ SEQUENCE 547 AA; 57919 MW; C326772AC1C155B2 CRC64;  
 OY 1 KKLQKGP GCGPP 13  
 DB 93 QREGSGFPGCPP 105

Query Match 59.3%; Score 48; DB 11; Length 547;  
 Best Local Similarity 53.8%; Pred. No. 42;  
 Matches 7; Conservative 3; Mismatches 0; Gaps 0;

RESULT 8  
 ID Q9V620 PRELIMINARY; PRT: 774 AA.  
 AC Q9V620:  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CG8991 protein.  
 GN Drosophila melanogaster (Fruit fly).  
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCBL\_Taxid=7227;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RP STRAIN-BERKELEY;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Branton R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Baldwin D.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Beasley E.M.,  
 RA Bailew R.M., Basu A., Baxendale J., Bhandari D., Bolshakov S.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotter P.,  
 RA Borokova D., Botchan M.R., Bouck J., Cadieu E., Center A., Chandra I.,  
 RA Burris K.C., Busam D.A., Butler H., Caden E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fioder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Stapleton M., Strong R., Sun E.,  
 RA Spier E., Spradling A.C., Turner R., Venler E., Wang A.H., Wang X.,  
 RA Svrlidskas R., Tector C., Turner R., Venler E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.C., Wu D., Yang S., Yao Q.A.,  
 RA Williams S.M., Woodage T., Worley K.G., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003824; AAF58619.1; -;  
 DR Flybase: FBgn003654; CG8991.  
 DR InterPro: IPR002965; P\_rich\_extensn.  
 DR PRINTS: PRO1217; PRICHEXTENSN.

SO SEQUENCE 774 AA; 83718 MW; 04A64D97952CF90D CRC64;

Query Match 59.3%; Score 48; DB 5; Length 774;  
Best Local Similarity 61.5%; Pred. No. 58;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKLQGGPGGAPP 13  
: | | | | |  
DB 366 QKSPGPGGAPP 378

## RESULT 9

O95TY2

ID O95TY2 PRELIMINARY; PRT; 813 AA.

AC O95TY2

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE GH22790P. (TREMBLrel. 20, Last annotation update)

GN CG8991.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Ephydroidea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC NCBI\_TaxID=7227;

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Gonzalez M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Nuno J., Paclet J., Paragay V., Park S., Phouanavong S., Wan K.,

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY058444; AL13673.1;

DR InterPro; IPR0033654; CG8991.

DR SEQUENCE 813 AA; 88199 MW; 9B9F9571EA08308C CRC64;

## Query Match

Best Local Similarity 59.3%; Score 48; DB 5; Length 813;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKLQGGPGGAPP 13  
: | | | | |  
DB 405 QKSPGPGGAPP 417

## RESULT 10

O9FLQ7

ID O9FLQ7 PRELIMINARY; PRT; 1289 AA.

AC O9FLQ7

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE G1AD23008.1. (TREMBLrel. 21, Last annotation update)

GN CG9425.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Eucosids II; Brassicales; Brassicaceae; Arabidopsidae.

OC NCBI\_TaxID=3702;

RP SEQUENCE FROM N.A.

RC STRAIN-COLUMBIA;

RA MEDLINE-98290546; PubMed-9628582;

RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,

RA Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen

RL DNA Res. 5:41-54(1998)."

DR EMBL; AB010070; BAB11454.1;

DR InterPro; IPR002965; P\_richextensn.

DR PRINTS; PR01582; KV33CHANNEL.

DR PRINTS; PR01217; PRICHEXTENS.

SO SEQUENCE 1289 AA; 137558 MW; 898E5A2A618F5E0 CRC64;

## Query Match

Best Local Similarity 59.3%; Score 48; DB 10; Length 1289;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 GKPGGAPP 13  
: | | | | |  
DB 1142 GKGPGAPP 1150

## RESULT 11

O96WL0

ID O96WL0 PRELIMINARY; PRT; 1292 AA.

AC O96WL0

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE TPR-containing protein Mq1.

GN MQL1.

OS Ustilago maydis (Smut fungus).

OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;

OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

OC NCBI\_TaxID=5270;

RP SEQUENCE FROM N.A.

RA Loubardou G., Kahmann R.

RT "Involvement of the TPR containing protein Mq1 in filamentous growth

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF28097; AAK58576.1;

DR InterPro; IPR001440; TPR.

DR Pfam; PF00515; TPR; 10.

DR SEQUENCE 1292 AA; 135886 MW; 543A2702C4E0D610 CRC64;

Query Match 59.3%; Score 48; DB 3; Length 1292;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 LQKPGGAPP 13  
: | | | | |  
DB 716 LAAGPGGAPP 726

## RESULT 12

O9VUH9

ID O9VUH9 PRELIMINARY; PRT; 2061 AA.

AC O9VUH9

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE CG9425 protein.

GN CG9425.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Ephydroidea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC NCBI\_TaxID=7227;

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RA MEDLINE-20196006; PubMed-10731132;

RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,

RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibergam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasio P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamas I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Glods R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
DR EMBL: AE003533; AAF49702.1;  
DR FLYBase: FBgn0036451; CG9425.  
DR InterPro: IPR002965; P\_c1ich\_extensn.  
DR InterPro: IPR001412; tRNA-synE\_1.  
DR InterPro: IPR000822; znf\_C2H2.  
DR InterPro: IPR000571; znf\_CCCH.  
DR Pfam: PF00642; zf-CCCH; 1.  
DR PRINTS: PR01217; PRICHEXTENS.  
DR SMART: SM00355; znf\_C2H2; 1.  
DR PROSITE: PS00178; AA\_TIRNA\_LIGASE\_1; UNKNOWN\_1.  
DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; UNKNOWN\_1.  
SQ SEQUENCE 2061 AA; 225386 MW; B6A1539B5B5CC0E CRC64;

Query Match 59.3%; Score 48; DB 5; Length 2061;  
Best Local Similarity 72.7%; Pred. No. 1.5e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 LOGKPGGPP 13  
Db 1361 LRGMPPGPP 1371

RESULT 13  
O8WNT3 PRELIMINARY; PRT; 104 AA.

AC O8WNT3;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Dopamine receptor D4 (fragment).  
GN DRD4.  
OS *Procyon lotor* (Raccoon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Carnivora; Fissipedia; Procyonidae; Procyon.  
OX NCBI\_TaxID=9654;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Inoue-Murayama M., Matsura N., Murayama Y., Niimi Y., Tsubota T.,  
RA Ito S.;  
RT "Sequence Comparison of Dopamine Receptor D4 Exon III Repetitive  
Region in Several Species of the Order Carnivora.";  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB069663; BAB79701.1;  
DR InterPro: IPR003993; trectace.  
DR PRINTS: PR01503; TREACLE.

KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 104 104  
SQ SEQUENCE 104 AA; 11491 MW; BC99F4C53ECE0F7A CRC64;

Query Match 58.0%; Score 47; DB 6; Length 104;  
Best Local Similarity 52.6%; Pred. No. 13;  
Matches 10; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

OY 2 KLOGK-----GPGGPPK 14  
Db 29 KLHGVRPRRSGCGPPPK 47

RESULT 14  
O9DWB2 PRELIMINARY; PRT; 262 AA.

AC O9DWB2;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE Pr90.  
GN R90.  
OS Rat cytomegalovirus (strain Maastricht).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Murinegaleovirus.  
OX NCBI\_TaxID=79700;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MAASTRICHT;  
RX MEDLINE=2036325; PubMed=10906222;  
RA Vink C., Beuken E., Bruggeman C.A.;  
RT "Complete DNA sequence of the rat cytomegalovirus genome.";  
RL J. Virol. 74:7656-7665(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MAASTRICHT;  
RX MEDLINE=20473137; PubMed=11018281;  
RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A.;  
RT "Rat cytomegalovirus R99 is a highly conserved gene which expresses a  
spliced transcript.";  
RL Virus Res. 69:119-130(2000).  
DR EMBL: AF232689; AAF99178.1;  
SQ SEQUENCE 262 AA; 27742 MW; 7C806385711307B7 CRC64;

Query Match 58.0%; Score 47; DB 12; Length 262;  
Best Local Similarity 70.0%; Pred. No. 30;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 OGGKPGGPP 13  
Db 18 RGRGPGGPP 27

RESULT 15  
O8WYU4 PRELIMINARY; PRT; 420 AA.

AC O8WYU4;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Hypothetical 45.8 kDa protein.  
GN PP6997.  
OS *Homo sapiens* (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,  
RA Wan D.F., Gu J.R.;  
RT "Novel human cDNA clones with function of inhibiting cancer cell  
growth.";

RI Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL: AF318356; AAL55863.1; -;  
DR InterPro: IPR000822; Znf\_C2H2.  
DR Pfam: PF00096; Zf-C2H2; 6.  
DR PRINTS: PR00048; ZINC\_FINGER.  
DR SMART: SM00355; znf\_C2H2; 6.  
DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; UNKNOWN\_6.  
DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 6.  
KW Hypothetical protein.  
SQ SEQUENCE 420 AA; 45771 MW; CB01FC26A489060C CRC64;

Query Match 58.0%; Score 47; DB 4; Length 420;  
Best Local Similarity 58.3%; Pred. No. 46;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 KKLQCKGPGGP 12  
||: : |||||  
Db 195 KKIKAKNPGGP 206

Search completed: April 11, 2003, 16:14:17  
Job time : 5.10604 secs



GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 ; Search time 0.822186 Seconds  
(without alignments)

706.250 Million cell updates/sec

Title: US-09-821-726A-3  
Perfect score: 81  
Sequence: 1 KKLQKGGPGGPPK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Capext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query length	ID	Description
1	81	100.0	199	1	CLIP_HUMAN
2	59	72.8	184	1	CLIP_MOUSE
3	50	61.7	673	1	UVRB_FCOLI
4	50	61.7	673	1	UVRB_SALTI
5	48	59.3	673	1	UVRB_SALTY
6	47	58.0	669	1	UVRB_XYLFA
7	46	56.8	427	1	MYCN_SERCA
8	46	56.8	830	1	DYNL_CAEEL
9	46	56.8	1103	1	DPOD_MESAU
10	46	56.8	1105	1	DPOD_MOUSE
11	45	55.6	402	1	GUNI_HUMIN
12	45	55.6	477	1	FES_FSVST
13	45	55.6	609	1	FES_FSVGA
14	45	55.6	820	1	FES_FELCA
15	45	55.6	822	1	FES_HUMAN
16	45	54.9	459	1	RN25_HUMAN
17	44	54.3	142	1	YRUB_KLEPN
18	44	54.3	218	1	RRAS_HUMAN
19	44	54.3	593	1	CC23_SCHPO
20	44	54.3	670	1	UVRB_PSEAE
21	44	54.3	919	1	NOS3_RAT
22	44	54.3	1048	1	AGOL_ARATH
23	44	54.3	1201	1	NOS3_MOUSE
24	44	54.3	1202	1	NOS3_HUMAN
25	44	54.3	1204	1	NOS3_BOVIN
26	44	54.3	1204	1	NOS3_PIG
27	44	54.3	1464	1	CAI3_MOUSE
28	44	54.3	1464	1	CAI3_BOVIN
29	43	53.1	1049	1	HB2A_RAT
30	43	53.1	252	1	CRB1_BOVIN
31	43	53.1	252	1	HB2F_MOUSE
32	43	53.1	263	1	HB2B_RAT
33	43	53.1	263	1	HB2B_MOUSE

34	43	53.1	263	1	HB2K_MOUSE	P06343 mus musculus
35	43	53.1	263	1	HB2S_MOUSE	P06345 mus musculus
36	43	53.1	263	1	HB2U_MOUSE	P06344 mus musculus
37	43	53.1	265	1	HB2D_MOUSE	P14483 mus musculus
38	43	53.1	265	1	HB2D_MOUSE	P01921 mus musculus
39	43	53.1	268	1	HB2X_HUMAN	P06342 mus musculus
40	43	53.1	360	1	OC3A_HUMAN	P05338 homo sapien
41	43	53.1	379	1	V671_CHLMU	Q01860 homo sapien
42	43	53.1	423	1	TBX2_CAEEL	Q9PK02 chlamydia m
43	43	53.1	736	1	DVL2_MOUSE	Q19691 caenorhabdit
44	43	53.1	860	1	ELT_MOUSE	O60838 mus musculus
45	43	53.1	860	1	ELT_MOUSE	P54320 mus musculus

## ALIGNMENTS

## RESULT 1

CLIP\_HUMAN STANDARD: PRT: 199 AA.

ID CLIP\_HUMAN

AC Q9NS71; 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE CALL protein.

GN CALL

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RP [1]

RF SEQUENCE FROM N.A.

RC TISSUE-Stomach;

RX MEDLINE-20296773; PubMed-10835488;

RA Yoshikawa Y, Mukai H, Hino F, Asada K, Kato I;

RT Jpn. J. Cancer Res. 91:459-463(2000).

RL "Isolation of two novel genes, down-regulated in gastric cancer."

CC -1- TISSUE SPECIFICITY: Expressed in stomach. No expression is

CC detected in cancer tissue or gastric cancer cell lines.

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CC DR EMBL; AB039886; BAA92433.1; -

DR MIM: 606402; -

SQ SEQUENCE 199 AA; 21999 MW; C099B8B9A1338D7A CRC64;

Query Match 100.0%; Score 81; DB 1; Length 199;

Best local similarity 100.0%; Pred. No. 0.00026;

Matches 14; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGPGGPPK 14

Db 118 KKLQKGGPGGPPK 131

## RESULT 2

CLIP\_MOUSE STANDARD: PRT: 184 AA.

ID CLIP\_MOUSE

AC Q9CR36; Q9D7K7; Q9CT25;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE CALL protein homology.

GN CALL

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

RA MEDLINE=86176773; PubMed=3008099;  
RX Beckendorf C, Spalk H, Barbiero A.P., van de Putte P.;  
RT "Structure of the *uvrB* gene of *Escherichia coli*. Homology with other  
RL DNA repair enzymes and characterization of the *uvrB* mutation.";  
RN Nucleic Acids Res. 14:2877-2890(1986).  
[2]  
RA SEQUENCE FROM N.A.  
RX MEDLINE=86176755; PubMed=3515321;  
RA Atikan E., Kulkarni M.S., Thomas D.C., Sancar A.;  
RT "Sequences of the *E. coli* *uvrB* gene and protein.";  
RL Nucleic Acids Res. 14:2637-2650(1986).  
[3]  
RN SEQUENCE FROM N.A.  
RX STRAIN-K12 / MG1655;  
RA MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Verdes J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of *Escherichia coli* K-12.";  
RL Science 277:1453-1474(1997).  
[4]  
RN SEQUENCE FROM N.A.  
RX STRAIN-O157:H7 / EDL933 / ATCC 700927;  
RX MEDLINE=21074935; PubMed=11206551;  
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";  
RL Nature 409:529-533(2001).  
[5]  
RN SEQUENCE FROM N.A.  
RX STRAIN-O157:H7 / RIMD 0509952;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayashi T., Matsuo K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasaki C., Ogatawara N., Yasunaga T.,  
RA Kubota S., Shibata T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*  
RT O157:H7 and genomic comparison with a laboratory strain K-12.";  
RL DNA Res. 8:11-22(2001).  
[6]  
RN SEQUENCE OF 168-673 FROM N.A.  
RX STRAIN-K12;  
RX MEDLINE=97061202; PubMed=8905232;  
RA Oshima T., Alpa H., Baba T., Fujita K., Hayashi K., Honjo A.,  
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K.,  
RA Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S.,  
RA Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,  
RA Nishimoto K., Wada C., Yamamoto Y., Yano M., Horiiuchi T.,  
RA "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome  
RT corresponding to the 12.7-28.0 min region on the linkage map.";  
RL DNA Res. 3:137-155(1996).  
[7]  
RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 619-673.  
RX MEDLINE=20123894; PubMed=10631326;  
RA Sohi M., Alexandrovich A., Moolenaar G., Vlasie R., Goosen N.,  
RA Venede X., Fontecilla-Camps J.C., Champness J., Sanderson M.R.;  
RT "Crystal structure of *Escherichia coli* *UvrB* C-terminal domain, and a  
RL model for *UvrB*-*uvrC* interaction.";  
RN FEBS Lett. 465:161-164(2000).  
[8]  
RN STRUCTURE BY NMR OF 619-673  
RX MEDLINE=99297571; PubMed=10771161;  
RA Alexandrovich A., Sanderson M.R., Moolenaar G.F., Goosen N.,  
RA Lane A.N.;  
RT "NMR assignments and secondary structure of the *UvrB* binding domain of  
RL FEBS Lett. 451:181-185(1999).  
[9]

```

CC -1- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
CC CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS
CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRB STIMULATES
CC THE ATPase ACTIVITY OF UVRB IN THE PRESENCE OF UV-IRRADIATED
CC DOUBLE-STRANDED DNA. IT ALSO ENHANCES THE ABILITY OF UVRB TO BIND
CC TO UV-IRRADIATED DUPLEX DNA.
CC -1- SUBUNIT: CONSISTS OF THREE SUBUNITS: UVRB, UVRB AND UVRB.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE UVRB FAMILY.
CC -1- SIMILARITY: CONTAINS 1 UVR DOMAIN.
-----
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-----
DR EMBL: X03722; CA27357.1; -
DR EMBL: X03678; CA27314.1; -
DR EMBL: AE000180; AAC73866.1; -
DR EMBL: AE005259; AAG55150.1; -
DR EMBL: AP002553; BAB34280.1; -
DR EMBL: D90716; BAA35437.1; -
DR PIR: A23765; BVCCUB.
DR PDB: 100J; 10-NOV-00.
DR PDB: 1ES2; 12-JUL-01.
DR ECO2DBASE: C080.0; 6TH EDITION.
DR Ecogene: EG1062; UVRB.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR004807; UVRB.
DR InterPro: IPR001943; UVRB/C.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF02151; UVR; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
DR TIGRFAMs: TIGR00631; uvrB; 1.
DR PROSITE: PS0151; UVR; 1.
DR SOS response: Excision nuclease; DNA repair; ATP-binding;
KW 3D-structure; Complete proteome.
KM NP_BIND 39 46 ATP (POTENTIAL).
FT DOMAIN 633 668 UVR.
FT SITE 630 631 CLEAVAGE.
FT CONFLICT 477 477 H -> R (IN REF. 2).
SQ SEQUENCE 673 AA; 76226 MW; 2F172045344FDAD7 CRC64;
OY 3 LOGKGPGCPPP 13
OY 1:1111111
DB 313 LSGRGPCEPPP 323

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RX MEDLINE-21534947; PubMed-11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Cornerton P.,
RA Croft A., Hamlin P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
CC -1- FUNCTION: The ABC excision nuclease is a DNA repair enzyme that
CC catalyzes the excision reaction of UV-damaged nucleotide segments
CC producing oligomers having the modified base(s). UVRB stimulates
CC the ATPase activity of UVRB in the presence of UV-irradiated
CC double-stranded DNA. It also enhances the ability of UVRB to bind
CC to UV-irradiated duplex DNA (By similarity).
CC -1- SUBUNIT: Consists of three subunits: uvrA, uvrB and uvrC.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE UVRB FAMILY.
-----
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-----
DR EMBL: AL627268; CAD05246.1; -
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR004807; UVRB.
DR InterPro: IPR001943; UVRB/C.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF02151; UVR; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
DR TIGRFAMs: TIGR00631; uvrB; 1.
DR PROSITE: PS0151; UVR; 1.
DR SOS response: Excision nuclease; DNA repair; ATP-binding;
KW Complete proteome.
KM NP_BIND 39 46 ATP (POTENTIAL).
FT DOMAIN 633 668 UVR.
FT SITE 630 631 CLEAVAGE.
FT CONFLICT 477 477 H -> R (IN REF. 2).
SQ SEQUENCE 673 AA; 76206 MW; 0618153EADAC890 CRC64;
OY 3 LOGKGPGCPPP 13
OY 1:1111111
DB 313 LSGRGPCEPPP 323

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RESULT 4
UVRB_SALTY STANDARD: PRT: 673 AA.
AC 082889;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exonuclease ABC subunit B.
GN UVRB OR STY0831.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN NCBI_TaxID=601;
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;

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RESULT 5
UVRB_SALTY STANDARD: PRT: 673 AA.
AC 082004;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exonuclease ABC subunit B.
GN UVRB OR STY0798.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN NCBI_TaxID=602;
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SCS1412 / ATCC 700720;
RC MEDLINE-21534948; PubMed-11677609;
RX MEDLINE-21534948; PubMed-11677609;

```

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewel N., Mullaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 RT LT2.";  
 RL Nature 413:852-856(2001).  
 CC -1- FUNCTION: The ABC excision nuclease is a DNA repair enzyme that  
 CC catalyzes the excision reaction of UV-damaged nucleotide segments  
 CC producing oligomers having the modified base(S). UVRB stimulates  
 CC the ATPase activity of UVRa in the presence of UV-irradiated  
 CC double-stranded DNA. It also enhances the ability of UVRa to bind  
 CC to UV-irradiated duplex DNA (by similarity).  
 CC -1- SUBUNIT: Consists of three subunits; UVRa, UVRB and UVRC.  
 CC -1- SIMILARITY: BELONGS TO THE UVRB FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AE008733; AAL19735.1; -  
 DR StGene; SG27272; UVRB.  
 DR InterPro: IPR001410; DEAD.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR InterPro: IPR004807; UVRB.  
 DR InterPro: IPR001943; UVRB/C.  
 DR Pfam: PF00271; helicase\_C; 1.  
 DR Pfam: PF02151; UVR; 1.  
 DR SMART: SM00487; DEXDC; 1.  
 DR SMART: SM00490; HELIC\_C; 1.  
 DR TIGRFAMs: TIGR00631; uvrB; 1.  
 DR PROSITE: PS50151; UVR; 1.  
 DR SOS response; Excision nuclease; DNA repair; ATP-binding;  
 KM Complete proteome.  
 KW NP-BIND 39 ATP (POTENTIAL).  
 FT DOMAIN 633 668 UVR.  
 FT SEQUENCE 673 AA; 76134 MW; 054E205FADA6C890 CRC64;  
 SQ  
 Query Match 61.7%; Score 50; DB 1; Length 673;  
 Best Local Similarity 72.7%; Pred. No. 11;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 LOGKGCGGPP 13  
 DB 313 LSGRGCGEPP 323  
 RESULT 6  
 CG48\_HUMAN STANDARD; PRT; 532 AA.  
 AC 09Y5J1: 09H4N6;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical WD-repeat protein CG1-48.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20272150; PubMed=10810093;  
 RA Lai C.-H., Chou C.-Y., Chang L.-Y., Lin C.-S., Lin W.-C.;  
 RT "Identification of novel human genes evolutionarily conserved in  
 RT *Caenorhabditis elegans* by comparative proteomics.";  
 RL Genome Res. 10:703-713(2000).  
 RN [2]

RP SEQUENCE OF 138-532 FROM N.A.  
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,  
 RA Margolin J.F.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TFR-ASP DOMAINS).  
 CC -1- SIMILARITY: BELONGS TO THE CG1-48 FAMILY OF WD-REPEAT PROTEINS.  
 CC -----  
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 CC -----  
 DR EMBL: AF151806; AAD34043.1; -  
 DR EMBL: AY007138; AAG01999.1; ALT\_INT.  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40; 8.  
 DR SMART: SM00320; WD40; 7.  
 DR PROSITE: PS00678; WD\_REPEATS\_1; 1.  
 DR PROSITE: PS50082; WD\_REPEATS\_2; 1.  
 DR PROSITE: PS50294; WD\_REPEATS\_REGION; 1.  
 DR Hypothetical protein; Repeat; WD repeat.  
 FT REPEAT 225 264 WD 1.  
 FT REPEAT 269 309 WD 2.  
 FT REPEAT 315 356 WD 3.  
 FT REPEAT 357 395 WD 4.  
 FT REPEAT 397 438 WD 5.  
 FT REPEAT 447 488 WD 6.  
 FT REPEAT 519 532 WD 6.  
 FT SEQUENCE 532 AA; 59103 MW; 2DA86FDF5DF7A1 CAC64;  
 SQ  
 Query Match 59.3%; Score 48; DB 1; Length 532;  
 Best Local Similarity 80.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 GKGCGGPPK 14  
 DB 8 GAGCGGPPK 17  
 RESULT 7  
 UVRB\_XYLFA STANDARD; PRT; 669 AA.  
 ID UVRB\_XYLFA  
 AC 09PER1;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Excinuclease ABC subunit B.  
 GN UVRB OR XP0967.  
 OS Xylella fastidiosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
 OC Xylella.  
 OC NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=9a5c;  
 RX MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvaranga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,  
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,  
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Fetto J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Fromme M., Furian L.R.,  
 RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhani A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,  
 RA Quaglio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,  
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi M.F., Verjovski-Almeida S., Vettore A.L.,  
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,  
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*."  
 RL Nature 406:151-159(2000).  
 CC -1- FUNCTION: The ABC excision nuclease is a DNA repair enzyme that  
 CC catalyzes the excision reaction of UV-damaged nucleotide segments  
 CC producing oligomers having the modified base(s). UVRB stimulates  
 CC the ATPase activity of UVRA in the presence of UV-irradiated  
 CC double-stranded DNA. It also enhances the ability of UVRA to bind  
 CC to UV-irradiated duplex DNA (by similarity).  
 CC -1- SUBUNIT: Consists of three subunits; uvrA, uvrB and uvrC.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
 CC -1- SIMILARITY: BELONGS TO THE UVRB FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE UVRB FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE UVRB FAMILY.  
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 CC -----  
 CC EMBL: AE003935; AAF8377.1; -  
 DR HSSP: P56981; 1D9X.  
 DR InterPro: IPR001410; DEAD.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR InterPro: IPR004807; UVRB.  
 DR InterPro: IPR001943; UVRB/EC.  
 DR Pfam: PF00271; Helicase\_C; 1.  
 DR Pfam: PF02151; UVR; 1.  
 DR SMART: SM00487; DEHC; 1.  
 DR SMART: SM00490; HELIC; 1.  
 DR TIGRfams: TIGR00631; uvrB; 1.  
 DR PROSITE: PS50151; UVR; 1.  
 KM SOS response: Excision nuclease; DNA repair; ATP-binding;  
 KM Complete proteome.  
 FT NP\_BIND 39 46 ATP (POTENTIAL).  
 FT DOMAIN 631 666 UVR.  
 SQ SEQUENCE 669 AA; 75557 MW; 26BA460383A7125E CRC64;  
 Query Match 58.0%; Score 47; DB 1; Length 669;  
 Best Local Similarity 61.5%; Pred. No. 28;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 KKLQKGGPGGPP 13  
 Db 311 RHLTGKAPGPP 323  
 RESULT 8  
 MYCN\_SERCA STANDARD; PRT; 427 AA.  
 ID MYCN\_SERCA  
 AC P26014;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE N-myc proto-oncogene protein.  
 GN MYCN.  
 OS Serinus canaria (Canary).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Aves; Neognathae; Passeriformes; Passeroidea;  
 OC Fringillidae; Carduelinae; Serinus.

OX NCBI\_Taxid=9135;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9114534; PubMed=1996121;  
 RA Collum R.G., Clayton D.F., Alt F.W.;  
 RT "Structure and expression of canary myc family genes."  
 RL Mol. Cell. Biol. 11:1770-1776(1991).  
 CC -1- SUBUNIT: EFFICIENT DNA BINDING. REQUIRES DIMERIZATION WITH ANOTHER  
 CC BHLH PROTEIN. BINDS DNA AS AN HETERODIMER WITH MAX  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 CC TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: M64598; AAA49540.1; -  
 DR EMBL: M64251; AAA49540.1; JOINED.  
 DR PIR: A39695; A39695.  
 DR HSSP: P25912; 1HLO.  
 DR TRANSFAC: T02381; -  
 DR InterPro: IPR001092; HLH\_Basic.  
 DR InterPro: IPR002418; TF\_Myc.  
 DR Pfam: PF00010; HLH; 1.  
 DR Pfam: PF01056; MYC\_N-term; 1.  
 DR PRINTS: PRO0044; LEUZ1PPMYC.  
 DR SMART: SM00353; HLH; 1.  
 DR PROSITE: PS00038; HLH; 1.  
 DR PROSITE: PS00888; HLH-2; 1.  
 KM Nuclear protein: DNA-binding; Proto-oncogene; phosphorylation.  
 FT MOD\_RES 212 219  
 FT DOMAIN 212 242  
 FT DOMAIN 220 242  
 FT NP\_BIND 343 356  
 FT DOMAIN 357 397  
 FT DOMAIN 396 417  
 FT MOD\_RES 224 224  
 FT MOD\_RES 226 226  
 FT MOD\_RES 226 226  
 SQ SEQUENCE 427 AA; 47140 MW; 6631FE6B15AE54B CRC64;  
 Query Match 56.8%; Score 46; DB 1; Length 427;  
 Best Local Similarity 61.5%; Pred. No. 25;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 KKLQKGGPGGPP 13  
 Db 144 EKLQKTPAPPP 156  
 RESULT 9  
 DYNL\_CAEEL STANDARD; PRT; 830 AA.  
 ID DYNL\_CAEEL  
 AC P39055; Q93176; Q950Y9;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dynamid (EC 3.6.1.50).  
 GN DYN-1 OR CO2C6.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Rhabditidae; Caenorhabditis.  
 OC NCBI\_Taxid=6239;  
 OX [1]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RP STRAIN=Bristol N2;  
 RX MEDLINE=97439883; PubMed=9294229;  
 RA Clark S.G., Shurland D.L., Meyerowitz E.M., Bargmann C.I.,  
 RA van der Bliek A.M.;

"A dynamin GTPase mutation causes a rapid and reversible temperature-inducible locomotion defect in *C. elegans*.";  
Proc. Natl. Acad. Sci. U.S.A. 94:10438-10443(1997).  
[2]  
REVIEWS TO C-TERMINUS.  
RA van der Bliek A.M.;  
RN Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).  
RC STRAIN-Bristol N2;  
RA Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: MICROTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN INVOLVED  
CC IN PRODUCING MICROTUBULE BUNDLES AND ABLE TO BIND AND HYDROLYZE  
CC GTP. MOST PROBABLY INVOLVED IN VESICULAR TRAFFICKING PROCESSES, IN  
CC PARTICULAR ENDOCYTOSIS.  
CC -1- CATALYTIC ACTIVITY: GTP + H<sub>2</sub>O = GDP + phosphate.  
CC -1- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED.  
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a (shown here) and b; may be  
CC produced by alternative splicing.  
CC -1- SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.  
CC -----  
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CC -----  
DR EMBL: L29031; AAB7228.2; -  
DR EMBL: Z79596; CAB01857.1; -  
DR EMBL: Z79596; CAC42251.1; -  
DR WormPep: C02C6.1a; CE07833.  
DR WormPep: C02C6.1b; CE07832.  
DR HSP: O05193; 2DYN  
DR InterPro: IPR001401; Dynamn.  
DR InterPro: IPR000375; Dynamn\_central.  
DR InterPro: IPR001310; GED.  
DR InterPro: IPR001849; PH.  
DR Pfam: PF00169; PH; 1.  
DR Pfam: PF00350; dynamn\_1.  
DR Pfam: PF01031; dynamn\_2; 1.  
DR Pfam: PF02212; GED; 1.  
DR PRINTS: PR00195; DYNAMIN.  
DR SMART: SM00053; DINC; 1.  
DR SMART: SM00302; GED; 1.  
DR SMART: SM00233; PH; 1.  
DR PROSITE: PS00410; DYNAMIN; 1.  
DR PROSITE: PS00003; PH DOMAIN; 1.  
KW Hydrolyase; Motor protein; GTP-binding; Microtubules; Multigene family;  
KW Endocytosis; Alternative splicing.  
FT NP\_BIND 40 47 GTP (BY SIMILARITY).  
FT NP\_BIND 138 142 GTP (BY SIMILARITY).  
FT NP\_BIND 207 210 GTP (BY SIMILARITY).  
FT DOMAIN 519 624 PH.  
FT VARSPLIC 817 830 PGSGPPNMAPPR -> VTPNSGAELIPARQVKKRP  
FT CONFLICT 734 734 (IN ISOFORM B).  
FT CONFLICT 734 734 R -> P (IN REF. 1).  
SQ SEQUENCE 830 AA; 93407 MW; FF681250E51AB8A5 CRC64;  
Query Match 56.8%; Score 46; DB 1; Length 830;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GPGGPP 13  
Db 818 GPGGPP 824

RESULT 10  
DPD\_MESAU

ID DPD\_MESAU STANDARD; PRT: 1103 AA.  
AC P97283; P97284;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE DNA polymerase delta catalytic subunit (EC 2.7.7.7).  
GN POLD1.  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxId=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Liu Z., Mishra N.C.;  
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: POSSIBLE TWO ENZYMAIC ACTIVITIES: DNA SYNTHESIS  
CC (POLYMERASE) AND AN EXONUCLEOLYTIC ACTIVITY THAT DEGRADES SINGLE  
CC STRANDED DNA IN THE 3' TO 5' DIRECTION. REQUIRED WITH ITS  
CC ACCESSORY PROTEINS (PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) AND  
CC REPLICATION FACTOR C (RFC) OR ACTIVATOR 1) FOR LEADING STRAND  
CC SYNTHESIS. ALSO INVOLVED IN COMPLETING OKAZAKI FRAGMENTS INITIATED  
CC BY THE DNA POLYMERASE ALPHA/PRIMASE COMPLEX (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate  
CC + (DNA)(N)  
CC -1- SUBUNIT: HETEROTETRAMER COMPOSED OF SUBUNITS OF 125 kDa, 50 kDa,  
CC 66 kDa and 12 kDa. THE 125 kDa SUBUNIT CONTAINS THE POLYMERASE  
CC ACTIVE SITE AND MOST LIKELY THE ACTIVE SITE FOR THE 3'-5'  
CC EXONUCLEASE ACTIVITY (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:  
CC ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR  
CC DIFFERENT REACTIONS OF DNA SYNTHESIS.  
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.  
CC -----  
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CC -----  
DR EMBL: U83704; AAB47254.1; -  
DR EMBL: U83705; AAB47255.1; -  
DR InterPro: IPR002064; DNA\_POL\_B.  
DR InterPro: IPR004578; POL2.  
DR Pfam: PF00136; DNA\_POL\_B; 1.  
DR Pfam: PF03104; DNA\_POL\_B\_exo; 1.  
DR PRINTS: PR00106; DNAPOLB.  
DR SMART: SM00486; POLBc; 1.  
DR TIGRFAMS: TIGR00592; pol2; 1.  
DR PROSITE: PS00116; DNA\_POLYMERASE\_B; 1.  
KW DNA-transferase; DNA-directed DNA polymerase; DNA replication;  
KW DNA-binding; Hydrolyase; Exonuclease; Zinc-finger; Nuclear protein.  
FT DOMAIN 4 19 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT ZN\_FING 1008 1025 C4-TYPE (POTENTIAL).  
FT ZN\_FING 1054 1072 C4-TYPE (POTENTIAL).  
FT VARIANT 64 64 MISSING (IN DELTA').  
FT VARIANT 386 386 P -> S (IN DELTA').  
SQ SEQUENCE 1103 AA; 123465 MW; 34AB5BF72DE53011 CRC64;  
Query Match 56.8%; Score 46; DB 1; Length 1103;  
Best Local Similarity 57.1%; Pred. No. 62;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKLGGKPGGPPK 14  
Db 4 KRLGGKPGGPPK 17

RESULT 11  
DPD\_MOUSE

ID DPOD\_MOUSE STANDARD; PRT: 1105 AA.  
 AC P52431; 054883;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE DNA polymerase delta catalytic subunit (EC 2.7.7.7).  
 GN POLDI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BA16/c;  
 RA MEDLINE=94085777; PubMed=8262377;  
 RT Cullmann G., Hindges R., Borchert T.V., Hubscher U.;  
 RT "Cloning of a mouse cDNA encoding DNA polymerase delta: refinement of  
 RT the homology boxes.";  
 RL Gene 134:191-200(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Svj;  
 RA Goldsby R.E., Singh M., Preston B.D.;  
 RT Mamm. Genome 9:92-93(1998).  
 RL -1- FUNCTION: POSSESSES TWO ENZYMAIC ACTIVITIES: DNA SYNTHESIS  
 (POLYMERASE) AND AN EXONUCLEOTIC ACTIVITY THAT DEGRADES SINGLE  
 ACCESORY PROTEINS (PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) AND  
 REPLICATION FACTOR C (RFC) OR ACTIVATOR 1) FOR LEADING STRAND  
 SYNTHESIS. ALSO INVOLVED IN COMPLETING OKAZAKI FRAGMENTS INITIATED  
 BY THE DNA POLYMERASE ALPHA/PRIMASE COMPLEX.  
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
 + [DNA](N).  
 CC -1- SUBUNIT: HETEROTETRAMER COMPOSED OF SUBUNITS OF 125 kDa, 50 kDa,  
 CC 66 kDa and 12 kDa. The 125 kDa SUBUNIT CONTAINS THE POLYMERASE  
 CC ACTIVE SITE AND MOST LIKELY THE ACTIVE SITE FOR THE 3'-5'  
 CC EXONUCLEIC ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:  
 CC ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR  
 CC DIFFERENT REACTIONS OF DNA SYNTHESIS.  
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.  
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 CC -----  
 DR EMBL: Z21848; CA79895.1;  
 DR EMBL: AF024570; AAB99910.1;  
 DR MGD: MG1:97741; PolDI.  
 DR InterPro: IPR002064; DNA\_POL\_B.  
 DR InterPro: IPR004578; Pol2.  
 DR Pfam: PF00136; DNA\_POL\_B.1.  
 DR Pfam: PF03104; DNA\_POL\_B-exo.1.  
 DR PRINTS: PRO0106; DNAPOLB.  
 DR SMART: SM00486; POLBc.1.  
 DR TIGRFS: TIGR00592; Pol2.1.  
 DR PROSITE: PS00116; DNA\_POLYMERASE\_B.1.  
 DR TRANSFERASE: DNA-directed DNA polymerase; DNA replication;  
 KW DNA-binding; Hydrolyase; Exonuclease; Zinc-finger; Nuclear protein;  
 KW DNA-binding; Hydrolyase; Exonuclease; Zinc-finger; Nuclear protein;  
 FT DOMAIN 4 19  
 FT 2N-FING 1010 1027 C4-TYPE (POTENTIAL).  
 FT 2N-FING 1056 1074 RPL -> GPP (IN REF. 2).  
 FT CONFLICT 112 114 E -> K (IN REF. 2).  
 FT CONFLICT 793 793 L -> F (IN REF. 2).  
 FT CONFLICT 1000 1000 S -> Y (IN REF. 2).  
 FT CONFLICT 1035 1035

FT CONFLICT 1045 1052 LEEFRL -> WKNSLRF (IN REF. 2).  
 SQ SEQUENCE 1105 AA: 123783 MW: 5355667620400564 CRC64;  
 Query Match  
 Best Local Similarity 57.1%; Pred. No. 62;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 OY 1 KRIQKGGGPPPK 14  
 Db 4 KRQGGGPPPKR 17  
 RESULT 12  
 GUN1\_HUMAN STANDARD; PRT: 402 AA.  
 ID GUN1\_HUMAN  
 AC P56680;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Endoglucanase I (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase).  
 GN Cel7B.  
 OS Humicola insolens.  
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.  
 OC NCBI\_TaxID=34413;  
 RN [1]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT S37W/P39W.  
 RX MEDLINE=97475713; PubMed=9335168;  
 RA Davies G.J., Ducros V., Lewis R.J., Borchert T.V., Schuelein M.;  
 RT "Oligosaccharide specificity of a family 7 endoglucanase: insertion  
 RT of potential sugar-binding subsites.";  
 RL J. Biochem. 57:91-100(1997).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MUTAGENESIS.  
 RX MEDLINE=98437137; PubMed=9761741;  
 RA Mackenzie L.F., Sulzenbacher G., Dwyer C., Jones T.A., Woeldike H.F.,  
 RA Schuelein M., Wilthers S.G., Davies G.J.;  
 RT "Crystal structure of the family 7 endoglucanase I (Cel7B) from  
 RT Humicola insolens at 2.2 A resolution and identification of the  
 RT catalytic nucleophile by trapping of the covalent glycosyl-enzyme  
 RT intermediate.";  
 RL Biochem. J. 335:409-416(1998).  
 CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE  
 CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:  
 CC (1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GUCCOSIDIC BONDS;  
 CC (2) EXOCELLULOBIODRASES WHICH CUT THE DISACCHARIDE CELLULOSE  
 CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;  
 CC (3) BETA-1,4-GUCCOSIDASES WHICH HYDROLYZE THE CELLULOSE AND OTHER  
 CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic  
 CC linkages in cellulose.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL  
 CC HYDROLASES).  
 DR PDB: 1A39; 02-MAR-99.  
 DR PDB: 2A39; 16-FEB-99.  
 DR InterPro: IPR001722; GH\_7.  
 DR Pfam: PF00840; Glyco\_Hydro\_7.1.  
 DR Prodom: PD186135; GH\_7.1.  
 KW Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein;  
 KW 3D-structure.  
 FT MOD\_RES 1 1  
 FT ACT\_SITE 197 197 PYROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 202 202 PROTON DONOR.  
 FT DISULFID 18 24  
 FT DISULFID 51 73  
 FT DISULFID 63 69  
 FT DISULFID 140 365  
 FT DISULFID 172 195  
 FT DISULFID 176 194  
 FT DISULFID 215 234  
 FT DISULFID 223 228  
 FT DISULFID 233 315





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FT DOMAIN 8 101 FCH.
FT DOMAIN 247 336 SH2.
FT DOMAIN 348 609 PROTEIN KINASE.
FT NP_BIND 354 362 ATP (BY SIMILARITY).
FT BINDING 377 377 ATP (BY SIMILARITY).
FT ACT_SITE 470 470 BY SIMILARITY.
FT MOD_RES 500 500 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 609 AA: 68769 MW: 5304919757CF73A3 CRC64:

Query Match 55.6% Score 45; DB 1; Length 609;
Best Local Similarity 66.7% Pred. No. 48;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 KLOGKGGCGPP 13
Db 174 KLEQLGGEPP 185

RESULT 15
FES_FELCA STANDARD; PRT; 820 AA.
ID FES_FELCA
AC P14238;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112) (C-FES).
GN FES OR FPS.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxId=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-8718954; PubMed=353615;
RA Roebroek A.J.M., Schalken J.A., Onnekink C., Bloemers H.P.J.,
RA van de Ven W.J.M.;
RT "Structure of the feline c-fes/fps proto-oncogene: genesis of a
RT retroviral oncogene.";
RL J. Virol. 61:2009-2016(1987).
CC -i CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -i SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FES/FPS
CC SUBFAMILY.
CC -i SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -i SIMILARITY: CONTAINS 1 FCH DOMAIN.
CC
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CC
DR EMBL: M16705; AAA30808.1; -;
DR EMBL: M16666; AAA30808.1; JOINED.
DR EMBL: M16667; AAA30808.1; JOINED.
DR EMBL: M16668; AAA30808.1; JOINED.
DR EMBL: M16669; AAA30808.1; JOINED.
DR EMBL: M16670; AAA30808.1; JOINED.
DR EMBL: M16671; AAA30808.1; JOINED.
DR EMBL: M16706; AAA30808.1; JOINED.
DR EMBL: M16672; AAA30808.1; JOINED.
DR EMBL: M16673; AAA30808.1; JOINED.
DR EMBL: M16674; AAA30808.1; JOINED.
DR EMBL: M16698; AAA30808.1; JOINED.
DR EMBL: M16700; AAA30808.1; JOINED.
DR EMBL: M16701; AAA30808.1; JOINED.
DR EMBL: M16702; AAA30808.1; JOINED.
DR EMBL: M16704; AAA30808.1; JOINED.
DR PIR: A27824; TVCTFF.
DR HSSP: P11362; IFGK.
DR InterPro: IPR001060; Cdc15_Fes_CIP4.

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DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00611; FCH; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR PRODOM: PD000093; SH2; 1.
DR SMART: SM00055; FCH; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS0133; FCH; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR TRANSFERASE: T550001; SH2; 1.
KW Phosphorylation; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
KW Phosphorylation; SH2 domain.
FT DOMAIN 1 94 FCH.
FT DOMAIN 458 547 SH2.
FT DOMAIN 559 820 PROTEIN KINASE.
FT NP_BIND 565 573 ATP (BY SIMILARITY).
FT BINDING 588 588 ATP (BY SIMILARITY).
FT ACT_SITE 681 681 BY SIMILARITY.
FT MOD_RES 711 711 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 820 AA: 92974 MW: F3A52B750236834E CRC64:

Query Match 55.6% Score 45; DB 1; Length 820;
Best Local Similarity 66.7% Pred. No. 64;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 KLOGKGGCGPP 13
Db 385 KLEQLGGEPP 396

```

Search completed: April 11, 2003, 16:11:52  
 Job time : 2.98885 secs



ZIP: 21702-5012







DB 637 LITKDDICPNHYSBGRAGSCPNYKSIYVKTPEISLNGNEHLSNPLNLTGTLNKKYM 696  
QY 150 AEEM-----QEASLPFYSGTCTTSLWMLVDSFC 179  
DB 697 KSNVELPEYKSGLANHGH-----DLSSVC 719

RESULT 12  
US-08-241-465B-19  
; Sequence 19, Application US/08241465B  
; Patent No. 5719125  
; GENERAL INFORMATION:  
; APPLICANT: FUJIO SUZUKI  
; APPLICANT: FUJIO HIRAKI  
; APPLICANT: KAZUHIRO TAKAHASHI  
; APPLICANT: JUNKO SUZUKI  
; APPLICANT: JUN KONDO  
; APPLICANT: ATSUKO KOHARA  
; APPLICANT: AKIKO MORI  
; APPLICANT: EI YAMADA  
; TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; COUNTRY: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,465B  
; FILING DATE: May 11, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-8850  
; TELEFAX:  
; ;  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 334 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-241-465B-19

Query Match 7.2% Score 72; DB 1; Length 334;  
Best Local Similarity 19.0%; Pred. No. 4.3;  
Matches 27; Conservative 27; Mismatches 76; Indels 12; Gaps 3;

QY 21 NYNIDVNDNNNGSGQSVSVNNEHNVANVNNNGWDSMNSIMDYNGFATRLFPCKT 80  
DB 76 HYTWSINGKLQDG-----SMEIDAGNNLETFKMGSGAEALAVNDPONGITGIFAGGEK 130  
QY 81 CIVHKMKKEVMPISQSLDALVKEKKLQK-GPGGPPPKGLMYSVNPKNVDDLKSGKNIA 139  
DB 131 CYTKAQQVKARIPVGAATKQSSISKLEKIMPVYKEENSLIWAVDQPKDMSFLSKVL 190  
QY 140 NMCRGI-----PTYMAEEMOE 155  
DB 191 ELGGDLPIFWLKPTYPKEIORE 212

RESULT 13  
US-08-241-465B-20  
; Sequence 20, Application US/08241465B

; Patent No. 5719125  
; GENERAL INFORMATION:  
; APPLICANT: FUJIO SUZUKI  
; APPLICANT: FUJIO HIRAKI  
; APPLICANT: KAZUHIRO TAKAHASHI  
; APPLICANT: JUNKO SUZUKI  
; APPLICANT: JUN KONDO  
; APPLICANT: ATSUKO KOHARA  
; APPLICANT: AKIKO MORI  
; APPLICANT: EI YAMADA  
; TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; COUNTRY: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,465B  
; FILING DATE: May 11, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-8850  
; TELEFAX:  
; ;  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 334 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-241-465B-20

Query Match 7.2% Score 72; DB 1; Length 334;  
Best Local Similarity 19.0%; Pred. No. 4.3;  
Matches 27; Conservative 27; Mismatches 76; Indels 12; Gaps 3;

QY 21 NYNIDVNDNNNGSGQSVSVNNEHNVANVNNNGWDSMNSIMDYNGFATRLFPCKT 80  
DB 76 HYTWSINGKLQDG-----SMEIDAGNNLETFKMGSGAEALAVNDPONGITGIFAGGEK 130  
QY 81 CIVHKMKKEVMPISQSLDALVKEKKLQK-GPGGPPPKGLMYSVNPKNVDDLKSGKNIA 139  
DB 131 CYTKAQQVKARIPVGAATKQSSISKLEKIMPVYKEENSLIWAVDQPKDMSFLSKVL 190  
QY 140 NMCRGI-----PTYMAEEMOE 155  
DB 191 ELGGDLPIFWLKPTYPKEIORE 212

RESULT 14  
US-08-227-108-16  
; Sequence 16, Application US/08227108  
; Patent No. 5807726  
; GENERAL INFORMATION:  
; APPLICANT: Blanchard, Claire  
; APPLICANT: Junien, Jean-Louis  
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Penile & Edmonds  
; STREET: 1155 Avenue of the Americas

```

; ATTORNEY/AGENT INFORMATION:
; NAME : Crissey, Todd M.
; REGISTRATION NUMBER: 37,807
; REFERENCE/DOCKET NUMBER: 5072-DI-66-TWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 734 622-7530
; TELEFAX: 734 622-1553
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-073-674-16

Query Match          7.2%; Score 72; DB 2; Length 380;
Best Local Similarity 23.1%; Pred. No. 5.2;
Matches   39; Conservative   30; Mismatches   50; Indels   50; Gaps   11.

QY    22 YNIDVN----DDNNAGSGQSVSYNNEHN-----VANVDNN-----GWDNQ- 60
      ||::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Db    38 YLEVNRIPIYGKKNNGTGOPEV-VFLQHGLASATNMWISNLPNNSLAFTLADAGYDVL 96

QY    61 -NSIWDYNGCFEATRLLFOKKTCI-----VHKMKKEWPSTQSIDLAVK--EKKLQK 109
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    97 GNS---RGNTVARRMRLYSPDSVEFEWAFAFPDEMAKYDLPA--TIDFTYKKTGOKQLHYV 151

QY    110 GGCGPPPKG-LMYSVPNPKVDLS-----KFGKNIANMCRGIP 146
       |::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    152 GHSGGTIGIFTAFSTNPSLAKRIKFVALAPVAIVKYTKSLINKLRFPV 200

```



R:Wehner, E.P., Nao, L., and Schaefer, S. 1993.  
Mol. Gen. Genet. 237, 351-358.  
A:Title: Molecular structure and genetic regulation of SFA, a gene responsible for re



Mon Apr 14 14:01:20 2003

us-09-821-726a-13.rpt

A:Molecule type: mRNA  
 A:Residues: 1-718 <KLA>  
 A:Cross-references: EMBL:X69167; NID:9393375; PIDN:CAA48917.1; PID:9393376  
 R:Chen, T.; Buntling, M.; Karim, F.D.; Thummel, C.S.  
 Dev. Biol. 151, 176-191, 1992  
 A:Title: Isolation and characterization of five *Drosophila* genes that encode an ets-related protein  
 A:Reference number: S28819; MUID:92249640; PMID:1577186  
 A:Accession: S28819  
 A:Molecule type: mRNA  
 A:Residues: 551-708 <GHE>  
 A:Cross-references: EMBL:M88472; NID:9157191; PIDN:AAC34200.1; PID:9157192  
 R:Chen, T.; Buntling, M.; Karim, F.D.; Thummel, C.S.  
 Dev. Biol. 151, 176-191, 1992  
 A:Title: Isolation and characterization of five *Drosophila* genes that encode an ets-related protein  
 A:Reference number: S28819; MUID:92249640; PMID:1577186  
 A:Accession: S28819  
 A:Molecule type: DNA  
 A:Residues: 540-561, 'R', 563-698 <PRI>  
 A:Cross-references: EMBL:M20408; NID:9157384; PIDN:AAA28521.1; PID:9157385  
 A:Note: the authors translated the codon AGA for residue 562 as Gln  
 A:Gene: Flybase:FBgn0003118  
 C:Genetics:  
 A:Gene: Flybase:FBgn0003118  
 A:Cross-references: Flybase:FBgn0003118  
 A:Introns: 645/3  
 A:Superfamily: pointed protein, splice form 2; ets DNA-binding domain homology; ets RII  
 C:Keywords: alternative splicing; DNA binding; nucleus; transcription factor  
 F:170-244/Domain: ets DNA-binding domain homology <ETS>  
 F:612-690/Domain: ets DNA-binding domain homology <ETS>

Query Match 9.2%; Score 91; DB 1; Length 718;  
 Best Local Similarity 27.1%; Pred. No. 1.6; Indels 44; Gaps 8;  
 Matches 38; Conservative 21; Mismatches 37

OY 15 LAPALANYNDVNDNNNGSGQSYSVNNEH---NVAANDNNGDWSNISTIDICNGF 70  
 DB 365 LPPAVOOSN---NENNTSSNTNNSSNNNNSSGSSNNSSNNNNNNNNNT---NEM 417  
 OY 71 AATRLFOKTCIVHKMKKVPSTIOSDALVKEKKIQGPGPGPPKGLMYSPNPKVDD 130  
 DB 418 AAAAIFQ-----HHLKEE--PGTON-----GNIGGIGGG-----SNSQNDPTD 453  
 OY 131 LSKFGKNIANMCRGIPTYMA 150  
 DB 454 LSSY-----GLPAHLA 464

RESULT 6  
 D71613  
 GAF domain protein (cyclic nt signal transduct.) PFB0510w - malaria parasite (Plasmodium falciparum)  
 C:Species: Plasmodium falciparum  
 C:Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000  
 C:Accession: D71613  
 R:Cardner, M.J.; Tettein, H.; Garucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.  
 Science 282, 1126-1132, 1998  
 A:Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.  
 A:Reference number: A71600; MUID:99021743; PMID:9804551  
 A:Accession: D71613  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1245 <GAR>  
 A:Cross-references: GB:AE001399; GB:AE001362; NID:93845200; PIDN:AAC71891.1; PID:9384520  
 A:Experimental source: clone 3D7  
 C:Genetics:  
 A:Gene: PFB0510w

Query Match 9.18; Score 90; DB 2; Length 1245;  
 Best Local Similarity 25.0%; Pred. No. 3.9; Indels 62; Gaps 7;  
 Matches 40; Conservative 15; Mismatches 43

OY 17 PALANYNDVND--DNNNAGSGQSYSVNNEHVAANDNNGDWSNISTIDICNGFPAIFR 74  
 DB 17 PALANYNDVND--DNNNAGSGQSYSVNNEHVAANDNNGDWSNISTIDICNGFPAIFR 74

DB 917 PNLTKNTKNNNDNIDNNN-----NNNNNNIDNNNNNGDNIYND--DLKRYLNTS 966  
 OY 75 LFOKKTCIVH-----KMKKEVPSIOSDALVKEKKIQGPGPGPPKGLM 120  
 DB 967 IFNKDLYVKHFVDILINKSLDEILIKMNYISERINSL-----LFHKG----- 1008  
 OY 121 YSNPKKVDLSKFGKNIANMCRGIPTYMAEOMQASLFP 160  
 DB 1009 -----MNLNDVTKL-----TMSNAYGCKCEFF 1030

RESULT 7  
 T18437  
 hypothetical protein C0405c - malaria parasite (Plasmodium falciparum)  
 C:Species: Plasmodium falciparum  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jun-2000  
 C:Accession: T18437  
 R:Lawson, D.; Bowman, S.; Barrell, B.  
 submitted to the EMBL Data Library, August 1997  
 A:Reference number: 218935  
 A:Accession: T18437  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-608 <LAN>  
 A:Cross-references: EMBL:298547; NID:e1325376; PID:e1325391; PIDN:CAB11116.1  
 A:Note: C0405c  
 C:Genetics:  
 A:Map position: 3  
 A:Gene: C0405c

Query Match 9.0%; Score 89; DB 2; Length 608;  
 Best Local Similarity 23.6%; Pred. No. 2;  
 Matches 52; Conservative 26; Mismatches 70; Indels 72; Gaps 11;

OY 19 LANVNDVNDNNNGSGQSYSVNNEHVAANDNNGDWSNISTIDICNGF 70  
 DB 396 ICHNN 104  
 OY 66 -----YGNFATRLFOKTCIVHKMKKVPSTIOSDALVKEKK 514  
 DB 455 KLVYIQSVREKKYINDVHEITVRLNTVKEFLKISVSEKLLDKKKRYFLGL 150  
 OY 105 -----KLGKPGPGPPKGLMYSPNPKVDDLSKFGKNIANMCRGIPTYMA 150  
 DB 515 KCTYHIDIDEPKIVFIAPNIEP-----SLN NIPDD--TLGKTIAR-CKEKNIPIVFA 564  
 OY 151 EEMQEKSLFPYSGTCYT---TSVLIVD-----ISFGGDPV 183  
 DB 565 LSKN-----LLGCKINRSOSIICIDNDSYIKCNDII 598

RESULT 8  
 T30918  
 hypothetical protein D1007.14 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
 C:Accession: T30918  
 R:Davidson, S.; Rohlfing, T.  
 submitted to the EMBL Data Library, August 1999  
 A:Reference number: The sequence of *C. elegans* cosmid D1007.  
 A:Accession: T30918  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-186 <DAV>  
 A:Cross-references: EMBL:AF003151; PIDN:AA854231.1  
 A:Experimental source: strain Bristol N2; clone D1007  
 C:Genetics:  
 A:Map position: 1  
 A:Introns: 15/2; 68/2; 87/2  
 A:Note: D1007.14

Query Match 8.9%; Score 88.5; DB 2; Length 186;  
 Best Local Similarity 24.0%; Pred. No. 0.52;

## RESULT 9

Query Match

## RESULT 10

Query Match

1

296

Query Match

Ресурси:





Mon Apr 14 14:01:26 2003

us-09-821-726a-13.rsp

GenCore version 5.1.4-p5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:33 : Search time 41.044 Seconds  
(without alignments)  
928.727 Million cell updates/sec

US-09-821-726a-13

Title: 994  
Perfect score: 1 MKFTVFGLGVLAPALA.....YTSVLMIVDISFGDTVEN 185

Sequence: BLOSUM62  
Scoring table: Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP-archaea:  
2: SP-bacteria:  
3: SP-fungi:  
4: SP-human:  
5: SP-invertebrate:  
6: SP-mammal:  
7: SP-mhc:  
8: SP-organelle:  
9: SP-phage:  
10: SP-plant:  
11: SP-rodent:  
12: SP-virus:  
13: SP-vertebrate:  
14: SP-unclassified:  
15: SP-bacteriophage:  
16: SP-archaeal:  
17: SP-archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245	24.6	191	11	09d077
2	195	19.6	184	11	09c056
3	98	9.9	568	5	09n138
4	97	9.8	588	5	0964f6
5	97	9.8	1208	5	097101
6	96.5	9.7	1844	5	097287
7	95.5	9.6	1318	5	0955p4
8	93.5	9.4	764	5	096234
9	93	9.2	586	5	0964f7
10	91.5	9.2	600	5	0964f5
11	91.5	9.2	600	5	095n13
12	91.5	9.2	628	5	08ssy0
13	90	9.1	604	5	0964f8
14	90	9.1	1245	5	08sx72
15	90	9.1	1245	5	096195
16					

17	89.5	9.0	1565	5	08t1m2
18	89	9.0	608	5	077331
19	88.5	8.9	186	5	001876
20	88	8.9	660	5	000885
21	88	8.9	3619	5	090573
22	87	8.8	798	5	08t200
23	87	8.8	1593	5	08t1f7
24	87	8.8	1650	5	077328
25	86.5	8.7	346	5	08ssv6
26	86	8.7	1060	5	077363
27	86	8.7	1258	5	08t1l7
28	86	8.7	2472	5	08t2m5
29	85	8.6	537	5	08t1k7
30	85	8.6	791	5	08t2u7
31	85	8.6	915	5	096n07
32	85	8.6	1064	5	025770
33	85	8.6	1256	5	023847
34	84.5	8.5	720	5	02bhn0
35	84.5	8.5	1855	5	09t7x5
36	84.5	8.5	2188	5	09t7x5
37	84.5	8.5	2188	5	096253
38	84.5	8.5	1817	5	096422
39	84	8.4	1979	5	096133
40	83.5	8.4	3275	16	08vkm3
41	83.5	8.4	3275	16	006304
42	83.5	8.4	3300	5	097239
43	83.5	8.4	3933	5	097239
44	83	8.4	212	5	08t1d8
45					

## ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	191 AA.
09d077	09d077		
AC	01-JUN-2001 (TREMUR)	17, Created	
DT	01-JUN-2001 (TREMUR)	17, Last sequence update	
DT	01-JUN-2001 (TREMUR)	17, Last annotation update	
DE	1190003M12R1K protein.		
GN	1190003M12R1K (Mouse).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	NCBI_TaxID=10090;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai U., Shinagawa A., Konno H., Adachi J., Fukuda S.,		
RA	Arakawa T., Hara A., Fukunishi K., Kiyosawa H., Konno H.,		
RA	Alizawa K., Izawa M., Nishi K., Bono H., Kasakawa T., Saito R.,		
RA	Saito T., Okazaki Y., Ashburner M., Batalov S., Kochia H.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kochia H.,		
RA	Fleischmann W., Gaasterland T., Alkaido I., Pesole G., Quackenbush J.,		
RA	Kuehl P., Lewis S., Matsuo Y., Suzuki R., Tomita M., Wagner L.,		
RA	Schirral L.M., Okido T., Furuno M., Konno H., Baldarelli R., Barsh G.,		
RA	Sakai K., Oki T., Fujita M., Carninci P., de Bonaldi M.,		
RA	Brownstein M.J., Hill D., Hoffmann M., Mazzarelli J., Kumbert P.,		
RA	Custincich S., Hill D., Hoffmann M., Mazzarelli J., Kumbert P.,		
RA	Lyons P., Marchionni L., Mashima J., Sakamoto N., Lee N.H.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Storch K.-F.,		
RA	Sasaki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Williams L.,		
RA	Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Williams L.,		
RA	Watanabe-Borja A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,		
RA	Hayashizaki Y.,		
RA	Functional annotation of a full-length mouse cDNA collection."		
RT	Nature 409:685-690(2001).		
DR	EMBL: AK004474; BAB23320.1;		
DR	MGI: 1916138; 1190003M12R1K.		

SO SEQUENCE 191 AA: 20772 MW: 76D7DB4796AEBB4D CRC64;  
 Query Match  
 Best Local Similarity 24.68; Score 245; DB 11; Length 191;  
 Matches 56; Conservative 37; Mismatches 71; Indels 12; Gaps 5;  
 QY 10 LGGVLAALANVINDVNDNNAGS-GGOOSVYNNHNANVNDNNAGSNNSNDXGN 68  
 DB 20 LGGVLAALANVINDVNDNNAGS-GGOOSVYNNHNANVNDNNAGSNNSNDXGN 68  
 QY 69 GFATRLFOKCTCYHKKKEVPSIOSLALYKKGKGGG--PPKGLMYSVNP 126  
 DB 78 DLAAKLFKMACVLAADPAFSLDITQAL-----GKQASHPTPTGLTYVLP 131  
 QY 127 KYDDLSKTKGNIAKRCGIPYAEKMOE-ASLFFVSGCTTSVMTVDISFGD 181  
 DB 132 RIKNLAQYGPDKICRAVPTTYAROOKEGTALTPDSCSELQSLFMSGLICGE 187  
 RESULT 2  
 ID 09C056 PRELIMINARY; PRT; 184 AA.  
 AC 09C056;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DE 1810036H07RIK (Tremblrel. 21, Last annotation update)  
 GN 1810036H07RIK  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=05/BL/6J; TISSUE=STOMACH AND PANCREAS;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Arakawa T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kondo S., Yamakata S.,  
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Saito R.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Koehle T.,  
 RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner J.,  
 RA Sakai K., Okido T., Suzuki R., Tomita M., Wagner J.,  
 RA Blake J., Boffelli D., Fujuno M., Aono H., Baldarelli R., Bashio T.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzaresi I., Sakamoto N.,  
 RA Nordone P., Ring B., Ringwald M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuk S.,  
 RA "Functional 1";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK008986; BAB25048.1;  
 DR EMBL: AK007705; BAB25201.1;  
 DR MGD: MGI:1913534; 1810036H07RIK.  
 DR PRINTS: PRO1559; DUFFYANTIGEN.  
 SQ SEQUENCE 184 AA: 20469 MW: 612A18FAB652230 CRC64;  
 Query Match  
 Best Local Similarity 19.68; Score 195; DB 11; Length 184;  
 Matches 51; Conservative 43; Mismatches 78; Indels 16; Gaps 5;  
 QY 1 MKFTTVEAGLGVFLPALANVINDVNDNNAGSGOOSVYNNHNANVNDNNAGSNNSNDXGN 68  
 DB 1 MKPLAVLVLSTFGIOSEAEIFNFPVSKNGNIGCTVITIDQNTATININISGSS 60  
 QY 61 NSIDYNGAATRLFOKCTCYHKKKEVPSIOSLALYKKGKGGG--PPKGLMYSVNP 126  
 DB 173 ILVSGIC 180

DB 61 TTFEDYKHGYIASRVLSRACVYIKMDKAIAPALDLOFLYEROTNN---AIDSEYTW 117  
 QY 121 YSNP-----KKYDDLSKTKGNIAKRCGIPYAEKMOE-ASLFFVSGCTTSVMTVDISFGD 181  
 DB 118 VYNNLKLRLTYK-DWFLFSGPIRLCKIMPLIEGVATKREVS-----TGACAKVGLG 172  
 QY 173 IVDISFGC 180  
 DB 173 ILVSGIC 180  
 RESULT 3  
 ID 09NL38 PRELIMINARY; PRT; 568 AA.  
 AC 09NL38;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DE N66 matrix protein.  
 OS Pinctada maxima.  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pterioidea;  
 OC Pterioidea; Pteridae; Pinctada.  
 NC NCB1\_TaxID=104660;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MACROPHAGE LAYER;  
 RX MEDLINE=20160475; PubMed=10694502;  
 RA Kono M., Hayashi N., Samata T.,  
 RT "Molecular mechanism of the macrophage layer formation in Pinctada  
 maxima".  
 RL Biochem. Biophys. Res. Commun. 269:213-218(2000).  
 DR EMBL: AB032613; BAA90540.1;  
 DR HSP: P23389; IDMY.  
 DR Interp: IPR002952; Eggshell.  
 DR Pfam: PF00194; carb. anhydrase; 3.  
 DR PRINTS: PRO1248; EGGSHL.  
 DR Matrix: PD000865; Euk\_Coatnd; 2.  
 SQ SEQUENCE 568 AA: 62377 MW: 4AD9242A96B642F CRC64;  
 Query Match  
 Best Local Similarity 9.98; Score 98; DB 5; Length 568;  
 Matches 41; Conservative 20; Mismatches 62; Indels 42; Gaps 7;  
 QY 27 NDDNNAGSGOOSVYNNHNANVNDNNAGSNNSNDXGN 68  
 DB 381 NGNNENNAGSGOOSVYNNHNANVNDNNAGSNNSNDXGN 68  
 QY 75 LFOKCTCYHKKKEVPSIOSLALYKKGKGGG--PPKGLMYSVNP 126  
 DB 441 YHSGGCIYKAKR-----LSRLICATVRRKREFFRNG-EKGLDVIDITPEMV----- 489  
 QY 135 GNIAKRCGIPYAEKMOE-ASLFFVSGCTTSVMTVDISFGD 181  
 DB 490 -----LP-----PMKRYHYTYEGSLTPPCNFTVLAWE 519  
 RESULT 4  
 ID 0964F6 PRELIMINARY; PRT; 588 AA.  
 AC 0964F6;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DE Merozoite surface protein 8.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NC NCB1\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K1;



FT	NON_TERM	1	1
SQ	SEQUENCE	1318 AA;	14494 MW; BIDA5CA0427066F6 CRC64;

```

RA Koonin E.V., Shalloom S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing X., Aston C., Lai Z., Schwartz D.C., Perlea M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Science 282;1126-1132(1998).
DR EMBL; AE001413; AAC71930.1; -.
KW Hypothetical protein.
SQ SEQUENCE 764 AA; 89327 MW; 0A80AF0090269A3E CRC64;

Query Match      9.4%; Score 93; DB 5; Length 764;
Best Local Similarity 22.6%; Pred. No. 2.6;
Matches 31; Conservative 25; Mismatches 41; Indels 40; Gaps 6

QY 20 ANYNIDVNDNNAGSGOOSVSYNNEHVAVDNNNGWDSNNSIMDYGNCFATRLFFOKK 79
   :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 335 SNHNHNINHHNSHNHNHNHNHNHNHNHNHNHNHNHNHNHNHNHNHYNYLYLTN-----YGR- 386
QY 80 TCIVNHKKKEVPMSIOSLDALVKEKKLGKGCGRRPKGLMT-SVPRNKVD-----DI 131
   Db 387 ----HNKNITPP-----PSGPPPNIKKYNVHPNHNYPNPPTGTL 424
QY 132 SKFGKIANNMCRGIPRY 148
   Db 425 QTFTNT--DSFPGLSST 439

RESULT 10

Q964F7 PRELIMINARY; PRT; 596 AA.
AC Q964F7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Merozoite surface protein 8.
GN MSP8.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D10;
RX MEDLINE=21273140; PubMed=11378201;
RA Black C.G., Wu F., Wang L., Hibbs A.R., Coppel R.L.;
RT "Merozoite surface protein 8 of Plasmodium falciparum contains two
RT epidermal growth factor-like domains.";
RL Mol. Biochem. Parasitol. 114:217-226(2001).
DR EMBL; AF325157; AAK63226.1; -.
DR InterPro; IPR000561; EGF-like.
DR SMART; SM00181; EGF_2.
SQ SEQUENCE 596 AA; 69301 MW; 1F60185C4B01C5FD CRC64;

Query Match      9.2%; Score 91.5; DB 5; Length 596;
Best Local Similarity 33.9%; Pred. No. 2.7;
Matches 21; Conservative 15; Mismatches 15; Indels 11; Gaps 3;

QY 21 NYNIDVNDNNAGS-GGOOSVSYNNEHVAVVDNNGGWSNNSIMDYGNCPA--ATRLFQ 77
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 59 NHNSMNNNNNNNNNDDNNNNINNHHNNNNNNNNNNNNNNNNNNNNNNNGNGISNFENKLF 110
QY 78 KK 79
   Db 111 KK 112

RESULT 11
Q964F5 PRELIMINARY; PRT; 600 AA.
```

```

Query Match          9.2%,   SCORE 91.5; DB 5; Length 600;
Best Local Similarity 33.9%; Pred. No. 2.7;
Matches 21; Conservative 15; Mismatches 15; Indels 11; Gaps

OY      21 NYNYDNDNNNAGS--GQGSVSYNNEHHVAVYDNNNGCDWSNTIDYGNGFA--ATRLFO 77
        |: :|::||| |:: || :| :||| |::|||: |::||: ||\
Db       59 NHNMSSMNNNNNNNNDDNNNNINNNNNNNNNNNNN-----NNGCGPSNFPKKFLG 110

OY      78 KK 79
         ||
Db     111 KK 112

RESULT 13
QBSSYO
ID QBSSYO PRELIMINARY; PRT: 628 AA.
```

[illegible]

RESULT 15

Q8SX72

ID Q8SX72

PRELIMINARY;

PRT;

868 AA.

AC Q8SX72;

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)

DE LD30050p.

CG9381.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_Taxid=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Change M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,

RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S.,

RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY094811; AAM1164.1; -

SQ SEQUENCE 868 AA; 92619 MW; E6FF05B4392EE3B CRC64;

QY 23 NIDVN----

Best Local Similarity 9.1%; Score 90; DB 5; Length 868;

Matches 31; Conservative 18; Mismatches 36; Indels 48; Gaps 5;

DB 86 NVNNGSGNSGNNNNNGN-----NNNNNGNISSNNNNNNNN-----123

QY 78 KKTCTVHKMKKEVMPSTIOSLDALVKEKKLQGGGCGPCKGLMYSVNPNKYVDLSEKFGKN 137

DB 124 -----KDNAPNCHS-----OGGPGCNSPDLGHNRGYNNGNNNGRGIGNG 163

QY 138 IAN-MCRGIPPTM 149

DB 164 IVNGNTMGPPDYM 176

Search completed: April 11, 2003, 16:14:20  
Job time : 44.044 secs

GenCore version 5.1.4-p5-4578  
1993 - 2003 CompuGen Ltd.

using SW model

OM protein - protein search, using OM  
Run on: April 11, 2003, 16:06:33 ; Search time 51.6281 seconds  
(without alignments)  
474.899 Million cell updates/sec

US-09-821-726A-16

Title:	Score:
TADILWLRMSFCGTSVEI	993
TADILWLRMSFCGTSVEI	993

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 18022000

Minimum	DB seq	length:	0
	DB seq	length:	200000000000

post-processing:	Minimum Match	0%
	Maximum Match	100%

Database :

A.Geneseq\_101002:\*

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1: /SID52/gcgdata/geneseq/geneseqp emb1/AA1981.DAT.\*

1: /SID52/gcgdata/geneseq/geneseqp emb1/AA1982.DAT.\*

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21: /SID52/gcgdata/geneseq/geneseqp emb1/AA2002.DAT.\*

22: /SID52/gcgdata/geneseq/geneseqp emb1/AA2003.DAT.\*

23: /S1562/505  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	936	94.3	184	23	ABP09922	Human ORFX protein
2	640	185.5	20	20	AAW99667	Human secreted pro
3	640	64.5	185	21	AAH24067	Human Prol1005 prot
4	640	64.5	185	21	AAH87272	Human signal pepti
5	640	64.5	185	21	AAI66586	Membrane-bound pro
6	640	64.5	185	22	AAI665209	Human Prol1005 (UNO
7	640	64.5	185	22	AAI60957	Human Prol1005 prot
8	640	64.5	185	22	AAI60957	Human angiotensin
9	640	64.5	185	23	ABP95422	Human Prol1005 prot
10	640	64.5	185	23	AAH84866	Human PRO protein

11	640	64.5	186	21	AAE383274
12	640	64.5	194	15	AAE69974
13	640	64.5	194	20	AAE76591
14	640	64.5	194	20	AAE3556
15	161	16.2	184	22	AAE04211
16	161	16.2	184	22	AAE04233
17	161	16.2	184	22	AAE64499
18	161	16.2	184	23	AAE64500
19	160	16.1	184	21	AAE65913
20	160	16.1	184	21	AAE65913
21	155	15.9	176	22	AAE29238
22	138.5	13.9	147	22	AAE04594
23	93	9.4	618	22	AAE63827
24	91	9.2	553	20	AAE55721
25	91	9.2	553	20	AAE53260
26	87	8.6	553	22	AAE41277
27	85.5	8.6	335	22	AAE89941
28	85.5	8.6	346	17	AAE55039
29	85.5	8.6	346	17	AAE91930
30	85.5	8.6	346	18	AAE35055
31	85.5	8.6	346	18	AAE19249
32	85.5	8.6	346	19	AAE43223
33	84.5	8.5	358	22	AAE38216
34	83.5	8.4	782	11	AAE06591
35	81.5	8.2	346	21	AAE82606
36	80.5	8.1	2295	21	AAE18180
37	80	8.1	95	22	AAE00897
38	80	8.1	2009	22	AAE74469
39	79.5	8.0	82	21	AAE54187
40	79.5	8.0	106	21	AAE75534
41	79.5	8.0	136	22	AAE63634
42	79.5	8.0	136	21	AAE57919
43	79.5	8.0	1215	21	AAE87788
44	79.5	8.0	1215	22	AAE87788
45	79	8.0	334	17	AAE00287

## ALIGNMENTS

RESULT 1	
ABP09922	
ID	ABP09922 standard; Protein: 184 AA.
AC	ABP09922:
XX	24-JUN-2002 (first entry)
XX	
XX	
DE	Human ORFX protein sequence SEQ ID NO:19826.
XX	
XX	Human: open reading frame: ORFX; gene therapy: cancer; cirrhosis;
KW	hyperproliferative disorder; psoriasis; benign tumour; hemorrhage;
KW	hyperproliferative disorder; osteoarthritis; neurodegenerative disorder;
KW	degenerative disorder; diabetes mellitus; systemic lupus erythematosus
KW	cardiovascular disease; hypothyroidism; cholesterol ester storage disease;
KW	immune deficiency; immune disorder; infectious disease;
KW	autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW	myasthenia gravis.
OS	Homo sapiens.
XX	
PN	WO200192523-A2.
XX	
PD	06-DEC-2001.
XX	
XX	29-MAY-2001: 2001WO-US10836.
XX	
XX	30-MAY-2000: 2000US-206132P.
PR	29-AUG-2000: 2000US-228716P.
XX	
XX	(CURA-) CURAGEN CORP.
PA	
PI	Shimkets RA, Leach MD;

CC present invention describes substantially purified human proteins  
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
CC in the specification), ABN15762 to ABN277252 encode the human ORFX  
CC proteins given in ABN00010 to ABN11500. ORFX proteins are useful for  
CC treating or preventing a pathology associated with an ORFX-associated  
CC syndrome in humans, and in the manufacture of a medicament for treating a  
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
CC sequences can be used in gene therapy. ORFX sequences can be used in the  
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
CC osteoarthritis, neurodegenerative disorders, disorders of liver,  
CC transplants, cardiovascular diseases, diabetes mellitus, hemorrhage,  
CC lung emphysema, hypertension, hypothyroidism, cholesterol disease,  
CC storage disease, various immune deficiencies, disorders related to organ  
CC diseases, autoimmune disorders such as multiple sclerosis, infectious  
CC arthritis, autoimmune thyroiditis, myasthenia gravis, rheumatoid  
CC disease and autoimmune inflammatory eye disease, graft-versus-host  
CC bone degenerative disorders, incisions, ulcers, for treating osteoporosis,  
CC protection or regeneration, or periodontal disease, and for gut  
CC repulsion injury in various tissues and conditions resulting from  
CC systemic cytokine damage.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pat\_sequences.  
CC Sequence 184 to 220

Sequence 184 AA;  
XX obtained in electronic format directly from WIPO  
SQ Sequence

Query Match	Score	DB	Length
Best Local Similarity	94.38;	23;	184;
Matches 172;	93.58;	23;	184;

	Conservative	7;	Mismatches	5;	Indels	0;	Gaps	0;
QY	1 MKLTMEVGLGCLLAAPGFAYTVNINCNCRGK							

61  
1 MKLTMEVVGLLGLLAAPGFAYTVNINGNDANDVGGGQSYSTINGVHNVAIDNNNGWDSW 60

61 NSLMIDYENSFAATRIEFSKSCSCIHRMKNKDAMSLÖDLDITMYKEÖKGKPGGAPKIDLMYS 120

121 VNPTRVEDLNTFGPKIAGMCGIPTVAEEIIPGNPBIYVSRGKGGK 120

121 INPTREVDVNTFGPKIASMCRGIPTYAAEEIPGPNQPLYSKRCYTANILWILRMSEFGCTS 180  
181 VETY 184

181 VETV 184

SULT 2  
W993667

AAW99667 standard; Protein, 185 AA.  
AAW99667

07-JUN-1999 (first entry)

Human secreted protein clone ej90\_5 protein

Human; secreted protein; nutritional; differentiation; immune stimulating; cytokine; cell proliferation; tissue growth; osteogenic; vascular

anti-inflammatory; cadherin; tumour invasion suppressor.

XX homo sapiens.  
PN WO9907840-A1.  
XX  
PD 18-FEB-1999.  
XX

06-AUG-1998; 98WO-US16318.

PR	04-AUG-1998;	98US-0130189.
PR	06-AUG-1997;	97US-0906708;
XX		

PA (GEMY ) GENETICS INST INC.  
X  
X  
I Acoustic m

WDT 11-11-61  
X I Jacobs K,  
X Merberg D, Racie LA, Steininger  
X

WPI; 1999-167419/14.  
N-PSDB; AAX19493.

New polynucleotides encoding secretory proteins of fetal kidney, adult testes, adult or adult retina cDNA

Claim 34; Page 98-99; 107pp; English

The present sequence represents a protein can have activities such as cell proliferation.

proliferation/differentiation (vaccines) or suppressing activity, tissue growth activity, chemokinesis.

...haemostatic and anti-inflammatory activity, suppressor activity, and tumour...

protein polynucleotides and proteins activities which would make them suitable for ameliorating medical conditions.

polynucleotides are also stated to be

ery Match	64.58;	Score 6
st Local Similarity	63.33	

1 MKLTMEVVCIGT 24; Misma

1 MKFTIVEAGLGLVFLAPALANYINYN-DNN

60 WNSLWDYENSFAATRLFSKSCIVHRMKNKDAM  
||:||||| ||:|||||  
60 WNSTEDYENSFAATRLFSKSCIVHRMKNKDAM

118 MYSVNPTRVEDLNTFGPKIAGMCPGIDTWT...

```
120 MYSVNPKNKVDLSKFCKNIANMCRGIPTYMAGE
```

1/8	GTSVE	182
180	GDIVE	184

67  
AB24067 standard; Protein; i85 AA

AB24067;

man PRO1005 protein sequence

Sequence ID NC



CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
CC nucleic acids can be used for the recombinant production of HSP, for  
CC detecting HSP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring), in gene therapy, as antisense,  
CC or genetic variations, and for chromosome mapping. HSP are also used to  
CC raise specific antibodies (Ab) and to screen for agonists and  
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic  
CC antagonists, in competitive drug screens, and for purification of HSP  
CC from natural sources.

Sequence 185 AA:

Query Match 64.58; Score 640; DB 21; Length 185;  
Best Local Similarity 63.88; Pred. No. 2,1e-60;  
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLMPVYGLGLAARFA-YTVNINSGNDGVDSSGOOSVINGVHNVANIDNNNGWDS 59  
Db 1 MKETIVFAGLGLVFLAPALANNINVN-DNNNAGSGOOSVNVNHNVANVDNNNGWDS 59  
QY 60 WNSLMDYENSFATRLFSKSCIVHRANKDAPSLDIDITVWKEOK--GKPGGAPPKDL 117  
Db 60 WNSIMDYNGFATRLFPKCTCTVHRANKKEVPSIQSLALVKEKLGKPGGAPPKDL 119  
QY 118 MYSVPTREDINTFGPIACMCRGIPYVAEEIPGNOPLYSKCYTADILMLMSFC 177  
Db 120 MYSVNPVNDLDSKFGKNIAMNCRGIPYVAEEIPGNOPLYSKCYTADILMLMSFC 179  
QY 178 GTSVE 182  
Db 180 GDVE 184

## RESULT 5

AY66666  
ID AY66666 standard; protein; 185 AA.

AC AY66666;

DT 05-APR-2000 (first entry)

XX Membrane-bound protein PRO1005.

XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
XX pharmacological; receptor Immunoadhesin; gene mapping.

OS Homo sapiens.

XX MO9963088-A2.

PD 03-DEC-1999.

PF 02-JUN-1999; 99WO-US12252.

XX 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 05-JUN-1998; 98US-0088655.

PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088828.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 12-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 16-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089112.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089536.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
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PR 23-JUN-1998; 98US-0090349.  
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PR 24-JUN-1998; 98US-0090538.  
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PR 25-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
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PR 25-JUN-1998; 98US-0090695.  
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PR 02-JUL-1998; 98US-0091478.  
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PR 02-JUL-1998; 98US-0091519.  
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PR 02-JUL-1998; 98US-0091633.  
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PR 07-JUL-1998; 98US-0091673.  
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 XX 20-JUL-1998; 98US-0093339.  
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 PR 04-AUG-1998; 98US-0095282.  
 PR 04-AUG-1998; 98US-0095285.  
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 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
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 PR 10-AUG-1998; 98US-0096143.  
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 PR 17-AUG-1998; 98US-0096765.  
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 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
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 PR 18-AUG-1998; 98US-0096950.  
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 PR 18-AUG-1998; 98US-0097022.  
 PR 18-AUG-1998; 98US-0097141.  
 PR 19-AUG-1998; 98US-0097218.  
 PR 20-AUG-1998; 98US-0097661.  
 PR 24-AUG-1998; 98US-0097951.  
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 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
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 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.  
 XX (GETH ) GENENTECH INC.  
 PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WJ, Yuan J;  
 XX WPI: 2000-072883/06.  
 DR N-PSDB: AA65023.  
 XX Membrane-bound proteins and related nucleotide sequences  
 PT claim 12: Fig 139; 822pp: English.  
 PS  
 XX The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 CC will also be useful for the preparation of PRO polypeptides, especially

CC by recombinant techniques.  
 XX Sequence 185 AA;  
 SQ Query Match 64.5%; Score 640; DB 21; Length 185;  
 Best Local Similarity 63.8%; Pred. No. 2,1e-60; Indels 4; Gaps 3;  
 Matches 118; Conservative 39; Mismatches 59  
 OY 1 MKLTMFVGLGLAAGPFA-YTVNINNGDNCVDSQDSVSINGVYANANIDNNNGWDS 59  
 DB 1 MKTTFVAGLLGVLPALANYNINVN-DDNNNAGSGQDSVYNNNEHNVANVNNNGWDS 59  
 OY 60 WNSLMDYENSFATRLFEKSCIVHMKNDAPSLQDIDTMVKQK--GKGGGAPPKDL 117  
 DB 60 WNSTMDYNGFAATRLFKKCTIVHMKNEVMPSTQSDALVKKRKLQGGKPGGPPPKGL 119  
 OY 118 MYSVNPTRVEDLMTFGKRTAGMCRGIPYVAEETPGPNOPLYSKKCYTADILMLRMSFC 177  
 DB 120 MYSVNPKNKVDLDSKFGKNIANMCKRGIPYVAEEMQASLFEVSGTCYTTSVLWIVDISFC 179  
 OY 178 GTSVE 182  
 DB 180 GDTVE 184  
 RESULT 6  
 AAB65209 standard: Protein; 185 AA.  
 ID AAB65209;  
 AC AAB65209;  
 XX 02-APR-2001 (first entry)  
 DT Human PRO1005 (UNC489) protein sequence SEQ ID NO:211.  
 DE Human; secreted and transmembrane protein; PRO; cytosolic;  
 XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay.  
 KM Homo sapiens.  
 OS WO200073454-A1.  
 PN 07-DEC-2000.  
 PD 30-MAR-2000; 2000WO-US08439.  
 PF 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 08-OCT-1999; 99US-0158663.  
 PR 01-DEC-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US30095.  
 PR 16-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US00219.  
 PR 05-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 XX (GETH ) GENENTECH INC.  
 PA

30-MAY-2000; 2000WO-US14941.

02-JUN-1999;	99WO-US12252.
22-JUN-1999;	99US-0140650.
23-JUN-1999;	99US-014037.
20-JUL-1999;	99US-0144758.
01-SEP-1999;	99WO-US20111.
08-SEP-1999;	99WO-US20594.
29-OCT-1999;	99US-0162506.
30-NOV-1999;	99WO-US28313.
01-DEC-1999;	99WO-US28634.
02-DEC-1999;	99WO-US28551.
16-DEC-1999;	99WO-US28551.
20-DEC-1999;	99WO-US30095.
06-JAN-2000;	2000WO-US30999.
11-FEB-2000;	2000WO-US00376.
18-FEB-2000;	2000WO-US03565.
18-FEB-2000;	2000WO-US04341.
02-MAR-2000;	2000WO-US04342.
03-MAR-2000;	2000WO-US05841.
10-MAR-2000;	2000WO-US18702.
15-MAR-2000;	2000WO-US06319.
30-MAR-2000;	2000WO-US06884.
17-MAY-2000;	2000WO-US08439.
	2000WO-US13705.

(GETH ) GENENTECH INC.

WPI; 2001-016509/02.  
N-PSDB; AAC91559.

Twenty eight nucleic acids encoding PRO polypeptides which are useful for treating various tumors, e.g. breast cancer, and other inflammatory, angiogenic and immunological disorders -

Claim 31, Fig 14; 188pp; English.

The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytic, hypothalamic and other glandular, macrophage, epithelial, stromal and osteocytic disorders, and inflammatory, angiogenic and immunological disorders.

sequence 185 AA;

Query Match	64.58;	Score 640;	DB 22;	Length 185;
Best Local Similarity	63.88;	Pred. No. 2.1e-60;		
Matches 118; Conservative	34.11;	W. 1.1e-10;		

[illegible]

20	1	MEFIVTLAGLGGELFALPALATANNINVN	-DDNNMSSGGGSVSNNEHNVAIVNNNGMDS	59
QY	60	WNSLMDYENFEAFATRLFEKSSCIYHAKMKDAMP	SLDDLTMYEKQ--GKGPGCAPPKDL	11
Db	60	WNSLMDYDGNFEAFATRLPQKTKTIVYHAKMK	EWMPISLOSLDALYERKLIKQKGGPGPGGL	11
QY	118	MYSNVLPREDINTGCPKTIAGKCRGIPITYAAEL	IPGPNQPLYEKCKCYTDTIMILRMSFC	17
Db	120	MYSNVNDKVDLSTKFGCIPIANMRCGIPITYAAE	EMQEASLFEFYSGTCYITSVLIMVLDISFC	179
QY	178	GSVSE	182	



XX 03-JAN-2002.  
 PD 20-JUN-2001; 2001WO-US19692.  
 XX 23-JUN-2000; 2000US-219637P.  
 XX 20-JUL-2000; 2000US-219556P.  
 PF 25-JUL-2000; 2000US-220624P.  
 PR 28-JUL-2000; 2000US-220664P.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23522.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 24-OCT-2000; 2000US-0665350.  
 PR 08-NOV-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-070923P.  
 PR 10-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US30873.  
 PR 20-DEC-2000; 2000US-0532678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 01-MAR-2001; 2001WO-US06520.  
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 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 01-JUN-2001; 2001WO-US17443.  
 XX 01-JUN-2001; 2001WO-US17800.  
 PA (GETH ) GENENTECH INC.  
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 DR WPI: 2002-090516/12.  
 DR N-PSDB: ABL88141.  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 XX infarction), endothelial or angiogenic disorders in a mammal.  
 XX Claim 11; Fig 140; 565pp; English.  
 PS ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytosolic,  
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC probes used in the exemplification of the present invention.  
 CC Sequence 185 AA;

Query Match  
 Best Local Similarity 64.5%; Score 640; DB 23; Length 185;  
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;  
 OY 1 MKITMFVVGILGLIAAFGFA-YTVNINCGNDGVNDGSGQSVSINGVHNVANINDNNNGWDS  
 Db 1 MKITMFVVGILGLIAAFGFA-PALANININ-N-DINNNGSGQSVSINGVHNVANINDNNNGWDS  
 OY 60 WNSLMDYENSFAATRLFSKSCIVHRNKKDAPSLDIDMVEOK--GKGPGAAPPDL 117  
 Db 60 WNSLMDYENSFAATRLFSKSCIVHRNKKDAPSLDIDMVEOK--GKGPGAAPPDL 117  
 OY 118 MYSVNPTRVEDLMTGPRITACMGRIPTVYAEIPPPNPLYSKCYTADILMLIRMSFC 177  
 Db 120 MYSVNPTRVEDLMTGPRITACMGRIPTVYAEIPPPNPLYSKCYTADILMLIRMSFC 177  
 OY 178 GTSVE 182  
 Db 180 GDTVE 184  
 RESULT 10  
 ID AU083665  
 AC AU083665 standard; Protein: 185 AA.  
 XX  
 DT 08-MAY-2002 (first entry)  
 DE Human PRO protein, Seq ID No 148.  
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW pericyte cell proliferation; chondrocyte cell proliferation;  
 OS Homo sapiens.  
 XX  
 PN WO200208288-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-US21066.  
 XX  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220585P.  
 PR 25-JUL-2000; 2000US-220605P.  
 PR 25-JUL-2000; 2000US-220607P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220638P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 26-JUL-2000; 2000US-220693P.  
 PR 28-JUL-2000; 2000US-220833P.  
 PR 23-AUG-2000; 2000WO-US20710.  
 PR 24-AUG-2000; 2000WO-US23522.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2000WO-US34956.  
 PR 10-MAY-2001; 2001WO-US06520.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PA (GETH ) GENENTECH INC.  
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
 DR WPI: 2002-172001/22.  
 DR N-PSDB: ABK33609.

Sequence 185 AA;

Matches 118; Conser

Db 1 MKFTIVFAGLLGV

DD 60 WNSLWDYGNNGFAA

DD 120 MIBVNFNNVDDLS

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ID AAB38329 standard;

DT 31-JAN-2001 (firs

KW Immunosuppressive;

XXXXXX

XX	19-OCT-2000
PD	

09-APR-1999 0900

PR 26-APR-1999; 99U

PS Claim 11; Page 598;

CC and proteins are used

CC diagnosis, treatment

angioinvasive, (1) the  
infections caused by

supporting cell culture

# 1. INTRODUCTION

Our first preference was

118 MYCINDBYEDT NMT

178 GTSVE 182

XX

XX

KW diagnosis; metastati

PN W09837187-A1.

PD 27-AUG-1998.  
 XX 18-FEB-1998; 98WO-JP00667.  
 PF 21-FEB-1997; 97JP-0052508.  
 XX (TAKI ) TAKARA SHUZO CO LTD.  
 PA Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;  
 PI WPI; 1998-467552/40.  
 XX  
 DR  
 PT Detection of cancer cells in tissue samples - by changes in mRNA  
 PT expression compared to normal tissue of specific cancer-associated  
 PT gene sequences  
 PS  
 PS Claim 14; Page 64-65; 92pp; Japanese.  
 CC The cancer associated proteins AAM6974-W69976 where used in the method  
 CC of the invention to detect cancer cells in tissue samples or biological  
 CC fluids. They are detected by monitoring the change in mRNA expression  
 CC as compared to normal tissue of one or more cancer-associated genes  
 CC whose cDNA stringently hybridises to cancer associated gene nucleic acid  
 CC fragments. The change in expression may be an increase or a decrease  
 CC compared to normal tissue. The mRNA expression may be determined by  
 CC PCR, Northern blotting or ribonuclease protection assay, or by  
 CC determining the change in the amount of protein encoded by the gene(s) as  
 CC compared to normal tissue, for example by using a labelled antibody  
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,  
 CC including detection of metastatic cancer cells in tissues other than the  
 CC primary tumour site.  
 CC  
 SQ Sequence 194 AA;  
 Query Match 64.5%; Score 640; DB 19; Length 194;  
 Best Local Similarity 63.8%; Pred. No. 2.2e-60;  
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;  
 QY 1 MKLTMFVGLLGLIAPGFA-YTVNINNGNDGNGSQSQSVSINGVHNVANINDNNNGMS 59  
 Db 10 MKFTTFAGLGLVFLAPALANNYNINVA-DNINNAGSQSQSVSNENHNVANVNDNNNGMS 68  
 QY 60 WNSLMDYENSFAATRLFSKSCIVHRMKNKDAMPSLDLDTMYEKQ--GKPGGAPPKDL 117  
 Db 69 WNSIMYGNCFATRLFOKKTCTIVHKMKEMVPSISLDAIVKEKKLOGKPGGPPKGL 128  
 QY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYAAEIPGPNOPLYSKCTADILMLIRMSFC 177  
 Db 129 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYAAEIPGPNOPLYSKCTADILMLIRMSFC 188  
 QY 178 GTSVE 182  
 Db 189 GDTVE 193  
 RESULT 13  
 AAY76591  
 ID AAY76591 standard; Protein; 194 AA.  
 XX  
 AC AAY76591;  
 XX  
 DT 10-APR-2000 (first entry)  
 XX  
 DE Human ovarian tumor EST fragment encoded protein 87.  
 KW Expressed sequence tag; EST; human; ovarian tumor; anticancer;  
 KW gene therapy; treatment.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE19817557-A1.  
 XX  
 PD 21-OCT-1999.

XX  
 PF 09-APR-1998; 98DE-1017557.  
 XX 09-APR-1998; 98DE-1017557.  
 PR (META-) METAGEN GES GENOMFORSCHUNG MBH.  
 XX  
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;  
 PI WPI; 1999-591920/51.  
 DR N-PSDB; AA277487.  
 DR  
 XX  
 PT New nucleic acid sequences expressed in ovarian, and some other, cancer  
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and  
 PT identification of therapeutic agents  
 PS  
 PS Claim 25; Page 279; 310pp; German.  
 CC This invention describes novel nucleic acid (cDNA) sequences (A) which  
 CC have anticancer activity and are highly expressed in ovarian tumor  
 CC tissue (and some also in testis and breast cancer tissue). The products  
 CC of the invention can be used for gene therapy. (A) are used (1) for  
 CC recombinant expression of polypeptides (B) and (11) to isolate complete  
 CC genes. (B) are used (1) to identify agents suitable for treatment of  
 CC ovarian cancer; (11) directly for treating this form of cancer  
 CC (including expression from gene therapy vectors) and (111) for generation  
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed  
 CC sequence tags) from a particular tissue type before comparison of the  
 CC expression patterns. This allows a significantly longer fragment of the  
 CC gene to be revealed, so should reduce the number of failures associated  
 CC with the fact that ESTs from different libraries may represent different  
 CC parts of the same unknown gene, distorting the estimated frequency of  
 CC occurrence in a particular tissue. AAY76505-Y76638 represent protein  
 CC fragments encoded by the human ovarian tumor cDNA library derived EST  
 CC fragments represented in AA277450-277572.  
 CC  
 SQ Sequence 194 AA;  
 Query Match 64.5%; Score 640; DB 20; Length 194;  
 Best Local Similarity 63.8%; Pred. No. 2.2e-60;  
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;  
 QY 1 MKLTMFVGLLGLIAPGFA-YTVNINNGNDGNGSQSQSVSINGVHNVANINDNNNGMS 59  
 Db 10 MKFTTFAGLGLVFLAPALANNYNINVA-DNINNAGSQSQSVSNENHNVANVNDNNNGMS 68  
 QY 60 WNSLMDYENSFAATRLFSKSCIVHRMKNKDAMPSLDLDTMYEKQ--GKPGGAPPKDL 117  
 Db 69 WNSIMYGNCFATRLFOKKTCTIVHKMKEMVPSISLDAIVKEKKLOGKPGGPPKGL 128  
 QY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYAAEIPGPNOPLYSKCTADILMLIRMSFC 177  
 Db 129 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYAAEIPGPNOPLYSKCTADILMLIRMSFC 188  
 QY 178 GTSVE 182  
 Db 189 GDTVE 193  
 RESULT 14  
 AAM23556  
 ID AAM23556 standard; Protein; 184 AA.  
 XX  
 AC AAM23556;  
 XX  
 DT 12-OCT-2001 (first entry)  
 XX  
 DE Human EST encoded protein SEQ ID NO: 1081.  
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition.



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QY 1 MKLMEVVGILLGLAAPGFAIV-NI---NGNDGVNDGSGOOSYSINGVHVANIDNNG 56
    | : : : : | : : : : | : : : : | : : : : |
Db 1 MKILVAFVLVLTFIGIOSHGEVFNISPSNNGV---QETVIDNEKNTAIIINHAG 56
    | : : : : | : : : : | : : : : | : : : : |
QY 57 WDSNNSLMDYENSFAATRLFSKSCIVHRMNRKDAMPLODLDTMWKEOKGKGGAPPKD 116
    | : : : : | : : : : | : : : : | : : : : |
Db 57 SCSSITIDYKHGYIASRVLRRACFIKMDHONITPPLNNLOWIYEKQA-----LD 108
    | : : : : | : : : : | : : : : | : : : : |
QY 117 LMYs-----VNP--TRVEDINTF--GPKIAGMCRGIPTYVAEELPGPNOLYSKKCYT 165
    | : : : : | : : : : | : : : : | : : : : |
Db 109 NMFSSKTYWVKYNPLESLIKVDWFLGSPIEKLCRHIPLYKGEVVENTHN-VGAGGCAR 167
    | : : : : | : : : : | : : : : | : : : : |
QY 166 ADILMLRMSFC 177
    | : : : : | : : : : | : : : : | : : : : |
Db 168 AGLLGILGISTC 179
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Search completed: April 11, 2003, 16:11:12  
 job time : 52.6281 secs



Mon Apr 14 14:01:50 2003

us-09-821-726a-16.ra1

Page 1

GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:08:13 ; Search time 18.6101 Seconds  
(without alignments)  
290.907 Million cell updates/sec

Title: US-09-821-726A-16

Perfect score: 993  
Sequence: 1 MKLIMFVGLGLIADGFA.....TADILWLRMSFGCTSVET 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2-6/ptodata/1/iaa/5A.COMB.pep:\*  
2: /cgn2-6/ptodata/1/iaa/5B.COMB.pep:\*  
3: /cgn2-6/ptodata/1/iaa/6A.COMB.pep:\*  
4: /cgn2-6/ptodata/1/iaa/6B.COMB.pep:\*  
5: /cgn2-6/ptodata/1/iaa/PCTUS.COMB.pep:\*  
6: /cgn2-6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	9.2	553	3	US-09-083-351-2
2	91	9.2	553	4	US-09-083-352-2
3	85.5	8.6	346	1	US-08-213-403-2
4	85.5	8.6	346	1	US-08-458-077-2
5	85.5	8.6	346	1	US-08-460-741-2
6	85.5	8.6	346	1	US-08-747-240-2
7	85.5	8.6	346	1	US-08-299-567-6
8	79.5	8.0	82	4	US-09-214-631-11
9	79.5	8.0	336	1	US-08-436-044-2
10	79.5	8.0	336	1	US-08-436-054-2
11	79.5	8.0	336	5	PCT-US95-08812-2
12	78	7.9	345	4	US-09-214-631-5
13	77.5	7.8	428	3	US-09-118-319-5
14	76	7.7	775	4	US-09-305-640-2
15	75	7.6	334	1	US-08-241-4658-19
16	75	7.6	334	1	US-08-241-4658-20
17	73.5	7.4	521	4	US-09-071-035-64
18	73.5	7.4	521	4	US-09-071-035-62
19	73	7.4	238	4	US-09-216-295-12
20	72	7.3	333	1	US-08-436-044-4
21	72	7.3	333	2	US-08-436-054-4
22	72	7.3	333	4	US-08-271-948-2
23	72	7.3	333	4	US-08-271-948-2
24	72	7.3	333	5	PCT-US95-08534-2
25	72	7.3	333	5	PCT-US95-08534-2
26	72	7.3	478	3	US-08-155-888-2
27	71	7.2	193	1	US-08-616-368A-1

28	71	7.2	193	4	US-09-054-298-1	Sequence 1, Appl
29	71	7.2	193	4	US-08-818-655-1	Sequence 1, Appl
30	70	7.0	193	1	US-08-616-368A-8	Sequence 8, Appl
31	70	7.0	193	1	US-08-616-368A-13	Sequence 13, Appl
32	70	7.0	193	2	US-08-739-485-1	Sequence 1, Appl
33	70	7.0	193	2	US-08-739-485-9	Sequence 9, Appl
34	70	7.0	193	4	US-09-054-298-8	Sequence 8, Appl
35	70	7.0	193	4	US-09-054-298-13	Sequence 13, Appl
36	70	7.0	193	4	US-08-818-655-8	Sequence 8, Appl
37	70	7.0	193	4	US-08-818-655-13	Sequence 13, Appl
38	70	7.0	312	1	US-08-525-505A-4	Sequence 4, Appl
39	70	7.0	312	1	US-08-525-505A-2	Sequence 2, Appl
40	70	7.0	992	1	US-08-127-499A-1	Sequence 1, Appl
41	70	7.0	992	1	US-08-482-847-1	Sequence 1, Appl
42	69.5	7.0	197	1	US-08-044-621D-29	Sequence 29, Appl
43	69.5	7.0	197	1	US-08-709-912-9	Sequence 9, Appl
44	69.5	7.0	197	2	US-09-047-370-9	Sequence 9, Appl
45	69.5	7.0	348	4	US-09-216-295-16	Sequence 16, Appl

#### ALIGNMENTS

RESULT 1  
US-09-083-351-2  
Sequence 2, Application US/09083351  
Patent No. 6087107  
GENERAL INFORMATION:  
APPLICANT: Sheffield, Val C.  
APPLICANT: Alward, Wallace L.M.  
APPLICANT: Stone, Edwin M.  
APPLICANT: Nishimura, Darryl  
APPLICANT: Palli, Shiva  
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR  
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN  
TITLE OF INVENTION: TRANSCRIPTION FACTOR  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HONG & ELLIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/083,351  
FILING DATE: 22-MAY-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UTA-029.02  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-083-351-2  
Query Match  
Best local similarity 9.2%; Score 91; DB 3; Length 553;  
Matches 38; Conservative 21; Mismatches 57; Indels 78; Gaps 9;  
14 LAAPGATYVINGNGNDGSGQGSVINGVHNA-----NIDNNNGW----- 57

Db 76 MKAPYSYIALIT---MAIONAPDKKITLNGIOTIMDRPEPPYRNKOGMONSIRHNLSL 132  
QY 58 -----DSWNSLMDYENS--FAATRLFSKSCSIYHRNNKDM 91  
Db 133 NECFVAVPRDDKPKGSGYWTLPDPSYNN---FENGSLRRRRRRKKKDAVAKDEKRL 189  
QY 92 -----PSLQDLDTWKEOKGKGPGAPPKDLMYSVPTREEDINTGPIAGMCRGIP 144  
Db 190 HKEPPPGRRPPAPPEQADGNAPGPP-----PVRIDIKTEN---GTC----- 233  
QY 145 TYVAEIEIPGNOPL 158  
Db 234 -----PSPPOPL 240

## RESULT 2

US-09-083-352-2  
; Sequence 2, Application US/09083352  
; Patent No. 6207450  
; GENERAL INFORMATION:  
; APPLICANT: Sheffield, Val C.  
; APPLICANT: Alward, Wallace L.M.  
; APPLICANT: Stone, Edwin M.  
; APPLICANT: Nishimura, Darryl  
; APPLICANT: Patil, Shiva  
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
; NUMBER OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HONG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/083,352  
; FILING DATE: 22-MAY-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: UIA-029.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-083-352-2

Query Match 9.2%; Score 91; DB 4; Length 553;  
Best Local Similarity 19.6%; Pred. No. 0.1;  
Matches 38; Conservative 21; Mismatches 57; Indels 78; Gaps 9;  
QY 14 LAAPGATVYVINGNDGNDVDSGQSVSINGVHVA-----NIDNNNGW----- 57  
Db 76 MKAPYSYIALIT---MAIONAPDKKITLNGIOTIMDRPEPPYRNKOGMONSIRHNLSL 132  
QY 58 -----DSWNSLMDYENS--FAATRLFSKSCSIYHRNNKDM 91  
Db 133 NECFVAVPRDDKPKGSGYWTLPDPSYNN---FENGSLRRRRRRKKKDAVAKDEKRL 189  
QY 92 -----PSLQDLDTWKEOKGKGPGAPPKDLMYSVPTREEDINTGPIAGMCRGIP 144

Db 190 HKEPPPGRRPPAPPEQADGNAPGPP-----PVRIDIKTEN---GTC----- 233  
QY 145 TYVAEIEIPGNOPL 158  
Db 234 -----PSPPOPL 240

## RESULT 3

US-08-213-403-2  
; Sequence 2, Application US/08213403  
; Patent No. 5512457  
; GENERAL INFORMATION:  
; APPLICANT: Lyman, Stewart D.  
; APPLICANT: Beckmann, M. Patricia  
; APPLICANT: Baum, Peter R.  
; APPLICANT: Carpenter, Melissa  
; TITLE OF INVENTION: No. 5512457el Cytokine Designated elk Ligand  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Apple Macintosh  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/213,403  
; FILING DATE: 15-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/977,693  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2807-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 346 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-213-403-2

Query Match 8.6%; Score 85.5; DB 1; Length 346;  
Best Local Similarity 23.1%; Pred. No. 0.21;  
Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11;  
QY 16 APGFATVYVINGNDGNDVDSGQSVSINGVHVAIDNNNG--WDSNNSLMDYENS--AAT 73  
Db 195 APG-----SRGSLGDSGK-----HEVNGEESKSGRSGSGGDDPDGFEFSKV 238  
QY 74 RLFSK--KSCIV-----HRNNKDMPSLQDLDTWKEOKGKGPGAP 113  
Db 239 ALFAAVAGAGVIFLLIIFLYVLLKLRHRRHKKHQOAAALSTLASPKGSGTAGTE 298  
QY 114 PKDLMYSVPTREEDINTGPIAGMCRGIP---KTAGMCRGIPTYVAEIEIPGNOPL---LTSK 161  
Db 299 FSDIILPLKTE---NNYCPHYEKVSG--DYGHPYIYQENP--FOSPANIYTK 345

RESULT 4  
US-08-458-077-2  
; Sequence 2, Application US/08458077

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CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,741
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-741-2

      8.6%; Score 85.5; DB 1; Length 346;
Query Match      23.1%; Pred. No. 0.21;
Best Local Similarity
Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11

QY 16 APEFAYTVNINSGNDGSSGQGSVINGVINVANIDNNNG-WDSWNSLWDYENSF-AAT 73
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QY 74 RLPSK-KKCIY-----HRMKDAMPISLDDITWYKEQKGGKPGCAP 113
Db 239 ALPFAAGAGCIVILIIIFLTVLLKLRKRHRKHTQQRRAALSLTLASPKGSGTAGTE 298
QY 114 PKDLMSVNPRTVEDLNTGCP---KTAGMCRGIPTYVAEELPGNP--LYSK 161
Db 299 PSDIILIRLRT-----NNYCPHYEKVSG-DYGHPIVIVGEMP-POSPANIYYK 345

RESULT 6
US-08-747-240-2
; Sequence 2, Application US/08747240
; Patent No. 5728613
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5728613el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:

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MEDIUM TYPE: floppy disk  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Apple System 7.1  
 SOFTWARE: Microsoft Word for Apple, Version 5.1a  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/747,240  
 FILING DATE: 12-NOV-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/213,403  
 FILING DATE: 15-MAR-1994  
 APPLICATION NUMBER: US 07/977,693  
 FILING DATE: 13-NOV-1992  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seese, Kathryn A.  
 REGISTRATION NUMBER: 32,172  
 REFERENCE/DOCKET NUMBER: 2807-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 587-0430  
 TELEFAX: (206) 233-0644  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 346 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-747-240-2

Query Match 8.6%; Score 85.5; DB 1; Length 346;  
 Best Local Similarity 23.1%; Pred. No. 0.21;  
 Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11;  
 QY 16 APGFAYTVNNGNDGSGQSVSINGVHNVANINNNNG-WDSWNSLMDYNSF-AAT 73  
 DB 195 APG-----SRGSLGDSGK-----HETVNOEKSGPGASGSSGDDPGFNSKV 238  
 QY 74 RLESK--KSCIV-----HRNKDAMPSLODDITVYKQKGGPGAP 113  
 DB 239 ALFAAVAGACVIFLLIIFLVLLKLRKRHRHTQORAAALSLTSLASPKSGSGTAGTE 298  
 QY 114 PKDLMYSVNPTRVEDLNTFGP---KIAGMCGIPTVVAEIPGPNP--LYSK 161  
 DB 299 PSDIILPLRTT-----NMCCHYEKVSQ-DYGHVYIVQEMP-POSPANITYK 345

RESULT 7  
 US-08-299-567-6  
 Sequence 6, Application US/08299567  
 Patent No. 5747033  
 GENERAL INFORMATION:  
 APPLICANT: Davis, et al.  
 TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 STREET: 777 Old Saw Mill River Road  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10591-6707  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/299,567  
 FILING DATE: 01-SEP-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kempier, Gail M.

REGISTRATION NUMBER: 32,143  
 REFERENCE/DOCKET NUMBER: REG 290  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 914-345-7400  
 TELEFAX: 914-345-7721  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 346 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-299-567-6

Query Match 8.6%; Score 85.5; DB 1; Length 346;  
 Best Local Similarity 23.1%; Pred. No. 0.21;  
 Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11;  
 QY 16 APGFAYTVNNGNDGSGQSVSINGVHNVANINNNNG-WDSWNSLMDYNSF-AAT 73  
 DB 195 APG-----SRGSLGDSGK-----HETVNOEKSGPGASGSSGDDPGFNSKV 238  
 QY 74 RLESK--KSCIV-----HRNKDAMPSLODDITVYKQKGGPGAP 113  
 DB 239 ALFAAVAGACVIFLLIIFLVLLKLRKRHRHTQORAAALSLTSLASPKSGSGTAGTE 298  
 QY 114 PKDLMYSVNPTRVEDLNTFGP---KIAGMCGIPTVVAEIPGPNP--LYSK 161  
 DB 299 PSDIILPLRTT-----NMCCHYEKVSQ-DYGHVYIVQEMP-POSPANITYK 345

RESULT 8  
 US-09-214-631-11  
 Sequence 11, Application US/09214631  
 Patent No. 6413730  
 GENERAL INFORMATION:  
 APPLICANT: Holland, Sacha  
 APPLICANT: Mbamalu, Geraldine  
 APPLICANT: Pawsan, Tony  
 TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED  
 TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR  
 FILE REFERENCE: 11757.23USMO  
 CURRENT APPLICATION NUMBER: US/09/214,631  
 EARLIER FILING DATE: 1999-03-12  
 EARLIER APPLICATION NUMBER: PCT/CA97/00473  
 EARLIER FILING DATE: 1997-07-04  
 EARLIER APPLICATION NUMBER: 60/021,272  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: Patent Ver. 2.0  
 SEQ ID NO 11  
 LENGTH: 82  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-214-631-11

Query Match 8.0%; Score 79.5; DB 4; Length 82;  
 Best Local Similarity 27.7%; Pred. No. 0.13;  
 Matches 23; Conservative 14; Mismatches 35; Indels 11; Gaps 5;  
 QY 84 HRNKDAMPSLODDITVYKQKGGPGAPPKDLMYSVNPTRVEDLNTFGP---KIAGMCG 140  
 DB 5 HRKHTQORAAALSLTSLASPKSGSGTAGTEPSDIILPLRTT-----NMCCHYEKVSQ-D 59  
 QY 141 RGIPTVVAEIPGPNP--LYSK 161  
 DB 60 YGHVYIVQEMP-POSPANITYK 81

RESULT 9  
 US-08-436-044-2  
 Sequence 2, Application US/08436044

Patent No. 5624899  
GENERAL INFORMATION:  
APPLICANT: Bennett, Brian D.  
APPLICANT: Matthews, William  
TITLE OF INVENTION: HTK LIGAND  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,044  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/277722  
FILING DATE: 20-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 90203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/952-9881  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 336 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-436-044-2

Query Match 8.0%; Score 79; DB 1; Length 336;  
Best local similarity 24.6%; Pred. No. 1.1;  
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9;

QY 49 ANIDNNNGMDSNLSMDYENSFAATRLFS--KKSCIV-----HRMK 88  
DB 209 SSTGNSAGHSNNLLGSE-----VALFAGIASGCIIFIVIIITLVLLKYYRRRRKHS 263  
QY 89 DAMPSLODDITMYKEQKGKGGAPPKDLMVSNPTREVDLNTGCP---KIAGMCGRIPT 145  
DB 264 PQHITLSTLSTLATPKRGNNNGSEPSDV---ITPLKTAD-SVFCPHYEKVSQ-DYGHVY 318  
QY 146 YVAEETPGPNP--LYSK 161  
DB 319 YIVQEMP-POSANITYK 335

RESULT 10  
US-08-436-054-2  
Sequence 2, Application US/08436054  
GENERAL INFORMATION:  
APPLICANT: Bennett, Brian D.  
APPLICANT: Matthews, William  
TITLE OF INVENTION: HTK LIGAND  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,054  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/277722  
FILING DATE: 20-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 90201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/952-9881  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 336 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-436-054-2

Query Match 8.0%; Score 79; DB 2; Length 336;  
Best local similarity 24.6%; Pred. No. 1.1;  
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9;

QY 49 ANIDNNNGMDSNLSMDYENSFAATRLFS--KKSCIV-----HRMK 88  
DB 209 SSTGNSAGHSNNLLGSE-----VALFAGIASGCIIFIVIIITLVLLKYYRRRRKHS 263  
QY 89 DAMPSLODDITMYKEQKGKGGAPPKDLMVSNPTREVDLNTGCP---KIAGMCGRIPT 145  
DB 264 PQHITLSTLSTLATPKRGNNNGSEPSDV---ITPLKTAD-SVFCPHYEKVSQ-DYGHVY 318  
QY 146 YVAEETPGPNP--LYSK 161  
DB 319 YIVQEMP-POSANITYK 335

RESULT 11  
PCT-US95-08812-2  
Sequence 2, Application PC/TUS9508812  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: HTK LIGAND  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08812  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000

1

10







Mon Apr 14 14:01:53 2003

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Page 1

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:11:18 ; Search time 18.31 Seconds  
(without alignments)  
614.367 Million cell updates/sec

Title: US-09-821-726A-16

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Scoring table: BLOSUM62  
Gapop 10.0 , Capext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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12: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	640	64.5	185	9	US-09-992-598-211
2	640	64.5	185	9	US-09-989-293A-211
3	640	64.5	185	9	US-09-989-735-211
4	640	64.5	185	9	US-09-990-444-211
5	640	64.5	185	9	US-10-001-054-14
6	640	64.5	185	9	US-09-989-730-211
7	640	64.5	185	9	US-09-990-436-211
8	640	64.5	185	9	US-09-991-181-211
9	640	64.5	185	9	US-09-993-687-211
10	640	64.5	185	9	US-09-997-653-211
11	640	64.5	185	9	US-09-997-653-211
12	640	64.5	185	9	US-09-993-667-211
13	640	64.5	185	9	US-09-990-438-211
14	640	64.5	185	9	US-09-990-562-211
15	640	64.5	185	9	US-09-997-428-211
16	640	64.5	185	9	US-09-997-666-211
17	640	64.5	185	9	US-10-227-884-148
18	640	64.5	185	9	US-09-990-711-211
19	640	64.5	185	9	US-10-230-163-148

20	640	64.5	185	9	US-09-989-726-211	Sequence 211, App
21	640	64.5	185	9	US-09-746-783-146	Sequence 146, App
22	640	64.5	185	9	US-09-980-437-211	Sequence 211, App
23	640	64.5	185	9	US-09-998-156-211	Sequence 211, App
24	640	64.5	185	9	US-10-218-631-148	Sequence 148, App
25	640	64.5	185	9	US-10-230-338-148	Sequence 148, App
26	640	64.5	185	9	US-09-991-157-211	Sequence 211, App
27	640	64.5	185	9	US-09-991-172-211	Sequence 211, App
28	640	64.5	185	9	US-09-997-514-211	Sequence 211, App
29	640	64.5	185	9	US-09-997-514-211	Sequence 105, App
30	640	64.5	185	9	US-10-050-704-105	Sequence 211, App
31	640	64.5	185	9	US-10-230-414-148	Sequence 211, App
32	640	64.5	185	9	US-09-990-443-211	Sequence 211, App
33	640	64.5	185	9	US-09-990-726-211	Sequence 211, App
34	640	64.5	185	9	US-09-997-559-211	Sequence 211, App
35	640	64.5	185	9	US-09-997-601-211	Sequence 211, App
36	640	64.5	185	9	US-09-989-729A-211	Sequence 211, App
37	640	64.5	185	9	US-09-990-440-211	Sequence 211, App
38	640	64.5	185	9	US-09-991-854-211	Sequence 211, App
39	640	64.5	185	9	US-09-997-349-211	Sequence 211, App
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41	640	64.5	185	9	US-09-997-628-211	Sequence 211, App
42	640	64.5	185	9	US-09-997-683-211	Sequence 211, App
43	640	64.5	185	10	US-09-989-722-211	Sequence 211, App
44	640	64.5	185	10	US-09-989-723-211	Sequence 211, App
45	640	64.5	185	10	US-09-989-279-211	Sequence 211, App

#### ALIGNMENTS

RESULT 1  
US-09-992-598-211  
Sequence 211, Application US/09992598  
Patient No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
CURRENT FILING DATE: 2001-11-14  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13

us-09-821-726a-16.rapp

1	PRIOR APPLICATION NUMBER: 60/0667770
2	PRIOR FILING DATE: 1997-11-24
3	PRIOR APPLICATION NUMBER: 60/075945
4	PRIOR FILING DATE: 1998-03-25
5	PRIOR APPLICATION NUMBER: 60/078910
6	PRIOR FILING DATE: 1998-03-20
7	PRIOR APPLICATION NUMBER: 60/083322
8	PRIOR FILING DATE: 1998-04-28
9	PRIOR APPLICATION NUMBER: 60/084600
10	PRIOR FILING DATE: 1998-05-07
11	PRIOR APPLICATION NUMBER: 60/087106
12	PRIOR FILING DATE: 1998-05-28
13	PRIOR APPLICATION NUMBER: 60/087607
14	PRIOR FILING DATE: 1998-06-02
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16	PRIOR FILING DATE: 1998-06-02
17	PRIOR APPLICATION NUMBER: 60/087759
18	PRIOR FILING DATE: 1998-06-02
19	PRIOR APPLICATION NUMBER: 60/087827
20	PRIOR FILING DATE: 1998-06-03
21	PRIOR APPLICATION NUMBER: 60/088021
22	PRIOR FILING DATE: 1998-06-04
23	PRIOR APPLICATION NUMBER: 60/088025
24	PRIOR FILING DATE: 1998-06-04
25	PRIOR APPLICATION NUMBER: 60/088026
26	PRIOR FILING DATE: 1998-06-04
27	PRIOR APPLICATION NUMBER: 60/088028
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31	PRIOR APPLICATION NUMBER: 60/088030
32	PRIOR FILING DATE: 1998-06-04
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41	PRIOR APPLICATION NUMBER: 60/088212
42	PRIOR FILING DATE: 1998-06-05
43	PRIOR APPLICATION NUMBER: 60/088217
44	PRIOR FILING DATE: 1998-06-05
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46	PRIOR FILING DATE: 1998-06-09
47	PRIOR APPLICATION NUMBER: 60/088734
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19	PRIOR FILING DATE: 1998-06-19
20	PRIOR APPLICATION NUMBER: 60/089948
21	PRIOR FILING DATE: 1998-06-19
22	PRIOR APPLICATION NUMBER: 60/089952
23	PRIOR FILING DATE: 1998-06-19
24	PRIOR APPLICATION NUMBER: 60/090246
25	PRIOR FILING DATE: 1998-06-22
26	PRIOR APPLICATION NUMBER: 60/090252
27	PRIOR FILING DATE: 1998-06-22
28	PRIOR APPLICATION NUMBER: 60/090254
29	PRIOR FILING DATE: 1998-06-22
30	PRIOR APPLICATION NUMBER: 60/090349
31	PRIOR FILING DATE: 1998-06-23
32	PRIOR APPLICATION NUMBER: 60/090355
33	PRIOR FILING DATE: 1998-06-23
34	PRIOR APPLICATION NUMBER: 60/090429
35	PRIOR FILING DATE: 1998-06-24
36	PRIOR APPLICATION NUMBER: 60/090431
37	PRIOR FILING DATE: 1998-06-24
38	PRIOR APPLICATION NUMBER: 60/090435
39	PRIOR FILING DATE: 1998-06-24
40	PRIOR APPLICATION NUMBER: 60/090444
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42	PRIOR APPLICATION NUMBER: 60/090445
43	PRIOR FILING DATE: 1998-06-24
44	PRIOR APPLICATION NUMBER: 60/090472
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67	PRIOR FILING DATE: 1998-06-26
68	PRIOR APPLICATION NUMBER: 60/091360
69	PRIOR FILING DATE: 1998-07-01
70	PRIOR APPLICATION NUMBER: 60/091478
71	PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 64.5%; Score 640; DB 9; Length 185;  
Best Local Similarity 63.8%; Pred. No. 1,2e-59;  
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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120 MYSVNPFRVLDLTFGPKIAGMCRGIPITYVAEIPGPNOPLXSKCYTDILMLRMSFC 179  
QY 178 GTSYE 182  
DB 180 GDTVE 184

## RESULT 2

US-09-989-293A-211

Sequence 211, Application US/09989293A

Patent No. US20020177164A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Bolstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Geider, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gueney, Austin L.

APPLICANT: Klijavio, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding The Same

FILE REFERENCE: P2730PIC66

CURRENT APPLICATION NUMBER: US/09/989,293A

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/049787

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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 64.5%; Score 640; DB 9; Length 185;  
Best Local Similarity 63.8%; Pred. No. 1.2e-59;  
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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DB 1 MFTTVFAGLLGVFLPALANYINVN-DDNNNGSGQGSVNNHHVAVANNNGWDS 59  
QY 60 WNSLWDYNSFAATPRLFSKSCIVHRMKNKDMPSLODLITWYKQK--GKPGGAPKDL 117  
DB 60 WNSLWDYNSFAATPRLFSKSCIVHRMKNKDMPSLODLITWYKQK--GKPGGAPKDL 119  
QY 118 MYSVNPTRVEDLMTFPGRIAGMCRGIPFYVAEEIPGPNOPLYSKCYTADILMTBSFC 177  
DB 120 MYSVNPTRVEDLMTFPGRIAGMCRGIPFYVAEEIPGPNOPLYSKCYTADILMTBSFC 179  
QY 178 GTSVE 182  
DB 180 GDIVE 184

RESULT 3  
US-09-989-735-211  
Sequence 211, Application US/09989735  
Publication No. US20020193299A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC61

Mon Apr 14 14:01:53 2003

us-09-821-726a-16.rapp

Page 5

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4	PRIOR FILING DATE: 1997-06-16
5	PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Query Match 64.5%; Score 640; DB 9; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.2e-59;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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QY 1 MKLTFVYVGLGLAAGFA-YTVNINGDNGNDGSGQSVSINGVHVNINNNNNWDS 59
Db 1 MKLTFVYVGLGLAAGFA-YTVNINGDNGNDGSGQSVSINGVHVNINNNNNWDS 59
QY 60 WNSLMDYENFSAATRLFSKSCIVHRNKKDAMPISLDDIDMNEOK--GKPGGAPPKDI 117
Db 60 WNSLMDYENFSAATRLFSKSCIVHRNKKDAMPISLDDIDMNEOK--GKPGGAPPKDI 117
QY 118 MYSVNPFRVDDLTDFGKTIAGMKRGIPYVAEIPGPNOPLYSKCKCYTADILMILMSC 177
Db 120 MYSVNPFRVDDLTDFGKTIAGMKRGIPYVAEIPGPNOPLYSKCKCYTADILMILMSC 177
QY 178 GTSVE 182
Db 180 GDTVE 184

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RESULT 4
US-09-990-444-211
Sequence 211, Application US/09990444
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey

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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenlu
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-09

Query Match 64.5% Score 640; DB 9; Length 185;  
 Best Local Similarity 63.8% Pred. No. 1.2e-59;  
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

OY 1 MKLTFVGLGILAPGFA-YTVNINGDGNVDGSGQSVSINGYHVAVDNNNGWDS 59  
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 DB 120 MYSVNPTRVEDLMTFGPKIAGMCRGIPYVAEETIPGPNOPLYSKKCYVADIILMISFC 179  
 OY 178 GTSVE 182  
 DB 180 GDTVE 184

RESULT 5  
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 Publication No. US20020192209A1  
 GENERAL INFORMATION:  
 APPLICANT: Genentech, Inc.  
 APPLICANT: Baker, Kevin  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Gurney, Austin  
 APPLICANT: Hebert, Carolyn  
 APPLICANT: Henzel, William  
 APPLICANT: Kabadoff, Rhonda  
 APPLICANT: Shelton, David  
 APPLICANT: Smith, Victoria  
 APPLICANT: Watanabe, Colin  
 APPLICANT: Wood, William  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
 TITLE OF INVENTION: CELL GROWTH  
 FILE REFERENCE: P3034RIJCT  
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 CURRENT FILING DATE: 2001-11-30  
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PRIOR APPLICATION NUMBER: PCT/US01/27099  
PRIOR FILING DATE: 2001-08-29  
NUMBER OF SEQ ID NOS: 91  
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ORGANISM: Homo Sapien  
US-10-001-054-14

Query Match 64.5%; Score 640; DB 9; Length 185;  
Best Local Similarity 63.8%; Pred. No. 1.2e-59;  
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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180 GDTVE 184  
Db 180 GDTVE 184  
RESULT 6  
US-09-989-730-211  
Sequence 211, Application US/09989730  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Iva J.  
APPLICANT: Napier, Mary A.

APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C69  
CURRENT FILING DATE: 2001-11-20  
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 PRIOR FILING DATE: 1998-07-09

Query Match 64.5% Score 640; DB 9; Length 185;  
 Best Local Similarity 63.8%; Pred. No. 1.2e-59;  
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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RESULT 7  
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 Sequence 211, Application US/09990436  
 Publication No. US20020198148A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Baton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
APPLICANT: Kijavich, Ivar J.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C14  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535

APPLICANT: Ferrara, Napoleon  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Klavio, Ivar J.  
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APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C53  
CURRENT APPLICATION NUMBER: 60/049787  
CURRENT FILING DATE: 2001-11-16  
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PRIOR FILING DATE: 1998-06-05  
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PRIOR FILING DATE: 1998-07-09

Query Match 64.5%; Score 640; DB 9; Length 185;  
Best Local Similarity 63.8%; Pred No. 1.2e-59;  
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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DB 60 WNSIWDYGNGFAATRLRLOKTKCTLVHKNKQVMPISLOSLALVYKELQCKGCGPPPKCL 119  
OY 118 MYSVNPFRVEDLNTFFGPKIAGMCGIPTVVAEETPGPNOLYKSKKXTDILWILMSPC 177  
DB 120 MTSVNPKNVDDLSKFGKNIAMKCGIPTVVAEEMQASLFFYSGTCITTSVIMTVISFC 179  
OY 178 GTSVE 182  
DB 180 GDTVE 184

RESULT 9  
US-09-933-687-211  
Sequence 211, Application US/09993687  
Publication No. US20020198149A1  
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
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 APPLICANT: Goddard, Audrey  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
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 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C11  
 CURRENT FILING DATE: 2002-11-14  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 64.5%; Score 640; DB 9; Length 185;  
Best Local Similarity 63.8%; Pred. No. 1,2e-59;  
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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DB 1 MKLTMEVVGILGLDAPGEA-YTVNINSGDGVDSGOOSVINGVHVNAINNNWDS 59  
QY 60 WNSIMDVGNGGPAATRLFFSKKSCIVHHRNKDAPSLDIDDTNVECK--GKPGGAPPPDL 117  
DB 60 WNSIMDVGNGGPAATRLFFSKKSCIVHHRNKDAPSLDIDDTNVECK--GKPGGAPPPDL 117  
QY 118 MYSVNPTRVEDLNTFGFKTIGKMGCRGTPTYAAEETPPGNOPLVSKCYTFADILMLMSFC 177  
DB 120 MYSVNPTRVEDLNTFGFKTIGKMGCRGTPTYAAEETPPGNOPLVSKCYTFADILMLMSFC 177  
QY 178 GTSVE 182  
DB 180 GDTVE 184

RESULT 10  
US-09-989-734-211  
Sequence 211, Application US/09989734  
Publication No. US20030003531A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 927301C64  
CURRENT FILING DATE: 2001-11-19  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match  
 Best Local Similarity 64.5%; Score 640; DB 9; Length 185;  
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 M K L T M F V V G L L G L A A P G F A - Y V I N I N G N D G N V D G S G Q O S V S I N G V H V A N I D N N N G N D S 59  
 D b 1 M K T I V A G L I G V L A P A L A N Y I N I N V - D D N N A G S G Q O S V S V N N E H V A N Y A N D N N G N D S 59  
 QY 60 W N S I M D Y E N S F A A T R L F S K S C I V H R M N D A M P S I O D D L T M Y K E O K - - G K G P G A P P K D L 117  
 D b 60 W N S I M D Y G N G F A A T R L F Q K T C I V H K M N E V P S I O S D A L V K E K K L O G K G P G P P K G L 119  
 QY 118 M Y S V N P R E D I N T E C P K A G M C R G I P T Y V A E I P G P N Q P L Y S K K C Y A D I L T I R S F C 177  
 D b 120 M Y S V N P K Y V D I S K F G K N I A N N C R I P T Y M A E M Q E A S L F Y S G T C T T S V L M I W I D I S F C 179



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Page 17

QY 178 GTSVE 182  
DB 180 GDIVE 184

RESULT 11  
US-09-997-653-211  
Sequence 211, Application US/09997653  
Publication No. US20030008297A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavio, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC38  
CURRENT APPLICATION NUMBER: US/09/997,653  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 64.5% Score 640; DB 9; Length 185;  
 Best Local Similarity 63.8% Pred. No. 1.2e-59;  
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QY 1 MRLTMVGLGLLAAPGFA-YTVNINGDGNVDSGQSVSYNGVHANYANDNNNGDMS 59  
 DB 1 MKFTTIFAGLIGVFLAPALANYINYN-DDNNAGSGQSVSYNHNANYANDNNNGDMS 59  
 QY 60 WNSLMDYENSPATRLFSKSCIVHRMKNDAAPSLDDDTWVKECK--GKPGGAPPKDL 117  
 DB 60 WNSIMDYGNFPAIRLFQKTCIVHRMKNKEVPSIOSIDALVKEKKLGKGGGPPPKGL 119

QY 118 MYSVNPTRVEDLNTPEKGIAGKCRGIPYVAEIPGPNOLYSKKCYTADIILMMSFC 177  
 DB 120 MYSVNPKNKVDLSKFGKINAMCRGIPYVAEIPGPNOLYSKKCYTADIILMMSFC 179  
 QY 178 GTSVE 182  
 DB 180 GDIVE 184

RESULT 12  
 US-09-993-667-211  
 Sequence 211, Application US/09993667  
 Publication No. US20030022187A1  
 GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Bolstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C4  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
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 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
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 PRIOR APPLICATION NUMBER: 60/065311  
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 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087827  
 PRIOR FILING DATE: 1998-06-03  
 PRIOR APPLICATION NUMBER: 60/088021



Db 1 MKFTVAGLGLVFLAPALANYINYN-DDNNAGSGQGSVSNHNNHANNVNDNNGMS 59  
 QY 60 WMSLMDYSPATRLRFKSKSCVHRMNDAMSLODDLTWKEQ--GKPGGADPPKDL 117  
 60 WMSLMDYSPATRLRFKSKSCVHRMNDAMSLODDLTWKEQ--GKPGGADPPKDL 117  
 Db 60 WMSLMDYSPATRLRFKSKSCVHRMNDAMSLODDLTWKEQ--GKPGGADPPKDL 117  
 QY 118 WMSVNRVEDINTGPKTAGMCRGIPYVAEIRPPNPOLYSKKCYTDJILMLMSC 177  
 120 WMSVNRVEDINTGPKTAGMCRGIPYVAEIRPPNPOLYSKKCYTDJILMLMSC 177  
 Db 120 WMSVNRVEDINTGPKTAGMCRGIPYVAEIRPPNPOLYSKKCYTDJILMLMSC 177  
 QY 178 GTSVE 182  
 180 GTSVE 184

RESULT 13

US-09-990-438-211

Sequence 211, Application US/09990438

Publication No. US20030027734A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C3  
 CURRENT APPLICATION NUMBER: US/09/990,438  
 PRIOR FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787  
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 PRIOR APPLICATION NUMBER: 60/066770  
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 PRIOR APPLICATION NUMBER: 60/075945  
 PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 60/078910  
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 PRIOR APPLICATION NUMBER: 60/088858  
 PRIOR FILING DATE: 1998-06-11  
 PRIOR APPLICATION NUMBER: 60/088861  
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 PRIOR APPLICATION NUMBER: 60/088876  
 PRIOR FILING DATE: 1998-06-11  
 PRIOR APPLICATION NUMBER: 60/089105  
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 PRIOR APPLICATION NUMBER: 60/089512  
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 PRIOR APPLICATION NUMBER: 60/089514  
 PRIOR FILING DATE: 1998-06-16  
 PRIOR APPLICATION NUMBER: 60/089532  
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 PRIOR APPLICATION NUMBER: 60/089599  
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 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089653  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089801  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089907  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089908

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Mon Apr 14 14:01:53 2003

PRIOR FILING DATE: 1998-06-18  
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 PRIOR FILING DATE: 1998-06-19  
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 PRIOR FILING DATE: 1998-06-19  
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 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090862  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
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 PRIOR FILING DATE: 1998-07-01  
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 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match

64.5%; Score 640; DB 9; Length 185;

Best Local Similarity 63.8%; Pred. No. 1.2e-59;  
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMPVGLIGLAPGFA-YTVNINCNDGNDVSGGOOSYSINGVNVANINDNNQWDS 59  
 Db 1 MKLTMPVGLIGLAPGFA-PALANYNINVN--DDNNNAGSGOOSVSVNNEHNVANINDNNQWDS 59

QY 60 WNSLMDYENSEFAATRLFSKKSCLVHRMKNKDAMPSTLDDIDFTVVKQK--GKPGCAPPKDL 117  
 Db 60 WNSLMDYENSEFAATRLFSKKSCLVHRMKNKDAMPSTLDDIDFTVVKQK--GKPGCAPPKDL 119

QY 118 MYSVNPVRVEDLMTFCPKIKGMRGIPYVAEIEGPNQPLYSKKCYADILMLRMSFC 177  
 Db 120 MYSVNPVRVEDLMTFCPKIKGMRGIPYVAEIEGPNQPLYSKKCYADILMLRMSFC 179

QY 178 GTSVE 182  
 Db 180 GTSVE 184

RESULT 14  
 US-09-990-562-211  
 Sequence 211, Application US/09990562  
 Publication No. US20030027985A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Baton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerlitsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Goddard, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C18  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/075945  
 PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/087106

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1	PRIOR APPLICATION NUMBER: 60/089801
2	PRIOR FILING DATE: 1998-06-18
3	PRIOR APPLICATION NUMBER: 60/089907
4	PRIOR FILING DATE: 1998-06-18
5	PRIOR APPLICATION NUMBER: 60/089908
6	PRIOR FILING DATE: 1998-06-18
7	PRIOR APPLICATION NUMBER: 60/089947
8	PRIOR FILING DATE: 1998-06-19
9	PRIOR APPLICATION NUMBER: 60/089948
10	PRIOR FILING DATE: 1998-06-19
11	PRIOR APPLICATION NUMBER: 60/089952
12	PRIOR FILING DATE: 1998-06-19
13	PRIOR APPLICATION NUMBER: 60/090246
14	PRIOR FILING DATE: 1998-06-22
15	PRIOR APPLICATION NUMBER: 60/090252
16	PRIOR FILING DATE: 1998-06-22
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60	PRIOR FILING DATE: 1998-07-01
61	PRIOR APPLICATION NUMBER: 60/091478
62	PRIOR FILING DATE: 1998-07-02
63	PRIOR APPLICATION NUMBER: 60/091519
64	PRIOR FILING DATE: 1998-07-01
65	PRIOR APPLICATION NUMBER: 60/091544
66	PRIOR FILING DATE: 1998-07-01
67	PRIOR APPLICATION NUMBER: 60/091626
68	PRIOR FILING DATE: 1998-07-02
69	PRIOR APPLICATION NUMBER: 60/091633
70	PRIOR FILING DATE: 1998-07-02
71	PRIOR APPLICATION NUMBER: 60/091978
72	PRIOR FILING DATE: 1998-07-07
73	PRIOR APPLICATION NUMBER: 60/091982

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
Query Match      64.5%; Score 640; DB 9; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.2e-59;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MLTMEVVLGLLAPGA-ITVNIINGNDGVDSGGOOSVINGVHNANIDNNNGMDS 59
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DB 1 MKETTFACLVFLPALANININ-NDNNAGSGOOSVYNNEHNANVNDNNNGMDS 59
   11 : 1111 : 11 : 11111111 : 1111 : 111111111111
QY 60 WNSLWDESFATRLSKKSCIVHRMKNDAFSLDLDITWKEOK--GKGFGAPPKDL 117
   1111111111111111111111111111111111111111111111111111111
DB 60 WNSLWDESFATRLSKKSCIVHRMKNDAFSLDLDITWKEOK--GKGFGAPPKDL 119
   1111111111111111111111111111111111111111111111111111111
QY 118 MYSVNPRTVEDLNTGCPKTLAGMCRGIPTYVAEELPPNPQPLVSKKCYTDIILMLMFC 177
   1111111111111111111111111111111111111111111111111111111
DB 120 MYSVNPRTVEDLNTGCPKTLAGMCRGIPTYVAEELPPNPQPLVSKKCYTDIILMLMFC 179
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QY 178 GTSVE 182
   1 : 111
DB 180 GDTVE 184

RESULT 15
US-09-997-428-211
; Sequence 211, Application US/09997428
; Publication No. US20030027162A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottlieb, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
; FILE REFERENCE: P2730P1C44
; CURRENT APPLICATION NUMBER: US/09/997,428
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
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 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
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PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 64.5%; Score 640; DB 9; Length 185;  
 Best Local Similarity 63.8%; Pred. No. 1.2e-59;  
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTFVGLGLLPAPGA-YTVNINCDGNVDSGQSVSTNGVHNTANDNNNGWDS 59  
 DB 1 MKFTIVFAGILGVFLPALANTYNNV-DNNNAGSGQSVSTNNHNTANDNNNGWDS 59  
 QY 60 MNSIMDYENSEFATRLFSKSCIVHRANKDAMPISLDDTWYKEDK--GKPGGAPPKDL 117  
 DB 60 MNSIMDYGNFATRLFKKTCIVHRMKEVMPISLSDLVKKEKLGKPGGPPKGL 119  
 QY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPYVAEIPGPNQPLYSKRCYTADILMLMSFC 177  
 DB 120 MYSVNPKNVDDLSKFGKNINAMNCRGIPYMAEEMQASLFFYSGTCYTTSLMIVDISPC 179  
 QY 178 GTSVE 182  
 DB 180 GDTVE 184

Search completed: April 11, 2003, 16:17:45  
 Job time : 19.31 secs



GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:53 ; Search time 19.8108 Seconds  
(without alignments)  
892.885 Million cell updates/sec

Title: US-09-821-726a-16

Perfect score: 993  
Sequence: 1 MKLTMFVYVGLGLLAAPGFA.....TADILMLRMSCGTSVENVY 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 73:\*

1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	9.0	345	2	Stral/Epi92 protei
2	88.5	8.9	842	2	hypothetical prote
3	86.5	8.7	658	2	hypothetical tureo
4	85.5	8.6	335	2	chondromodulin-1 p
5	85.5	8.6	346	2	elk ligand - human
6	85.5	8.6	539	2	phosphoenolpyruvat
7	85	8.6	345	2	phosphoenolpyruvat
8	84	8.5	643	2	hypothetical gene
9	83.5	8.4	782	2	lipoprotein associat
10	81	8.2	617	2	lipoprotein [impor
11	80.5	8.1	547	2	hypothetical prote
12	80.5	8.1	728	2	diacylglycerol kin
13	80.5	8.1	2295	2	probable membrane
14	80	8.1	3194	2	toxin-like outer m
15	80	8.1	3197	2	phosphoenolpyruvat
16	79.5	8.0	1215	2	chitinase A [impor
17	79	8.0	186	2	hypothetical prote
18	79	8.0	336	2	hepatoma transmem
19	79	8.0	138170	2	gene hrad protein
20	78	7.9	362	2	hypothetical prote
21	78	7.9	642	2	hypothetical prote
22	77.5	7.8	407	2	regulatory protein
23	77.5	7.8	419	2	hypothetical prote
24	77.5	7.8	459	2	hypothetical prote
25	77.5	7.8	1109	2	hypothetical prote
26	77.7	7.8	363	2	hypothetical prote
27	76.5	7.7	194	2	beta-cysteine-rich
28	76.5	7.7	493	1	cellulase (EC 3.2.
29	76.5	7.7	504	2	mucin (clone pgm31

30	76	7.7	631	2	T07670	probable protein k
31	76	7.7	1278	2	A71609	probable secreted
32	75.5	7.6	194	2	S41761	cysteine-rich prot
33	75.5	7.6	397	2	S64841	hypothetical prote
34	75.5	7.6	421	2	E64819	yeblu protein - Esc
35	75.5	7.6	421	2	B90741	hypothetical prote
36	75.5	7.6	421	2	E85591	hypothetical prote
37	75	7.6	331	2	AG2679	conserved hypothet
38	75	7.6	352	2	E97461	MYB DNA-binding-li
39	75	7.6	423	2	T51794	hypothetical prote
40	74.5	7.5	404	2	S50648	hypothetical prote
41	74.5	7.5	624	2	B82108	flagellar hook-ass
42	74.5	7.5	747	2	S46608	TTA1 protein - ye
43	74.5	7.5	1045	2	S23570	pol polyprotein ho
44	74.5	7.5	1362	2	A75207	amylolipulanase P
45	74	7.5	241	2	S71473	endo-1,4-beta-xyla

## ALIGNMENTS

## RESULT 1

148780  
Stral/Epi92 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence.revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: 148780; A55507; A55062; S52670  
R:Bouillet, P.; Ould-Abdelghani, M.; Vitale, S.; Garnier, J.M.; Schubaur, B.; Doll  
Dev. Biol. 170, 420-433, 1995  
A:Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in p19 embryone  
A:Reference number: 148780; MUID:9537533; PMID:7649373  
A:Accession: 148780  
A:Status: preliminary; translated from GR/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-345 <RPS>  
A:Cross-references: EMBL:Z48781; NID:9747858; PIDN:CAA8695.1; PID:9747859  
R:Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A  
Genomics 24, 127-132, 1994  
A:Title: Genomic organization and chromosomal localization of mouse Epi92, a gene enc  
A:Reference number: A55507; MUID:95203867; PMID:7896266  
A:Accession: A55507  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-345 <PLE>  
A:Cross-references: GB:U07598  
R:Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.  
J. Biol. Chem. 269, 26606-26609, 1994  
A:Title: cDNA cloning and characterization of a ligand for the Cck5 receptor protein-  
A:Reference number: A55062; MUID:95014510; PMID:7929389  
A:Accession: A55062  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-89, 'T', 91-345 <SHA>  
A:Cross-references: GB:U12963; NID:9575928; PIDN:AAA53231.1; PID:9575929  
C:Genetics:  
A:Gene: Epi92

Query Match 9.0%; Score 89; DB 2; Length 345;  
Best Local Similarity 23.1%; Pred. No. 1.2;  
Matches 40; Conserves 26; Mismatches 57; Indels 50; Gaps 10;

OY	16	APGEVYTVNINDGNVGS-----GQSVSINGVHNVANIDNNNGWDSNSIMDYENSPA 71
DB	195	APG-----RSGQSDSGKHETVQDEKSGGAGCGSGDSDSPFNSKVAL-----FA 241
OY	72	ATRLPSKKSCTV-----HAMKNDAMPSTLDDDTTWKKEQKCGPGCAP 113
DB	242	AV-----GAGCVIFLLIIFLVLLKLRKRHRHQOAAALSTLSPKSGSTAGTE 297
OY	114	PKDLVSNPPEVEDLNTFGP---KIAGMCRGIPYVAEIEPGNPQ--LYSK 161
DB	298	PSDIIIPLTTE---NNICPHEKVSQ-DYGHPIYIOEMP-POSPANITYK 344



C:Date: 15-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 28-May-1999  
C:Accession: S46993  
R:Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrar, T.; Kozlowski, J. 13, 3757-3762, 1994  
EMBO J.  
A:Title: Molecular characterization of a family of ligands for eph-related tyrosine kinases  
A:Reference number: S46993; MUID:9434923; PMID:8070404  
A:Accession: S46993  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-346 <BEC>  
A:Cross-references: GB:009304; NID:g538366; PIDN:AAA53093.1; PID:g538367

Query Match	8.6%;	Score	85.5;	DB	2;	Length	346;
Best Local Similarity	23.1%;	Pred.	No. 2.5;				
Matches	40;	Conservative	23;	Mismatches	61;	Indels	49;
						Gaps	11;

```

QY      16  A G C A T Y T I N I G N D N N D G S G C G S Y S I N G Y I N V A N I D I N N G - W D S M S L M D Y E N S F - A A T /
      11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      195  A G C ----- S R C L G D S D G K ----- H E T V N O E K S G S P G A S G C S S G G P D C F F N S K V 238
QY      74  R L F S K - K S C I Y ----- H R M K D A P S I Q D D I P T W K E D G K G P G C A P 113
      11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      239  A L F A A V A G A C V I F L I I I F L Y L L L K L R K R H R K H Q R A A L S T L S A P G C S G A G T E 298
QY      114  P E D L M A Y S N P F V E D L N T E G P - K I A M C G C I P T Y A A E I P G N O P - I Y S K 161
      11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      299  P E D I I I P L E T T E --- N N I C P H E V A S G - D I G H P Y I Y O E M P - P O S A N I I Y K 345

```

phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - *Salmonella enterica* subsp. *enterica*  
AF0998  
C:species: *Salmonella enterica* subsp. *enterica* serovar Typhi  
A:Note: this species has also been called *Salmonella typhi*  
C:date: 09-Nov-2001  
C:sequence-revision 09-Nov-2001  
C:text-change 27-Nov-2001  
C:accession: AF0998

Query Match	8.6%	Score 85.5:	DB 2:	Length 539:
Best Local Similarity	23.4%	Pred. No. 4.4:		
Matches 47; Conservative	32;	Mismatches 65;	Indels 57;	Gaps 11;

```

Oy      1  MKLTMFV--GLGLLAAGFATVYINQDNCN-----DSGQOASVINGVHNAID  52
Db      210  MKKMFESVNYTLPLGLASMHCSANV-CEKGDVAVFQLSTGKTLTSTPKRRLIG-D  267
Oy      53  NNNQMSDMSNLMDYENS-PAATRLFLSKS--CIYHRMKNKAMP-----93
Db      268  DEHQMD-DGVFNPEGGYAKTIKLSKAEPELYHAIIRDALLENVAREDDVDGDS  324
Oy      94  -----LQDLTMVYKQCKGP-----GGAPKDLMTSVNPTREDLNT  133
Db      327  KTEPTRVSYPIYHIDNLIVKSPVSKAGHATKVIETLADAEVLDPVSKL-TANOTYHFLSG  385
Oy      132  FGPKIAGMCGI-----PTYVA  148
Db      386  FTAKLACTERGVTEPTTFESA  406

```

RESULT 7  
I58406

LERK-2 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence-revision 26-Jul-1996 #text-change 05-Nov-1999  
C:Accession: 158406  
R:Flatcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hol  
Oncogene 9, 3241-3248, 1994  
A>Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily con  
A:Reference number: 158406; MUID:95022634; PMID:7956548

Query Match	8.6%	Score 85:	DB 2:	Length 345:
Best Local Similarity	23.1%	Pred. No. 2.8:		
Matches 40:	Conservative 24:	Mismatches 59:	Indels 50:	Gaps 10:

```

OY      16 AGGAAATVAINCNDQNVGS-----GGGVSATNGVHNAINDNNNGMSMSLWYENSA /
Db      195 AFG-----KSGQSDSGKHETVYNQQLKSGKAGAGSSGDTDFPMSKAL-----FA 241
OY      72 ATRLEKSKSCI-----HRMKDAMPSLDLDLTWYKEQKGKGGPGAR 113
Db      242 AV-----GAGCVIFLLITFLVLLKLRKHKKHQQQAALLSLSTLAPSGDGGTAGTE 297
OY      114 PKDLMYSNPTREVEDLNTGPR--KIAGMCKGIPYYAAEELPGMOP--LYSK 161
Db      298 PSLIIILPLKTFE-----NNYCPHYEKVSG-DYGHAPYYIOEMP-POSPANIIYKK 344

```

RESULT 8  
 S17997  
 hypothetical gene COX1 intron 3 protein - yeast (*Kluyveromyces marxianus* var. *lactis*)  
 C|Species: mitochondrion *Kluyveromyces marxianus* var. *lactis*, *Candida sphaerica*  
 C|Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 08-Dec-2000  
 C|Accession: S17997  
 R|Hardy, C.M.; Clark-Walker, G.D.  
 Curr. Genet. 20: 99-114, 1991  
 A|Title: Nucleotide sequence of the COX1 gene in *Kluyveromyces lactis* mitochondrial DNA  
 A|Reference number: S17993; M0ID:92035081; PMID:1657415

F:1-324/Region: cox1 exons 1 to 3 encoded  
F:325-643/Region: cox1 intron encoded

```

.. Query Match      8.5%; Score 84; DB 2; Length 943;
Best Local Similarity 26.9%; Pred. No. 7.6;
Matches 29; Conservative 20; Mismatches 39; Indels 20; Gaps

Oy 24 NNNNNCNGVSGCGGASLNGVHNVAINDNNMGDSMNSLMDYEN--SFATRLFSKRS 80
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 347 NNNNNNNNNNNPPOGSPVIGMTAGMKTIVNNNSYSSNNNNNNYKRLTICTNLYS--- 403
      | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 81 CTVRRMKKDMAPLQDLDFYVKQKKKKGGGAPRDLWYSVNPFRVED 128
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 404 ---NLAKREYNTMM--TKYIK-----IPNNIMIMINGILLTD 437

```

## RESULT 9

RESULT 11  
T25478

Query Match	8.18;	Score 80.5;	DB 2;	Length 728;
Best Local Similarity	24.18;	Pred. No. 19;		
Matches 34;	Conservative 27;	Mismatches 57;	Indels 23;	Gaps 7





GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:33 ; Search time 40.8222 Seconds  
(without alignments)  
928.727 Million cell updates/sec

Title: US-09-821-726A-16

Perfect score: 993  
Sequence: 1 MKLMEYVGLGLAAGFA.....TADILWLIRMSFGTSVEY 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP-archaea:\*  
2: SP-bacteria:\*  
3: SP-fungi:\*  
4: SP-human:\*  
5: SP-invertebrate:\*  
6: SP-mammal:\*  
7: SP-mhc:\*  
8: SP-organelle:\*  
9: SP-plant:\*  
10: SP-rodent:\*  
11: SP-virus:\*  
12: SP-virus:\*  
13: SP-vertebrate:\*  
14: SP-unclassified:\*  
15: SP-rvivirus:\*  
16: SP-bacteriophage:\*  
17: SP-archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	234	23.6	191	11	09D0T7	09d0t7 mus muscu
2	167.5	16.9	184	11	09C0S6	09c0s6 mus muscu
3	93	9.4	618	5	09V629	09v629 drosophila
4	91	9.2	577	5	09V615	09v615 drosophila
5	89.5	9.0	292	5	025762	025762 plasmodium
6	88.5	8.9	860	5	019852	019852 caenorhabd
7	88	8.9	2206	12	099FJ4	099fj4 porcine tes
8	88	8.9	2206	12	099FJ3	099fj3 porcine tes
9	86.5	8.7	658	3	059779	059779 schistosacc
10	86	8.7	531	16	093JF5	093jf5 streptomyc
11	85	8.6	2206	12	099FJ5	099fj5 porcine tes
12	84	8.5	319	8	034834	034834 kiuyveromy
13	83.5	8.4	782	5	090431	090431 plasmodium
14	83.5	8.4	782	5	090429	090429 plasmodium
15	83.5	8.4	782	5	090414	090414 plasmodium
16	83.5	8.4	782	5	025730	025730 plasmodium

17	83.5	8.4	782	5	026007	026007 plasmodium
18	83.5	8.4	3322	16	08X0Z5	08X0Z5 ralsionia s
19	82.5	8.3	493	9	09JMM8	09JMM8 bacterioph
20	82	8.3	602	6	09GL34	09GL34 bos taurus
21	82	8.3	757	17	08TIV7	08TIV7 methanosarc
22	81	8.2	553	11	09QWR9	09QWR9 mus musculu
23	81	8.2	547	5	0980P1	0980P1 mycoplasma
24	80.5	8.1	782	5	P91006	P91006 caenorhabdi
25	80.5	8.1	782	5	025875	025875 plasmodium
26	80.5	8.1	1332	5	09BNI7	09BNI7 drosophila
27	80.5	8.1	1332	5	09BNI7	09BNI7 drosophila
28	80.5	8.1	2295	5	09TY98	09TY98 plasmodium
29	80.5	8.1	2295	5	09TY98	09TY98 plasmodium
30	80	8.1	2009	5	09VXM0	09VXM0 drosophila
31	80	8.1	3194	16	09ZLM3	09ZLM3 helicobacte
32	79.5	8.0	494	2	005527	005527 comamonas a
33	79.5	8.0	1215	1	09UWR7	09UWR7 pyrococcus
34	79.5	8.0	1960	5	09UOK8	09UOK8 plasmodium
35	79.5	8.0	2432	12	09IQP4	09IQP4 aichi virus
36	79	8.0	186	5	001876	001876 caenorhabdi
37	79	8.0	338	4	015333	015333 homo sapien
38	78.5	7.9	501	5	09BID4	09BID4 anopheles g
39	78	7.9	319	3	096067	096067 neurospora
40	78	7.9	642	5	017169	017169 caenorhabdi
41	78	7.9	664	5	027435	027435 plasmodium
42	77.5	7.8	419	5	077316	077316 plasmodium
43	77.5	7.8	428	3	012646	012646 neocallimas
44	77.5	7.8	439	3	092401	092401 agaricus bl
45	77.5	7.8	458	10	09FVH2	09FVH2 arabidopsis

## ALIGNMENTS

RESULT 1  
ID 09D0T7 PRELIMINARY: PRT: 191 AA.  
AC 09D0T7  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE 1190003M12Rik protein.  
GN 1190003M12Rik.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,  
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Mazarrelli J., Mombaerts P.,  
RA Lyons P., Marchionni L., Mashima J., Rodriguez I., Sakamoto N.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weyt C., Whitaker C., Williams L.,  
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
RA Hayashikawa Y.,  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL: AK004474; BMB23320.1;  
MGD: MGI:1916138; 1190003M12Rik.

```

SQ SEQUENCE 191 AA: 20772 MW: 76D7DB4796A8B4D CRC64;
Query Match 23.6%; Score 234; DB 11; Length 191;
Best Local Similarity 31.1%; Pred. No. 1,4e-14;
Matches 56; Conservative 40; Mismatches 66; Indels 18; Gaps 7;

OY 3 LIMEVYGLGLLAAPGFAATVNINGDNG-NVDS-QGQSVSINGVHNVANIDNNNGDSW 60
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 21 VVVFELV-----PALATL-----NTSDSYPLDSVGTGTHVDAALGVYSIRNSVQSEW 69
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 61 NSLMDYENFAATRLFSKSCICVHRMKNKDMPSLDL-DTWKEQKGGKGGAPPDLMY 119
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 70 DEVMYKNNLLAKLESKMACVLAQMDPAFSLDITQALGQASGHPY---PTRGLEY 126
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 120 SYNPRVEDLNTFGPKIACMGCPITYVA-EELIPGNQPLYSKCYTADILMLRMSFG 178
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 127 TVLPSRIKMLAQGYVPIKDLCAVPTYPFARQCKEGTALMDPSCELOLLSLWGLSTIG 186
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
OY 09C0S6 PRELIMINARY; PRT; 184 AA.
ID 09C0S6;
AC 09C0S6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE 1810036H07RIK protein.
GN 1810036H07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH, AND PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shunagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aekawa T., Hara A., Fukunishi Y., Konno H., Adachi Y., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Katsukawa T., Saito R.,
RA Kodota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita W., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008986; BAB26008.1; -
DR EMBL; AK007451; BAB25046.1; -
DR EMBL; AK007705; BAB25201.1; -
DR MGD; MGI:1913534; 1810036H07RIK.
DR PRINTS; PR01559; DUFFYANTIGEN.
SQ SEQUENCE 184 AA: 20469 MW: 612A18FABE652230 CRC64;

Query Match 16.9%; Score 167.5; DB 11; Length 184;
Best Local Similarity 25.7%; Pred. No. 3,1e-08;
Matches 46; Conservative 46; Mismatches 76; Indels 11; Gaps 5;

OY 5 MFEVGLGLLAAPGFAATVNINGDNGSGQSVSINGVHNVANIDNNNGDSWNSLW 64
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 8 LVVLSTFGIOSEAELTFNFVPSKNG---GNIDETVTIDNQWNTATINIHSGSCSSSTIF 64
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 65 DYENSEFAATRLFSKSCICVHRMKNKDMPSLDLDTYVKQKGGKGGAPPKDLMYSVNP- 123
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

```





DR EMBL: U42834; AAA83583.2; .  
 DR HSP: Q61193; 1RLF.  
 DR InterPro: IPR000651; RasGEFN.  
 DR InterPro: IPR001895; RasGEF\_CDC25.  
 DR InterPro: IPR00159; RA\_domain.  
 DR Pfam: PF00788; RA\_1.  
 DR Pfam: PF00617; RasGEF; 1.  
 DR Pfam: PF00618; RasGEF; 1.  
 DR SMART: SM00314; RA; 1.  
 DR SMART: SM00147; RasGEF; 1.  
 DR SMART: SM00229; RasGEF; 1.  
 DR PROSITE: PS00720; GDS\_CDC25; 1.  
 DR Hypothetical protein.  
 KW SEQUENCE 860 AA; 96122 MW; 16088524FBC65CA5 CRC64;

Query Match 8.9%; Score 88.5; DB 5; Length 860;  
 Best Local Similarity 25.0%; Pred. No. 7.6;  
 Matches 27; Conservative 15; Mismatches 61; Indels 5; Gaps 2;

QY 29 DGNVDSGQGSVINGVHANNINNNNGWSLMDYENSFAATRLFSKSKCIVHMK 88  
 DB 600 DGRDGGPPGVPPLSGTSTPSSANASMTGSGSEFPSSLFPYS---HSRK 655  
 QY 89 DAMPSLQDLDTMVEKQKGGAPPKDLMYSVNPTRVEDLNTFGRPT 136  
 DB 656 SGESSLQEVKTSW-STRASADGTSIGTSLRSATPIRTLAEEVDSKV 702

RESULT 7

QY 099FJ4 PRELIMINARY; PRT; 2206 AA.  
 AC 099FJ4;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 OS Porcine teschovirus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Teschovirus.  
 OX NCBI\_TaxID=118140;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VIR 3764/86;  
 RX MEDLINE=21105197; Pubmed=11160660;  
 RA Zell R., Dauber M., Krumholz A., Henke A., Birch-Hirschfeld E.,  
 RA Stelzner A., Prager D., Wurm R.;  
 RT "Porcine teschovirus Comprise at Least Eleven Distinct Serotypes;  
 RT Molecular and Evolutionary Aspects.";  
 RL J. Virol. 75:1620-1631(2001).  
 DR EMBL: AF296113; AAK12406.1; .  
 DR HSP: Q88590; 1TME.  
 DR InterPro: IPR004004; Calli.pol\_hel.  
 DR InterPro: IPR001676; RHV.  
 DR InterPro: IPR000605; RNA\_helicase.  
 DR InterPro: IPR001205; RNA\_pol\_P3D.  
 DR Pfam: PF00073; Thv. 2.  
 DR Pfam: PF00680; RNA\_dep.RNA\_pol; 1.  
 DR Pfam: PF00910; RNA\_helicase; 1.  
 DR PRINTS: PR00918; CALICVIRUSNS.  
 SQ SEQUENCE 2206 AA; 247376 MW; 76FDA9AA1ADA08E CRC64;

Query Match 8.9%; Score 88; DB 12; Length 2206;  
 Best Local Similarity 24.1%; Pred. No. 27;  
 Matches 52; Conservative 18; Mismatches 66; Indels 80; Gaps 11;

QY 4 TMFVGLGILAAPGAYVNING---NDGNVDSGQGSVINGVHANNINNNNGMD- 58  
 DB 275 TRFHGGCLGVFAIPERSVFSKLOGIPLYDGKNDG-----ANSNI-----MDK 317  
 QY 59 -----SNLSLMYENS-----FATRLFSKSKCIVH-----RMN 87  
 DB 318 FTTWHNPDMAMFGAWYSHDPTDTHKWKPKLEQYGGISPSOLF---CFPHQLINPRTN 373

QY 88 KDAMPLODLD-----TMVEKQKGGAPPKDLMYSVNPTRVEDLNT 131  
 DB 374 SSATLCLEPVDGCPITDVTVHCMAIVVYLRELTVALGGTPTSDINVSAPC---DVEY 430  
 QY 132 FGPKIAGMCRG-IPTYVAEEIPGNPLYSKCKYTA 166  
 DB 431 HGLRQDSMYGPIPKF---DIDASKALFSSSTOPYTA 463

RESULT 8

QY 099FJ3 PRELIMINARY; PRT; 2206 AA.  
 AC 099FJ3;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 OS Porcine teschovirus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Teschovirus.  
 OX NCBI\_TaxID=118140;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VIR 2500/99;  
 RX MEDLINE=21105197; Pubmed=11160660;  
 RA Zell R., Dauber M., Krumholz A., Henke A., Birch-Hirschfeld E.,  
 RA Stelzner A., Prager D., Wurm R.;  
 RT "Porcine teschovirus Comprise at Least Eleven Distinct Serotypes;  
 RT Molecular and Evolutionary Aspects.";  
 RL J. Virol. 75:1620-1631(2001).  
 DR EMBL: AF296113; AAK12407.1; .  
 DR HSP: Q88590; 1TME.  
 DR InterPro: IPR004004; Calli.pol\_hel.  
 DR InterPro: IPR001676; RHV.  
 DR InterPro: IPR000605; RNA\_helicase.  
 DR InterPro: IPR001205; RNA\_pol\_P3D.  
 DR Pfam: PF00073; Thv. 2.  
 DR Pfam: PF00680; RNA\_dep.RNA\_pol; 1.  
 DR Pfam: PF00910; RNA\_helicase; 1.  
 DR PRINTS: PR00918; CALICVIRUSNS.  
 SQ SEQUENCE 2206 AA; 247391 MW; 24C81E3E20C37405 CRC64;

Query Match 8.9%; Score 88; DB 12; Length 2206;  
 Best Local Similarity 24.1%; Pred. No. 27;  
 Matches 52; Conservative 20; Mismatches 64; Indels 80; Gaps 12;

QY 4 TMFVGLGILAAPGAYVNING---NDGNVDSGQGSVINGVHANNINNNNGMD- 58  
 DB 275 TRFHGGCLGVFAIPERSVFSKLOGIPLYDGKNDG-----ANSNI-----MDK 317  
 QY 59 -----SNLSLMYENS-----FATRLFSKSKCIVH-----RMN 87  
 DB 318 FTTWHNPDMAMFGAWYSHDPTDTHKWKPKLEQYGGISPSOLF---CFPHQLINPRTN 373  
 QY 88 KDAMPLODLD-----TMVEKQKGGAPPKDLMYSVNPTRVEDLNT 131  
 DB 374 SSATLCLEPVDGCPITDVTVHCMAIVVYLRELTVALGGTPTSDINVSAPC---DVEY 430  
 QY 132 FGPKIAGMCRG-IPTYVAEEIPGNPLYSKCKYTA 166  
 DB 431 HGLRQDSMYGPIPKF---DIDASKALFSSSTOPYTA 463

RESULT 9

QY 059779 PRELIMINARY; PRT; 658 AA.  
 AC 059779;  
 DT 01-AUG-1998 (Tremblrel. 07, Created)  
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)  
 DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 OS Hypothetical 69.7 kDa ASN/THR-rich protein C320.02C in chromosome III.  
 SC Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RC Wood V., Rajandream M.A., Barrell B.G., Medler H., Wambutt R.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 468-658 FROM N.A.  
 RC STRAIN=972;  
 RC Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL022245; CA18304.1;  
 DR EMBL: AL031764; CA21105.1;  
 KM Hypothetical protein.  
 SQ SEQUENCE 658 AA; 69695 MW; 63082230B6488AC5 CRC64;  
 Query Match 8.7%; Score 86.5; DB 3; Length 658;  
 Best Local Similarity 25.4%; Pred. No. 8.5;  
 Matches 36; Conservative 26; Mismatches 53; Indels 27; Gaps 7;  
 QY 1 MKLTFVGLGLLAPGF---AYTVINGNDGNDGSGOQSVSINGVNV---ANI-- 51  
 Db 321 METITVGNNDSPSQNFSGKTFVSNANSSNSN-DGSSSKSLDVGSFVNAFKQLVND 379  
 QY 52 ---DNNNGWDSNLSMDYENSFAT-RLFSKKSCLVHRMNDAMPPLSDLDITVKEQKG 107  
 Db 380 NSSNNSSGNDSTRTGAAVFAAGKFFSOHSCDLASGNKSAOEGONFLSWESE--- 436  
 QY 108 GPGGAPKDL---YSVNPTR 125  
 Db 437 -----AKNLAKTKTYSANQSO 452  
 RESULT 10  
 O93JF5 PRELIMINARY; PRT; 531 AA.  
 ID O93JF5;  
 AC 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Hypothetical protein STRAC16H6.07.  
 GN STRAC16H6.07 OR SC05972 OR SCBAC16H6.07.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Collins M.R., Harris D.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RX MEDLINE=97000351; Pubmed=8843436;  
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
 RL Mol. Microbiol. 21:77-96(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2).";  
 RL Nature 417:141-147(2002).  
 DR EMBL: AL596162; CAC44586.1;  
 DR InterPro: IPR000051; SAM\_bind.  
 KM Hypothetical protein.  
 SQ SEQUENCE 531 AA; 58656 MW; 714F103D5C29B3F CRC64;  
 Query Match 8.7%; Score 86; DB 16; Length 531;  
 Best Local Similarity 28.4%; Pred. No. 7.3;  
 Matches 27; Conservative 12; Mismatches 34; Indels 22; Gaps 4;  
 QY 96 DLDTWKEQKGGPGGAPKDLMSVNV--PFRVEDL-----NFGPKIAGCGRIPITYV 147  
 Db 92 DAVALLVRGKGGKGGAPPAALAQYVNDPRYAASSLLAVLSSVSSAMRGYCKSRPERA 151  
 QY 148 AEELP-----GPN--OPLYSKCYTADI 168  
 Db 152 AESLPLRVEITPALPARGPDIVRLPEPLGWTVDV 186  
 RESULT 11  
 O99FJ5 PRELIMINARY; PRT; 2206 AA.  
 ID O99FJ5;  
 AC 099FJ5;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Polyprotein.  
 OS Porcine teschovirus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Teschovirus.  
 OX NCBI\_TaxID=118140;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VIR 918-19/85;  
 RX MEDLINE=21105197; Pubmed=11160660;  
 RA Zell R., Dauber M., Krumbholz A., Henke A., Birch-Hirschfeld E.,  
 RA Stelzner A., Prager D., Wurm R.;  
 RT "Porcine teschovirus: Comprise at Least Eleven Distinct Serotypes;  
 Molecular and Evolutionary Aspects.";  
 RL J. Virol. 75:1620-1631(2001).  
 DR EMBL: AF296111; AAK12405.1;  
 DR HSSP: Q88590; TMF.  
 DR InterPro: IPR004004; Calic1\_pol\_hel.  
 DR InterPro: IPR001676; RNV.  
 DR InterPro: IPR000605; RNA\_helicase.  
 DR InterPro: IPR001205; RNA\_pol\_P3D.  
 DR Pfam: PF00073; rnv; 2.  
 DR Pfam: PF00680; RNA\_dep\_PNA\_pol; 1.  
 DR Pfam: PF00910; RNA\_helicase; 1.  
 DR PRINTS: PR00918; CALICVIRUSNS.  
 SQ SEQUENCE 2206 AA; 247295 MW; 113CC439CB2C774F CRC64;  
 Query Match 8.6%; Score 85; DB 12; Length 2206;  
 Best Local Similarity 23.6%; Pred. No. 52;  
 Matches 51; Conservative 21; Mismatches 64; Indels 80; Gaps 12;  
 QY 4 TMFVGLGLLAPGFAYTVNNG---NDGAVDGGGQSVSINGVNVANNDNNNGMD- 58  
 Db 275 TRHGGCLGFAIFSVSKLOGIPLTYDGNKG-----NVSNT-----MDR 317  
 QY 59 --SWNS-----LMDYNSF-----AATRLFSKKSCLVH-----RMN 87  
 Db 318 FTTHNPDAMFGAMYSHTADKDKHMYKPKLEQYGISPSOLF-----CFPHLLINPRN 373

QY 88 KDMPSLQDID-----TWKEQKGGKPGAPKDLMSVNPTRVEDLMT 131  
 Db 374 SSATLCLPFDGCPITDVTVCWPAIVVVYLRRLTVALGTSVDLINSVAPC---DVEY 430  
 QY 132 FGKINGMCRG-IPYVAEIEEPNPLYSKCYTA 166  
 Db 431 HGLRQDSMTGPIPKF---DIDASKALFSSSTQPYTA 463

RESULT 12  
 ID Q34834 PRELIMINARY; PRT; 319 AA.  
 AC Q34834;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Intron orf.  
 OS Kluveromyces lactis (Yeast).  
 OG Mitochondrion.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluveromyces.  
 OX NCBI\_TaxID=28985;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K8;  
 RX MEDLINE=92035081; PubMed=1657415;  
 RA Hardy C.M., Clark-Walker G.D.;  
 RT "Nucleotide sequence of the COX1 gene in Kluveromyces lactis  
 RT mitochondrial DNA: Evidence for recent horizontal transfer of a group  
 RT II Intron."  
 RL Curr. Genet. 20:99-114(1991).  
 DR EMBL; X57546; CAA40768.1; -;  
 DR InterPro; IPR004860; IAGLIDAGC\_2.  
 DR Pfam; PF03161; IAGLIDAGC\_2; 1.  
 KW Mitochondrion.  
 SO SEQUENCE 319 AA; 37564 MW; 476288776D11F85 CRC64;

Query Match 8.5%; Score 84; DB 8; Length 319;  
 Best Local Similarity 26.9%; Pred. No. 6;  
 Matches 29; Conservative 20; Mismatches 39; Indels 20; Gaps 4;  
 QY 24 NINGDNGVSGQGSVINGVHNVANIDNNQWDSNLSMDYEN---SFAATRLFSKKS 80  
 Db 23 NHHNNNNNNPFGQSPYIGMTAGMKIYNNNSYNNNNNYNNKLTITGTNLS--- 79  
 QY 81 CIVHRNKKDAMPISLQDIDTWKEQKGGKPGAPKDLMSVNPTRVED 128  
 Db 80 ---NLNKKYNNNTM-IKYMIK-----IPNNIMIMINGILTTD 113

RESULT 13  
 ID Q90431 PRELIMINARY; PRT; 782 AA.  
 AC Q90431;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE Rhoptyr-associated protein 1 (Fragment).  
 GN Rapi.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Saul A.;  
 RT "Efficacy of vaccines containing Rhoptyr-Associated Proteins RAPI and  
 RT RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF205282; AAF23403.1; -;  
 FT NON\_TER 782  
 SO SEQUENCE 782 AA; 90066 MW; B344948D5806F7DC CRC64;  
 Query Match 8.4%; Score 83.5; DB 5; Length 782;

Best Local Similarity 24.0%; Pred. No. 20;  
 Matches 35; Conservative 21; Mismatches 63; Indels 27; Gaps 6;  
 QY 26 NGDNG-NDVSGGQGSVINGVHNVANIDNNQWDSNLS---LMDYENSPATRLFSKSC 81  
 Db 18 NVADGIVNNGDNNYKGTI--INDFNFDYNYWPIPKKEFLNLYEDKFSSEPLEKSS 75  
 QY 82 IVHRNKKDAMPISLQDIDTWKEQKGGKPGAPK-----DLMSVNPTRV 126  
 Db 76 V-----DDGNTLNTDITSTSNKSSK-KHGGRSVRSASAAALIEDDSKDDMEKASPSVY 129  
 QY 127 EDLMTFGPKTAGMCRGIPYVAEIEP 152  
 Db 130 KTSPTSGTQTSGILKSSSPSSSKSSP 155

RESULT 14  
 ID Q90429 PRELIMINARY; PRT; 782 AA.  
 AC Q90429;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE Rhoptyr-associated protein 1.  
 GN Rapi.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVO;  
 RA Saul A.;  
 RT "Efficacy of vaccines containing Rhoptyr-Associated Proteins RAPI and  
 RT RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF205284; AAF23405.1; -;  
 SO SEQUENCE 782 AA; 90041 MW; 27FEA9BC930434E CRC64;

Query Match 8.4%; Score 83.5; DB 5; Length 782;  
 Best Local Similarity 24.0%; Pred. No. 20;  
 Matches 35; Conservative 21; Mismatches 63; Indels 27; Gaps 6;  
 QY 26 NGDNG-NDVSGGQGSVINGVHNVANIDNNQWDSNLS---LMDYENSPATRLFSKSC 81  
 Db 18 NVADGIVNNGDNNYKGTI--INDFNFDYNYWPIPKKEFLNLYEDKFSSEPLEKSS 75  
 QY 82 IVHRNKKDAMPISLQDIDTWKEQKGGKPGAPK-----DLMSVNPTRV 126  
 Db 76 V-----DDGNTLNTDITSTSNKSSK-KHGGRSVRSASAAALIEDDSKDDMEKASPSVY 129  
 QY 127 EDLMTFGPKTAGMCRGIPYVAEIEP 152  
 Db 130 KTSPTSGTQTSGILKSSSPSSSKSSP 155

RESULT 15  
 ID Q90414 PRELIMINARY; PRT; 782 AA.  
 AC Q90414;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE Rhoptyr associated protein-1.  
 GN Rapi-1.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RCCL/HN;  
 RA Li X.R., Luo S.H., Yu X.B., Shan Z.X., Ma C.L.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF206631; AAF15365.1; -;

SO SEQUENCE 782 AA; 90082 MW; 8E1F4CF283903FD CRC64;

Query Match 8.4%; Score 83.5; DB 5; Length 782;

Best Local Similarity 24.0%; Pred. No. 20;

Matches 35; Conservative 21; Mismatches 63; Indels 27; Gaps 6;

QY 26 NGNDG-NVDSGGQOSVSIKGVHNYANIDNNNGWDSWNS--LMDYENSFAATRLFSKKS 81  
 18 NVADGINVNDGNNYKTI--INDFNFDYNYWTPINKKEFLNSYEDDFSSSEFLNKSS 75  
 QY 82 IVHRMNDAMPSTLQDLDTWVKEQKGGPGGAPK-----DLMTSVNPTRV 126  
 76 V-----DDGININLDTSTSNKSSK-KHGKRSRVRSASAAALLEEDSKDMEFKASPSVY 129  
 Db 127 EDLNTFGPKIAGMCRGIPYVAEEIP 152  
 130 KTSTPSGTGTSGLKSSSPSTKSSP 155

Search completed: April 11, 2003, 16:14:27  
 Job time : 45.8222 secs



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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:08:13 ; Search time 4.24796 Seconds  
(without alignments)  
290.907 Million cell updates/sec

Title: US-09-821-726A-13\_COPY\_78\_119  
Perfect score: 221  
Sequence: 1 KKTCLVHKMKREKVPISQSL.....LVKKKLLQGGKGGPPPKGL 42

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59.5	26.9	269	2	US-07-857-224B-14 Sequence 14, Appl
2	59.5	26.9	269	2	US-07-857-224B-16 Sequence 16, Appl
3	57	25.8	467	4	US-09-002-361-3 Sequence 3, Appl
4	57	25.8	496	4	US-09-002-361-2 Sequence 2, Appl
5	53.5	24.2	494	4	US-09-126-420A-26 Sequence 2, Appl
6	53.5	24.2	542	1	US-08-701-380-2 Sequence 13, Appl
7	53.5	24.2	542	1	US-08-032-365A-13 Sequence 6, Appl
8	53	24.0	3174	2	US-09-477-451-3 Sequence 3, Appl
9	52	23.5	199	4	US-09-497-779A-6 Sequence 24, Appl
10	52	23.5	248	4	US-09-452-239-26 Sequence 119, App
11	52	23.5	248	4	US-08-484-905-119 Sequence 119, App
12	52	23.5	265	2	US-08-481-985B-119 Sequence 39, Appl
13	52	23.5	265	2	US-08-481-985B-119 Sequence 39, Appl
14	52	23.5	265	2	US-08-481-985B-119 Sequence 39, Appl
15	52	23.5	298	4	US-08-207-481-39 Sequence 182, App
16	52	23.5	298	5	PCT-US95-02689-41 Sequence 182, App
17	52	23.5	331	2	US-08-997-080-182 Sequence 182, App
18	52	23.5	331	2	US-08-997-080-182 Sequence 182, App
19	52	23.5	331	4	US-09-095-855-182 Sequence 182, App
20	52	23.5	331	4	US-09-324-542-182 Sequence 182, App
21	52	23.5	331	4	US-09-205-426-182 Sequence 18, Appl
22	51	23.1	247	4	US-09-452-239-182 Sequence 2, Appl
23	50.5	22.9	386	4	US-08-875-082-2 Sequence 2, Appl
24	50.5	22.9	752	4	US-09-817-180-2 Sequence 4, Appl
25	50.5	22.9	822	4	US-09-817-180-4 Sequence 2, Appl
26	50	22.6	428	1	US-08-332-576-2 Sequence 2, Appl
27	50	22.6	428	5	PCT-US95-13672-2 Sequence 2, Appl

28	50	22.6	673	4	US-09-078-347A-2	Sequence 2, Appl
29	49.5	22.4	469	1	US-08-363-215-1	Sequence 1, Appl
30	49.5	22.4	469	3	US-08-807-342B-6	Sequence 6, Appl
31	49	22.2	168	1	US-08-441-139-10	Sequence 10, Appl
32	49	22.2	280	4	US-09-383-586-18	Sequence 18, Appl
33	49	22.2	855	4	US-09-813-819-2	Sequence 2, Appl
34	49	22.2	855	4	US-09-920-048-2	Sequence 10, Appl
35	48.5	21.9	224	4	US-09-091-899-10	Sequence 20, Appl
36	48.5	21.9	376	4	US-08-874-569B-20	Sequence 37, Appl
37	48.5	21.9	1440	4	US-09-357-251-37	Sequence 48, Appl
38	48.5	21.9	1512	4	US-09-443-184-48	Patent No. 5223423
39	48.5	21.9	3025	6	US-08-997-080-141	Sequence 141, App
40	48	21.7	73	2	US-08-997-362-141	Sequence 141, App
41	48	21.7	73	4	US-09-095-855-141	Sequence 141, App
42	48	21.7	73	4	US-09-324-542-141	Sequence 141, App
43	48	21.7	73	4	US-09-205-426-141	Sequence 141, App
44	48	21.7	73	4	US-09-562-737-70	Sequence 70, Appl
45	48	21.7	503	4		

## ALIGNMENTS

RESULT 1  
US-07-857-224B-14  
Sequence 14, Application US/07857224B  
Patent No. 5958784  
GENERAL INFORMATION:  
APPLICANT: Jenner, Steven A.  
TITLE OF INVENTION: Predicting Folded Structures of Proteins  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESS: Steven A. Jenner  
STREET: Hadlaubstrasse 151  
CITY: Zurich  
STATE: none  
COUNTRY: Switzerland  
ZIP: (note: this is an international post code) CH-8092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/857,224B  
FILING DATE: 03/25/92  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA: none  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (International) 41 1 632 2830  
TELEFAX: (International) 41 1 262 2437  
TELEX: none  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
ORGANISM: human  
FEATURE: Protein kinase; Table 8 Column 15  
PUBLICATION INFORMATION:  
AUTHORS: Hanks, S. K.  
AUTHORS: Hunter, T. M.  
AUTHORS: Hunter, T. M.  
TITLE: The protein kinase family  
JOURNAL: Science  
VOLUME: 241  
PAGES: 42-52  
DATE: 1988  
US-07-857-224B-14

Query Match 26.9%; Score 59.5; DB 2; Length 269;  
Best Local Similarity 39.4%; Pred. No. 3.1;  
Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

Qy 9 MKKEVMPISLSDALVKEK---LQKRGPGGP 38  
Db 34 LKKDVIQDDVDCTLVEKRVLALGGRGPGRP 66

RESULT 2  
US-07-857-224B-16

; Sequence 16, Application US/07857224B  
; Patent No. 5958784

; GENERAL INFORMATION:

; APPLICANT: Bener, Steven A.

; TITLE OF INVENTION: Predicting folded structures of proteins

; NUMBER OF SEQUENCES: 114

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Steven A. Bener

; STREET: Hadlaubstrasse 151

; CITY: Zurich

; STATE: none

; COUNTRY: Switzerland

; ZIP: (note: this is an international post code) CH-8092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

; OPERATING SYSTEM: Macintosh 7.0

; SOFTWARE: Microsoft Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/857,224B

; FILING DATE: 03/25/92

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (International) 41 1 632 2830

; TELEFAX: (International) 41 1 262 2437

; TELEX: none

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 269

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; DESCRIPTION: protein

; ORGANISM: human

; PUBLICATION INFORMATION:

; AUTHORS: Hanks, S. K.

; AUTHORS: Quinn, A. M.

; AUTHORS: Hunter, T.

; TITLE: The protein kinase family

; JOURNAL: Science

; VOLUME: 241

; PAGES: 42-52

; DATE: 1988

; US-07-857-224B-16

Query Match 26.9%; Score 59.5; DB 2; Length 269;  
Best Local Similarity 39.4%; Pred. No. 3.1;  
Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

Qy 9 MKKEVMPISLSDALVKEK---LQKRGPGGP 38  
Db 34 LKKDVIQDDVDCTLVEKRVLALGGRGPGRP 66

RESULT 3  
US-09-002-361-3

; Sequence 3, Application US/09002361

; Patent No. 6329516

; GENERAL INFORMATION:

; APPLICANT: Halling, Blaik

; TITLE OF INVENTION: Lepidopteran GABA-gated chloride

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dechert Price & Rhoads

; STREET: 997 Lenox Drive, Building 3, Suite 210

; CITY: Lawrenceville

; STATE: NJ

; COUNTRY: USA

; ZIP: 08543

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: IBM Compatible

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/002,361

Query Match 25.8%; Score 57; DB 4; Length 467;  
Best Local Similarity 36.8%; Pred. No. 12;  
Matches 14; Conservative 8; Mismatches 8; Indels 8; Gaps 2;

Qy 8 MKKEVMPISLSDALVKEKLGKPGG----PPK 40  
Db 314 QMKRQRTAVOKMAA---EKKMQIDGPPGSAEPIPPR 348

RESULT 4  
US-09-002-361-2

; Sequence 2, Application US/09002361  
; Patent No. 6329516

; GENERAL INFORMATION:

; APPLICANT: Halling, Blaik

; TITLE OF INVENTION: Lepidopteran GABA-gated chloride

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dechert Price & Rhoads

; STREET: 997 Lenox Drive, Building 3, Suite 210

; CITY: Lawrenceville

; STATE: NJ

; COUNTRY: USA

; ZIP: 08543

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: IBM Compatible

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/002,361

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bloom, Allen

; REGISTRATION NUMBER: 29,135

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 609-520-3214

; TELEFAX: 609-520-3259

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 467 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-002-361-3



FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bloom, Allen  
REGISTRATION NUMBER: 29,135  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-520-3214  
TELEFAX: 609-520-3259  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 496 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-002-361-2

Query Match 25.8%; Score 57; DB 4; Length 496;  
Best Local Similarity 36.8%; Pred. No. 13;  
Matches 14; Conservative 8; Mismatches 8; Indels 8; Gaps 2;

QY 8 KMKKEVMSIOSLALVKEKKLOGKPGG-----PPPK 40  
Db 343 QMKRFTAVQKMA---EKKMIDGPSSAEIPPPR 377

RESULT 5  
US-09-126-420A-26  
Sequence 26, Application US/09126420A  
Patent No. 6376753  
GENERAL INFORMATION:  
APPLICANT: BATTARD, YANNICK  
APPLICANT: ROBINEAU, TIBURCE  
APPLICANT: DURST, FRANCIS  
APPLICANT: WERCK-REICHART, DANIELE  
APPLICANT: DIDIERJEAN, LUC  
TITLE OF INVENTION: PURIFIED CYTOCHROME P450 CYP76B1 FROM HELIANTHUS  
TITLE OF INVENTION: PARTICULAR FOR THE DEGRADATION OF ENVIRONMENTAL  
TITLE OF INVENTION: POLLUTANTS AND FOR ALTERING THE RESISTANCE OF PLANTS S  
FILE REFERENCE: 03715.0032  
CURRENT APPLICATION NUMBER: US/09/126,420A  
CURRENT FILING DATE: 1998-07-30  
PRIOR APPLICATION NUMBER: 60/054,351  
PRIOR FILING DATE: 1997-07-31  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 494  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-126-420A-26

Query Match 24.2%; Score 53.5; DB 4; Length 494;  
Best Local Similarity 40.6%; Pred. No. 38;  
Matches 13; Conservative 5; Mismatches 9; Indels 5; Gaps 1;

QY 13 VMSIOSLALV-----KEKKLOGKPGGPP 39  
Db 8 LVASVAFSLVLMVSKRKRLSPGPTP 39

RESULT 6  
US-08-701-380-2  
Sequence 2, Application US/08701380  
Patent No. 5686598  
GENERAL INFORMATION:

APPLICANT: NORTH, Michael  
APPLICANT: NISHINA, Patsy  
APPLICANT: MAGGERT, Juergen  
TITLE OF INVENTION: GENES ASSOCIATED WITH RETINAL  
TITLE OF INVENTION: DYSTROPHIES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/701,380  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SHERWOOD, Pamela J.  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: A-63565/PJS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-494-8700  
TELEFAX: 415-494-8771  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 542 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-701-380-2

Query Match 24.2%; Score 53.5; DB 1; Length 542;  
Best Local Similarity 35.4%; Pred. No. 42;  
Matches 17; Conservative 7; Mismatches 15; Indels 9; Gaps 2;

QY 1 KKTCTYHKKMKKEVMSIOSLALVKEKKLOGKPGG-----PPPK 42  
Db 135 KKEKILLPPKK--PLREKSSADLKERAKAGPRDGLSPPPPKPL 179

RESULT 7  
US-09-032-365A-13  
Sequence 13, Application US/09032365A  
Patent No. 6114502  
GENERAL INFORMATION:  
APPLICANT: No. 6114502th, Michael  
APPLICANT: Nishina, Patsy  
APPLICANT: Maggert, Juergen  
APPLICANT: No. 6114502en-Traulh, Konrad  
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH  
TITLE OF INVENTION: NEUROSENSORY DEFECTS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bozicevic & Reed, LLP  
STREET: 285 Hamilton Avenue, Suite 200  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/032,365A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: SEQ-2C1P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-327-3400  
TELEFAX: 650 327-3231  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 542 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-032-365A-13

Query Match 24.2%; Score 53.5; DB 3; Length 542;  
Best Local Similarity 35.4%; Pred. No. 42;  
Matches 17; Conservative 7; Mismatches 15; Indels 9; Gaps 2;

QY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLOGKPGG-----PPPKGL 42  
Db 135 KKEKILPPKK---PLREKSSADLKERAKKAGPPRGDLSPPPPKPL 179

RESULT 8  
US-08-477-451-3  
Sequence 3, Application US/08477451  
Patent No. 5928865  
GENERAL INFORMATION:  
APPLICANT: Covacci, Antonello  
TITLE OF INVENTION: Helicobacter Pylori CagI Region  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,451  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McClung, Barbara G.  
REGISTRATION NUMBER: 33,113  
REFERENCE/DOCKET NUMBER: 0335.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2708  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3174 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-451-3

Query Match 24.0%; Score 53; DB 2; Length 3174;

Best Local Similarity 42.3%; Pred. No. 3,6e+02;  
Matches 11; Conservative 7; Mismatches 6; Indels 2; Gaps 1;  
QY 6 VHKMKKEVMPSTQSLDALVKEKKLOG 31  
Db 871 VHRLEKEQI--IOMLOTIIRNKKFQG 894

RESULT 9  
US-09-497-779A-6  
Sequence 6, Application US/09497779A  
Patent No. 6297368  
GENERAL INFORMATION:  
APPLICANT: DEPINHO, RONALD A.  
TITLE OF INVENTION: MYC HOMOLOG REGION II - ASSOCIATED PROTEIN AND USES THEREOF  
FILE REFERENCE: 96700-609  
CURRENT APPLICATION NUMBER: US/09/497,779A  
CURRENT FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: US 08/946,692  
PRIOR FILING DATE: 1997-10-08  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 199  
TYPE: PRT  
ORGANISM: MOUSE  
US-09-497-779A-6

Query Match 23.5%; Score 52; DB 4; Length 199;  
Best Local Similarity 34.0%; Pred. No. 21;  
Matches 16; Conservative 5; Mismatches 14; Indels 12; Gaps 2;

QY 8 KMKKEVMPSTQSLDALVKEK-----KLOG-KGPGGPPPKGL 42  
Db 20 KKKSSPPHLOKITKLTVKSEVLAQSPLSKLRGPKAKRGCPKGL 66

RESULT 10  
US-09-452-239-24  
Sequence 24, Application US/09452239  
Patent No. 6465229  
GENERAL INFORMATION:  
APPLICANT: Ratajski, Antoni J.  
APPLICANT: Fader, Gary M.  
TITLE OF INVENTION: Plant Caffeoil-CoA O-methyltransferase  
FILE REFERENCE: BB1284 US MA  
CURRENT APPLICATION NUMBER: US/09/452,239  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: 60/110,594  
EARLIER FILING DATE: 1998-December-02  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 24  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (7)  
US-09-452-239-24

Query Match 23.5%; Score 52; DB 4; Length 248;  
Best Local Similarity 32.3%; Pred. No. 27;  
Matches 10; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLOG 31  
Db 126 EKAGVAHKIDFREGPALPLDLVLIKDEKNGK 156

RESULT 11  
US-09-452-239-26

Sequence 26, Application US/09452239  
Patent No. 6465229  
GENERAL INFORMATION:  
APPLICANT: Rafalski, Antoni J.  
APPLICANT: Fader, Gary M.  
APPLICANT: Cahoon, Rebecca E.  
TITLE OF INVENTION: Plant Caffey1-CoA O-Methyltransferase  
FILE REFERENCE: B81284 US NA  
CURRENT APPLICATION NUMBER: US/09/452,239  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: 60/110,594  
EARLIER FILING DATE: 1998-December-02  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 26  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Glycine max  
US-09-452-239-26

Query Match 23.5%; Score 52; DB 4; Length 248;  
Best Local Similarity 32.3%; Pred. No. 27;  
Matches 10; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 KTCIVHKKMKVPSIOSDALVKKKKG 31  
DB 126 EKAGVAHKIDFREGPALPLIDVLKDEKNKG 156

RESULT 12  
US-08-484-905-119  
Sequence 119, Application US/08484905  
Patent No. 5976551  
GENERAL INFORMATION:  
APPLICANT: Motiez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: An Altered Major Histocompatibility  
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the  
NUMBER OF SEQUENCES: 127  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS-/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,905  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Potler, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 03495.0106-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 119:

SEQUENCE CHARACTERISTICS:  
LENGTH: 265 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-905-119

Query Match 23.5%; Score 52; DB 2; Length 265;  
Best Local Similarity 81.8%; Pred. No. 29;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 32 KPGGPPPKGL 42  
DB 253 KPGGPPPKGL 263

RESULT 13  
US-08-481-985B-119  
Sequence 119, Application US/08481985B  
Patent No. 6011146  
GENERAL INFORMATION:  
APPLICANT: Motiez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: Altered Major Histocompatibility Complex  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS-/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,985B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0106-04000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 119:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-481-985B-119

Query Match 23.5%; Score 52; DB 3; Length 265;  
Best Local Similarity 81.8%; Pred. No. 29;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 32 KPGGPPPKGL 42  
DB 253 KPGGPPPKGL 263

```

RESULT 14
US-08-370-476-119
; Sequence 119, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Castrouge, Armande
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flunegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370.476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-370-476-119

Query Match 23.5%; Score 52; DB 4; Length 265;
Best Local Similarity 81.8%; Pred. No. 29;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 32 KPGGPPPKGL 42
Db 253 KPGGPPPKGL 263

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RESULT 15
US-08-207-481-39
; Sequence 39, Application US/08207481
; Patent No. 5820866
; GENERAL INFORMATION:
; APPLICANT: Kappler, John W.

```

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; APPLICANT: Marrack, Philippa
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL
; REGULATION
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH
; STREET: 1700 LINCOLN STREET, SUITE 3500
; CITY: DENVER
; STATE: COLORADO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,481
; FILING DATE: 04-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-207-481-39

Query Match 23.5%; Score 52; DB 2; Length 298;
Best Local Similarity 81.8%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 32 KPGGPPPKGL 42
Db 286 KPGGPPPKGL 296

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Search completed: April 11, 2003, 16:16:38  
 Job time : 5.24796 secs

Mon Apr 14 14:01:41 2003

us-09-821-726a-13\_copy\_78\_119.rpr

GenCore version 5.1.4-p5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: April 11, 2003, 16:07:53 ; Search time 4.52202 Seconds  
(without alignments)  
892.885 Million cell updates/sec

Title: US-09-821-726a-13\_COPY\_78\_119  
Perfect score: 221  
Sequence: 1 KKTGIVHKMKKEVMPSTISL.....LVKKKLGKGGPGPPPKGL 42

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	29.0	1677	2	T14267
2	61.5	27.8	311	2	H82966
3	59.5	26.9	682	1	KIRBGC
4	59.5	26.9	697	1	KIRBGC
5	59.5	26.9	697	1	KIRBGC
6	59.5	26.9	697	2	JN0548
7	59.5	26.9	697	2	D24664
8	57.5	26.7	759	2	T43031
9	57.5	26.0	634	2	B70381
10	57.5	26.0	2459	2	H36812
11	57.5	25.8	997	2	S4457
12	55.5	25.1	444	2	H82821
13	55.5	24.9	160	2	R89841
14	55.5	24.9	230	2	G83993
15	55.5	24.9	380	2	T29445
16	54.5	24.7	477	1	TVMCS
17	54.5	24.7	820	1	TVCNPF
18	54.5	24.4	875	1	ITECAP
19	54.5	24.4	875	1	B91018
20	54.5	24.4	891	2	AC0149
21	54.5	24.4	966	2	A71080
22	53.5	24.2	494	2	A32030
23	53.5	24.2	502	1	HURFAB
24	53.5	24.0	233	1	T04084
25	53.5	24.0	240	1	HURFAB
26	53.5	24.0	263	1	A37048
27	53.5	24.0	875	2	D85862
28	52.5	23.8	98	2	S15106

30	52.5	23.8	156	2	S74733	hypothetical prote
31	52.5	23.8	303	1	S28392	protein-tyrosine-p
32	52.5	23.8	488	2	JC7510	benzoate X recepto
33	52.5	23.8	383	2	A97295	fusion of Uroporph
34	52.5	23.8	592	2	T29402	hypothetical prote
35	52.5	23.8	712	2	T12452	hypothetical prote
36	52.5	23.8	1189	2	S56852	hypothetical prote
37	52.5	23.5	148	2	T26759	major histocompat
38	52.5	23.5	233	2	I59495	H-2 class II histo
39	52.5	23.5	238	2	A53278	H-2 class II histo
40	52.5	23.5	252	1	H1MSBF	H-2 class II histo
41	52.5	23.5	263	1	H1MSBK	H-2 class II histo
42	52.5	23.5	263	1	H1MSBU	H-2 class II histo
43	52.5	23.5	263	1	H1MSBS	H-2 class II histo
44	52.5	23.5	263	2	A61389	H-2 class II histo
45	52.5	23.5	263	2	A61389	H-2 class II histo

ALIGNMENTS

RESULT 1  
T14267  
Xin protein, stage early embryo - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: T14267  
R:Wang, D.Z., Lin, J.J.C.  
submitted to the EMBL Data Library, March 1998  
A:Description: Involvement of a novel gene, Xin, in cardiac looping.  
A:Reference number: 217948  
A:Accession: T14267  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1677 <MAN>  
A:Cross-references: EMBL:AF051945; NID:q2970645; PID:q2970646; PIDN:MAC06023.1  
A:Experimental source: cardiac muscle; stage early embryo

Query Match 29.0%; Score 64; DB 2; Length 1677;  
Best Local Similarity 30.6%; Pred. No. 17;  
Matches 11; Conservative 10; Mismatches 3; Indels 12; Gaps 1;  
Qy 5 IVHKMKKEVMPSTISLALVKKKLGKGGPGPPK 40  
Db 561 MIHQEEO-----KPEEGKGGPGPPPE 584

RESULT 2  
H82966  
Probable transcription regulator PA5437 [imported] - Pseudomonas aeruginosa (strain P  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: H82966  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
..; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: H82966  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-311 <STO>  
A:Cross-references: GB:AE004956; GB:AE004091; NID:9951760; PIDN:AA08822.1; GSPDB:GN  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA5437  
C:Superfamily: transcription activator LysR-type  
Query Match 27.8%; Score 61.5; DB 2; Length 311;  
Best Local Similarity 37.5%; Pred. No. 5.8; Indels 7; Gaps 2;  
Matches 15; Conservative 7; Mismatches 11

OY 4 C1VHKMKVPSIQSLDLVKEK-----LOGK--GFGC 36  
 Db 270 CLVHAKGKRLSPVAQAFVAFVEERKALISQLAGRPAGPGC 309

## RESULT 3

KIRBOG  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 30-Sep-1992 #sequence-revision 30-Sep-1992 #text-change 11-Jun-1999  
 R:Accession: C24664  
 R:Comments: L.; Parker, P.D.; Rhee, L.; Yang-Feng, T.L.; Chen, E.; Waterfield, M.D.; Fra  
 Science 233, 859-866, 1986  
 A:Title: Multiple, distinct forms of bovine and human protein kinase C suggest diversity  
 A:Accession: C24664  
 A:Reference: A94291, PMID:86289426; PMID:3755548  
 A:Molecule type: mRNA  
 A:Residues: 1-682 <OHN>  
 A:Cross-references: GB:M13976; NID:9163525; PIDN:AAA30704.1; PID:9163526  
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-st  
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,  
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may  
 C:Superfamily: The zinc-stabilized regions bind diacylglycerol and phorbol esters.  
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bindin  
 F:3-13/Region: pseudophosphorylation motif  
 F:6-11/Region: pseudophosphorylation motif  
 F:86-135/Domain: protein kinase C zinc-binding repeat homology <K21>  
 F:136-249/Domain: protein kinase C C2 region homology <K22>  
 F:334-599/Domain: protein kinase C2 region homology <K23>  
 F:21-51,54,70/Region: protein kinase ATP-binding motif  
 F:34,37,59,62/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:86,116,119,135/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:99,102,124,127/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:365/Active site: Lys #status predicted  
 F:653,640/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

## Query Match

Best Local Similarity 26.9%; Score 59.5; DB 1; Length 682;  
 Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

OY 9 MKKEVPSIQSLDLVKEK---LOGKPGGPP 38  
 Db 367 LKDVIVODDDVDTLVEKRVLALGGKPGGPP 399

## RESULT 4

KIRTCG  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1992 #sequence-revision 30-Sep-1992 #text-change 11-Jun-1999  
 R:Accession: A05105; S02129; I55317  
 R:Comments: J.L.; Lee, M.H.; Sultzman, L.A.; Kriz, R.W.; Loomis, C.R.; Hewick, R.M.; Bell,  
 Cell 46, 491-502, 1986  
 A:Title: Cloning and expression of multiple protein kinase C cDNAs.  
 A:Reference number: A50883; MUID:86272097; PMID:3755379  
 A:Molecule type: mRNA  
 A:Residues: 1-697 <KNO>  
 A:Cross-references: GB:M13707; NID:9206186; PIDN:AAA1874.1; PID:9206187  
 R:Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y.  
 Nucleic Acids Res. 16, 5199-5200, 1988  
 A:Title: Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat brain prote  
 A:Reference number: S02129; MUID:88262515; PMID:3387228  
 A:Molecule type: mRNA  
 A:Residues: 1-697 <KNO>  
 A:Cross-references: EMBL:X07287; NID:956917; PIDN:CAA30267.1; PID:956918  
 J:Chen, K. Biol. Chem. 265, 19961-19965, 1990

A:Title: Characterization of the 5'-flanking region of the rat protein kinase C gamma  
 A:Reference number: I55317; MUID:91060619; PMID:2246272  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-56 <RES>

A:Cross-references: GB:M55417; NID:9206184; PIDN:AAA1873.1; PID:9554487  
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine  
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol este  
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane  
 C:Keywords: The zinc-stabilized regions bind diacylglycerol and phorbol esters.  
 A:Genes: PRKC-gamma

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k  
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin  
 F:18-28/Region: pseudophosphorylation motif  
 F:21-26/Region: pseudophosphorylation motif  
 F:36-85/Domain: protein kinase C zinc-binding repeat homology <K21>  
 F:101-150/Domain: protein kinase C zinc-binding repeat homology <K22>  
 F:151-264/Domain: protein kinase C C2 region homology <K23>  
 F:349-614/Domain: protein kinase C2 region homology <K24>  
 F:357-365/Region: protein kinase ATP-binding motif  
 F:36,66,69,85/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:49,52,74,77/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:101,131,134,150/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:114,117,139,142/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:380/Active site: Lys #status predicted  
 F:648,655/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

## Query Match

Best Local Similarity 26.9%; Score 59.5; DB 1; Length 697;  
 Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

OY 9 MKKEVPSIQSLDLVKEK---LOGKPGGPP 38  
 Db 382 LKDVIVODDDVDTLVEKRVLALGGKPGGPP 414

## RESULT 5

KIRBOG  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 30-Sep-1992 #sequence-revision 30-Sep-1992 #text-change 11-Jun-1999  
 R:Accession: A28708  
 R:Comments: S.; Kawasaki, H.; Kono, Y.; Inagaki, M.; Hidaka, H.; Suzuki, K.  
 Biochemistry 27, 2083-2087, 1988  
 A:Title: A fourth type of rabbit protein kinase C.  
 A:Reference number: A28708; MUID:88241036; PMID:2837282  
 A:Molecule type: mRNA  
 A:Residues: 1-697 <OHN>  
 A:Cross-references: GB:M19338; NID:9165651; PIDN:AAA3144.1; PID:9165652  
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine  
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol este  
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane  
 C:Superfamily: The zinc-stabilized regions bind diacylglycerol and phorbol esters.  
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin  
 F:18-26/Region: pseudophosphorylation motif  
 F:21-26/Region: pseudophosphorylation motif  
 F:36-85/Domain: protein kinase C zinc-binding repeat homology <K21>  
 F:101-150/Domain: protein kinase C zinc-binding repeat homology <K22>  
 F:151-264/Domain: protein kinase C C2 region homology <K23>  
 F:349-614/Domain: protein kinase C2 region homology <K24>  
 F:357-365/Region: protein kinase ATP-binding motif  
 F:36,66,69,85/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:49,52,74,77/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:101,131,134,150/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:114,117,139,142/Binding site: zinc (His, Cys, Cys, Cys) #status predicted  
 F:380/Active site: Lys #status predicted  
 F:648,655/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

## Query Match

Best Local Similarity 26.9%; Score 59.5; DB 1; Length 697;

	Best Local Similarity	39.4%	Pred. No. 24:	10:	Indels	3:	Gaps
Matches	13:	Conservative	7:	Mismatches	38		
OY	9	MKREYVPSIQSLDALVKEKK--	LOGKPGGPGP	38			
	::::: :	: :	:::	:			
Db	382	LKKDVIIVQDDVDVCTLYEKRYLALGGKRGPGGPP	414				

[illegible]

RESULT 7  
D24664  
Protein kinase C (EC 2.7.1.-) gamma - human  
C.Species: Homo sapiens (man)  
C.Date: 30-Jun-1988 #sequence: revision 10-May-1996 #text\_change 23-Mar-2001  
C.Accession: D24664.1 S1611: S3637  
C.Crossens: L.: Parker, P.J.: Rhee, L.: Yang-Feng, T.L.: Chen, E.: Waterfield, M.D.: Fed  
Science 233, 859-866, 1986  
Script: Multiple, distinct forms of bovine and human protein kinase C suggest diversity  
A.Reference number: A94291; MUID:86289426; PMID:3755548  
A.Accession: D24664RNA  
A.Molecule type: mRNA  
A.Residues: 1-313, 'YS', 316, 'T', 318 <CON>  
A.Note: the authors translated the codon GCA for residue 170 as Ser and AGC for residue  
R:Hong, H.  
Submitted to the EMBL Data Library, September 1992  
A.Description: Partial cDNA sequence of human protein kinase C zeta.  
A.Reference number: S25605  
A.Accession: S31611  
A.Status: preliminary  
A.Structure type: mRNA  
A.Residues: 162-697 HUNG  
A.Cross-references: EMBL:215114; NID:935496; PIDN:CA178820.1; PID:935497

R.:Kochs, G.; Hummel, R.; Meyer, D.; Hug, H.; Marime, D.; Sarte, T.F.  
Eur. J. Biochem. 216, 597-606, 1993  
A>Title: Activation and substrate specificity of the human protein kinase C alpha and  
A:Reference number: S56836; MUID:9387312; PMID:8375396  
A:Accession: S36837  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 162-697 <KC>  
A:Cross-references: EMBL:Z15114; NID:g35496; PIDN:CAA78820.1; PID:g35497  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

C:Genetics:  
A:Gene: GKB:PRKG; GDB:128017; OMIM:176980  
A:Cross-references: 19q13.4-19q13.4  
A:Map position: protein kinase C alpha; protein kinase C C2 region homology; protein K  
C:Superfamily: protein kinase C alpha; phosphotransferase; serine/threonine  
C:Keywords: ATP; autophosphorylation; phosphoprotein; homology <R1>  
C:Keywds/domain: protein kinase C zinc-binding repeat homology <KC2>  
F:36-150/Domain: protein kinase C C2 region homology <KC2>  
F:101-264/Domain: protein kinase C C2 region homology <KC2>  
F:131-264/Domain: protein kinase C C2 region homology <KC2>  
F:349-614/Domain: protein kinase C C2 region homology <KC2>  
F:357-365/Region: protein kinase C C2 region homology <KC2>

F:357-365/Region: protein kinase C C2 region homology <KC2>

Query Match 26.9%; Score 59.5; DB 2; Length 697;  
Best Local Similarity 39.4%; Pred. No. 24; Indels 3; Gaps 1;  
Matches 13; Conservative 7; Mismatches 10;

9 MKKEYMPSIQSDALVKKR--LOGKGCGP 38  
:::|: :|: ||: |::|||  
Db 382 LKRDVIYDDVDCTIVKEKVALGRCGGCRP 414

RESULT 8  
T43031  
DNA topoisomerase (EC 5.99.1.2) III - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 11-Jan-2000 #sequence-revision 11-Jan-2000 #text-change 17-Mar-2000  
C:Accession: T43031  
R:Kim, Y.C.; Koo, H.S.  
submitted to the EMBL Data Library, April 1998  
A:Description: cDNA cloning and overexpression of Caenorhabditis elegans DNA topoisom  
A:Reference number: Z22296  
A:Accession: T43031  
A:Status: Preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1759 <KIM>  
A:Cross-references: EMBL:AF057032; PIDDN:AAC13567.1  
C:Genetics:  
A:Gene: TOP3  
A:Superfamily: DNA topoisomerase I topA  
C:Keywords: isomerase

Query Match  
Best Local Similarity 26.7%; Score 59; DB 2; Length 759;  
Matches 17; Conservativity 26.2%; Pred. No. 30; 17; Indels 24; Gaps 2;  
Mismatches 7; Mismatches 37

1 KKTCTVHKMKKEVMP-----IGSLDALYKKKKLOGKGPGSP---- 37  
||| : |||  
566 KEICDGRQKOEVLDQIGKYRAIVESERKIGVLGYSLOLRIDLNNOAGCGPGGCGGG 625  
||| : |||

DB 38 - PRKG 41  
QX 11:1  
DB 626 GPPEG 630

RESULT 9  
B70381  
cell division protein FtsH - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence-revision 08-May-1998 #text-change 02-Feb-2001  
C:Accession: B70381  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;  
Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A:Reference number: A70300; MUID:98196666; PMID:9537320  
 A:Status: B70381  
 A:Molecule type: DNA  
 A:Residues: 1634 <AOF>  
 A:Cross-references: GB:AE000714; NID:92983446; PID:AA07029.1; PID:92983448; GB:AE00065  
 A:Experimental source: strain VPS  
 C:Keywords: cell division protein ftsH; ftsH/SEC18/CD48-type ATP-binding domain homology  
 F:169-379/Domain: ftsH/SEC18/CD48-type ATP-binding domain homology  
 F:195-202/Region: nucleotide-binding motif A (P-loop)  
 Query Match  
 Best Local Similarity 26.0%; Score 57.5; DB 2; Length 634;  
 Matches 15; Conservative 7; Mismatches 10; Indels 5; Gaps 1;  
 Db 160 IEVKEVEKEITELKDPVAFKRL-----GRRPKGV 191  
 RESULT 10  
 H36812  
 C:Species: salmistrine herpesvirus 1 (strain 11)  
 A:Title: host salmistrine herpesvirus 1  
 C:Date: 16-Oct-1992 #sequence\_revision 16-Oct-1992 #text\_change 08-Oct-1999  
 R:Albrecht, J.  
 Submitted to the EMBL Data Library, January 1992  
 A:Description: Primary structure of the herpesvirus salmistrine genome.  
 A:Reference number: A36806  
 A:Accession: H36812  
 A:Molecule type: DNA  
 A:Residues: 12469 <ALB>  
 A:Cross-references: GB:X64346; NID:660320; PID:CAA45687.1; PID:660385  
 R:Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Blesinger, B.; Newman, C.; W  
 J. Virol. 66, 5047-5058, 1992.  
 A:Title: Primary structure of the herpesvirus salmistrine genome.  
 A:Contents: annotation; protein-coding frames  
 A:Note: neither protein nor nucleotide sequence is given  
 C:Genetics: 64  
 A:Gene: 64  
 Query Match  
 Best Local Similarity 26.0%; Score 57.5; DB 2; Length 2469;  
 Matches 16; Conservative 7; Mismatches 9; Indels 7; Gaps 2;  
 Db 1122 ILTKVEEVELESVKML-----KEAKLSLDPNGPVPFPK 1156  
 RESULT 11  
 S44457  
 C:Species: Sordaria fimicola  
 C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Nov-1999  
 R:Merrow, M.W.  
 EMBL J. 13, 2257-2266, 1994  
 A:Title: Intergenic complementation of a circadian rhythmicity defect: phylogenetic co  
 A:Accession: S44457; MUID:94252311; PMID:8194516  
 A:Molecule type: DNA  
 A:Residues: 1997 <MER>  
 A:Cross-references: EMBL:L14467; NID:9310366; PID:AAA20825.1; PID:9530050  
 C:Genetics: 1997

C:Keywords: circadian rhythm  
 Query Match  
 Best Local Similarity 32.8%; Score 57; DB 2; Length 997;  
 Matches 17; Conservative 10; Mismatches 12; Indels 14; Gaps 3;  
 Db 320 KKKLVBRRLQLTGKISGRNQRIPSPSDALVSEGTIM-APRPPEG 370  
 RESULT 12  
 H82821  
 C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
 R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa  
 A:Reference number: A82515; MUID:20365717; PMID:10910347  
 A:Accession: H82821  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1444 <SIM>  
 A:Cross-references: GB:AE003884; GB:AE003849; NID:99105127; PID:AAF83121.1; GSPDB:CN  
 R:Simpson, A.J. Source: strain 945C  
 Briones, M.R.S.; Bueno, M.R.P.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvaranga, R.  
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facinani, A.P.; Ferreira, A.J.S.; Carre  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Klafjima, J.P.; Krieger, J.E.; Kuramae, E.E.; La  
 A:Authors: Matella, A.M.B.N.; Madeira, L.M.F.; Matsukuma, A.Y.; Marins, M.V.; Martins  
 Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Miyaki, C.  
 M.; Tsubako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics: 1  
 A:Gene: XF0310  
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain F; NADH dehydrogenase (ubiquinon  
 Query Match  
 Best Local Similarity 25.1%; Score 55.5; DB 2; Length 444;  
 Matches 15; Conservative 9; Mismatches 11; Indels 9; Gaps 2;  
 Db 45 LKTIPEEKIPPEVID-MVKOSNLKRGAGFPGLKMSFMKG 87  
 RESULT 13  
 B89841  
 C:Species: Staphylococcus aureus  
 C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
 R:Kuroda, M.; Ohba, T.; Uchiyama, T.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O  
 ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K  
 C:; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Lancet 357, 1225-1240, 2001  
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
 A:Reference number: A89758; MUID:21311952; PMID:11418146  
 A:Accession: B89841  
 A:Molecule type: DNA  
 A:Residues: 1160 <KUR>  
 A:Cross-references: GB:BA000018; PID:913700588; PID:BA81885.1; GSPDB:GN00149  
 A:Experimental source: strain N315







GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:33 : Search time 9.31811 Seconds  
(without alignments)  
928.727 Million cell updates/sec

Title: US-09-821-726a-13\_COPY\_78\_119  
Perfect score: 221  
Sequence: 1 KKTCTVHKMKKEVMPSTQSL.....LVKEKKLQKGGPGPPPKGL 42

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21:  
1: SP-archaea:  
2: SP-bacteria:  
3: SP-fungi:  
4: SP-human:  
5: SP-invertebrate:  
6: SP-mammal:  
7: SP-mhc:  
8: SP-organellar:  
9: SP-phage:  
10: SP-plant:  
11: SP-rodent:  
12: SP-virus:  
13: SP-vertebrate:  
14: SP-unclassified:  
15: SP-rviro:  
16: SP-bacteriaph:  
17: SP-archaeop:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	64	29.0	1677	11 070373	070373 mus musculu
2	62.5	28.3	467	4 09H9F1	09H9F1 homo sapien
3	61.5	27.8	311	16 09H9C9	09H9C9 pseudomonas
4	59	26.7	637	11 08R2Y1	08R2Y1 mus musculu
5	58	26.2	136	4 09H1L1	09H1L1 homo sapien
6	58	26.2	281	16 097T2	097T2 clostridium
7	58	26.2	707	4 09NMP3	09NMP3 homo sapien
8	58	26.2	707	4 09H52	09H52 homo sapien
9	58	26.2	707	4 09H261	09H261 homo sapien
10	58	26.2	1821	4 08WMO0	08WMO0 homo sapien
11	57.5	26.0	227	11 08R134	08R134 mus musculu
12	57.5	26.0	306	4 09NVM2	09NVM2 homo sapien
13	57.5	26.0	1582	4 09H301	09H301 homo sapien
14	57.5	26.0	1602	4 09H2T5	09H2T5 homo sapien
15	57.5	26.0	1634	4 09H314	09H314 homo sapien
16	57	25.8	438	11 0990B1	0990B1 mus musculu

17	57	25.8	438	11 091VC4	091VC4 mus musculu
18	57	25.8	494	5 09XZW0	09XZW0 heliothis v
19	57	25.8	496	5 018468	018468 heliothis v
20	56.5	25.6	434	6 08S001	08S001 macaca mula
21	56.5	25.6	464	5 09V8D8	09V8D8 drosophila
22	56	25.3	222	5 09V7T2	09V7T2 drosophila
23	55.5	25.1	322	13 09PTB4	09PTB4 brachydanio
24	55.5	25.1	388	16 09F339	09F339 streptomyce
25	55.5	25.1	444	16 09PGC10	09PGC10 xyella fas
26	55	24.9	160	16 099V55	099V55 staphylococ
27	55	24.9	160	16 099V55	022948 caenorhabd
28	55	24.9	494	6 08S068	08S068 sus scrofa
29	55	24.9	850	2 08VW80	08VW80 rhodococcus
30	55	24.9	1714	10 09FPM3	09FPM3 arabidopsis
31	54	24.4	438	11 09WV78	09WV78 rattus norv
32	54	24.4	468	2 09X681	09X681 clostridium
33	54	24.4	485	2 0936F0	0936F0 marinomonas
34	54	24.4	618	16 09RRK22	09RRK22 streptomyce
35	54	24.4	783	11 09QY56	09QY56 mus musculu
36	54	24.4	862	11 09EPY1	09EPY1 mus musculu
37	54	24.4	875	2 047245	047245 escherichia
38	54	24.4	875	16 08XE30	08XE30 escherichia
39	54	24.4	880	2 054355	054355 serralia ma
40	54	24.4	891	16 08ZGR5	08ZGR5 yersinia pe
41	54	24.4	996	17 08Z627	08Z627 pyrococcus
42	54	24.4	1779	11 08VDD9	08VDD9 mus musculu
43	53.5	24.2	198	16 099ZEF2	099ZEF2 streptococ
44	53.5	24.2	502	16 09XTU7	09XTU7 streptomyce
45	53.5	24.2	899	11 099K26	099K26 mus musculu

## ALIGNMENTS

RESULT 1  
ID 070373 PRELIMINARY; PRT: 1677 AA.  
AC 070373;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Xin.  
GN Xin.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART MUSCLE;  
RX PubMed=9159189;  
RA Wang D.-Z., Hu X., Lin J.L.-C., Kitten G.T., Solursh M., Lin J.J.-C.;  
RT "Differential display of mRNAs from the atrioventricular region of  
developing chicken hearts at stages 15 and 21.";  
RL Front. Biosci. 1:al-015(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART MUSCLE;  
RX MEDLINE=99146891; PubMed=10021346;  
RA Wang D.-Z., Reiter R.S., Lin J.L.-C., Wang Q., Williams H.S.,  
Krob S.L., Schultheiss T.M., Evans S., Lin J.J.-C.;  
RT "Regulation of a novel gene, Xin, in cardiac morphogenesis.";  
RL Development 126:1281-1294(1999).  
DR EMBL; AF051945; AAC06023.1; -;  
DR GDB; MGI:133878; Xin.  
SQ SEQUENCE 1677 AA; 182085 MW; A201CFCA710C7FF CRC64;

Query Match 29.0%; Score 64; DB 11; Length 1677;  
Best Local Similarity 30.6%; Pred. No. 23;  
Matches 11; Conservative 10; Mismatches 3; Indels 12; Gaps 1;  
QY 5 IVHKMKKEVMPSTQSLDLVKEKKLQKGGPGPPPK 40  
::: :::: | :: ::|||

Db 561 MHQEQO-----KPEEEKGKGGPPPE 584

## RESULT 2

09H9F1

AC 09H9F1; PRELIMINARY; PRT; 467 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE CDNA FLJ12800 fis, clone NT2RP2002079, weakly similar to histone H1,

DE gonadal.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Isocai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

RT "NEO human cDNA sequencing project.";

RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK022862; BAB14278.1; -

DR InterPro; IPR000637; AT\_hook.

DR SMART; SM00384; AT\_hook.1.

SQ SEQUENCE 467 AA; 49648 MW; 287B1BF4CF30B1A1 CRC64;

Query Match 28.3%; Score 62.5; DB 4; Length 467;

Best Local Similarity 37.8%; Pred. No. 9.6;

Matches 14; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 4 CIVHKKKEVMPISQSLDALVKEKKLOGKGGPPPK 40

Db 191 CLGAKHKAOSL-QLSLADSPKLRKSSGPGGNPRK 226

RESULT 3

09HTC9

AC 09HTC9; PRELIMINARY; PRT; 311 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Probable transcriptional regulator.

GN PA5437.

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas.

OX NCBI\_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=20437337; PubMed=10984043;

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltzer S.N., Tolentino E., Westbrook-Wadman S., Yuan Y.,

RA Brody L.L., Coulter L.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reitzer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an

RT opportunistic pathogen.";

CC Nature 406:959-964(2000).

CC -1- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.

DR EMBL; AE004956; AG08822.1; -

DR InterPro; IPR000847; HTH\_LysR.

DR InterPro; IPR005119; LysR\_subst.

DR Pfam; PF00126; HTH1.1; -

DR Pfam; PF03466; LysR\_substrate; 1.

DR PRINTS; PR00039; HTHLYSR.

DR PROSITE; PS00044; HTH\_LYSR\_FAMILY; UNKNOWN\_1.

KW DNA-binding; Transcription regulation; Complete proteome.

SQ SEQUENCE 311 AA; 34642 MW; 1660ABEF28B0522C CRC64;

Query Match 27.8%; Score 61.5; DB 16; Length 311;

Best Local Similarity 37.5%; Pred. No. 8.5;

Matches 15; Conservative 7; Mismatches 11; Indels 7; Gaps 2;

QY 4 CIVHKKKEVMPISQSLDALVKEKK-----LQCK--GGG 36

Db 270 CLVHAKGKRSLPYAQAFAVFERERALLSOLAGRFAPG 309

## RESULT 4

08R2Y1

AC 08R2Y1; PRELIMINARY; PRT; 637 AA.

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE Similar to cleavage stimulation factor, 3, pre-RNA subunit 2, 64 kDa,

DE tau.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC026995; AAH26995.1; -

SQ SEQUENCE 637 AA; 66407 MW; A279955579AC37FE CRC64;

Query Match 26.7%; Score 59; DB 11; Length 637;

Best Local Similarity 40.5%; Pred. No. 37;

Matches 15; Conservative 4; Mismatches 12; Indels 6; Gaps 2;

QY 5 IVHKKKEVMPISQSLDALVKEKKLOGKGGPPPKG 41

Db 190 ILHR-KIHTPLPG-----KSQVSGPGGPGPSG 220

## RESULT 5

09H1L1

AC 09H1L1; PRELIMINARY; PRT; 136 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE BA303K20.1 (Novel protein) (Fragment).

GN BA303K20.1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Matthews L.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL445589; CAC18786.2; -

FT NON TER 1

SQ SEQUENCE 136 AA; 15646 MW; 9105441005458049 CRC64;

Query Match 26.2%; Score 58; DB 4; Length 136;

Best Local Similarity 33.3%; Pred. No. 10;

Matches 12; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 5 IVHKKKEVMPISQSLDALVKEKKLOGKGGPPPK 40

Db 76 LLSKVFSEVWQVOILESMRCSGTIOCKFHSSPPK 111

## RESULT 6

097TT2

ID Q97TW2 PRELIMINARY: PRT: 281 AA.  
AC Q97TW2:  
DT 01-OCT-2001 (TREMBlrel. 18, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE G1P0 related phosphodiesterase.  
GN CAP0015.  
OS Clostridium acetobutylicum.  
OC Plasmid pSOL.  
OC Bacteria: Firmicutes: Bacillus/Clostridium group: Clostridia:  
OC Clostridiales: Clostridiaceae: Clostridium.  
OX NCBI\_TaxID=1488;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;  
RA MEDLINE-21359325; PubMed-11466286;  
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,  
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,  
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
RA Bennett G.N., Koonin E.V., Smith D.R.:  
RT "Genome sequence and comparative analysis of the solvent-producing  
RT bacterium Clostridium acetobutylicum."  
RL J. Bacteriol. 183:4823-4838(2001).  
DR EMBL: AE01438; AAK76761.1; -.  
DR InterPro: IPR004129; GDPD.  
DR Pfam: PF03009; GDPD: 1.  
KM Plasmid; Complete proteome.  
SQ SEQUENCE 281 AA; 32023 MW; A19BC118FDEC6A10 CRC64;

Query Match 26.2%; Score 58; DB 16; Length 281;  
Best Local Similarity 36.0%; Pred. No. 21;  
Matches 9; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 1 KKTCTVHKMKKEVMPSTQSDALVK 25  
DB 171 EKKCLVHSMSTYRLVQKSLDSEIK 195

RESULT 7  
ID Q9NWP3 PRELIMINARY: PRT: 707 AA.  
AC Q9NWP3:  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE KAI1A571 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-LEAL MUCOSA;  
RA Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,  
RA Hirao M., Ohmori Y., Ota T., Suzuki Y., Ohayashi M., Nishi T.,  
RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.:  
RT "NEO human cDNA sequencing project."  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AK000712; BAA91336.1; -.  
DR InterPro: IPR001487; Bromodomain.  
DR Pfam: PF00439; bromodomain; 2.  
DR PRINTS: PRO0503; BROMODOMAIN.  
DR SMART: SM00297; BROMO: 2.  
DR PROSITE: PSS0014; BROMODOMAIN\_2; 2.  
SQ SEQUENCE 707 AA; 80344 MW; FB8344D6B3B15AF7 CRC64;

Query Match 26.2%; Score 58; DB 4; Length 707;  
Best Local Similarity 43.6%; Pred. No. 55;  
Matches 17; Conservative 3; Mismatches 15; Indels 4; Gaps 1;

OY 6 VHKMKKEVMPSTQSDALVK 40  
DB 565 VPIRDEVLPSTGNCFLSETNNVKEDLLQKKNRGGRPK 603

RESULT 8  
ID Q96H52 PRELIMINARY: PRT: 707 AA.  
AC Q96H52:  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Pleckstrin homology domain interacting protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-SKIN;  
RA Strausberg R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC008909; AAH08909.1; -.  
DR InterPro: IPR001487; Bromodomain.  
DR Pfam: PF00439; bromodomain; 2.  
DR PROSITE: PSS0014; BROMODOMAIN\_2; 2.  
SQ SEQUENCE 707 AA; 80287 MW; C0F903A46BBE109F CRC64;

Query Match 26.2%; Score 58; DB 4; Length 707;  
Best Local Similarity 43.6%; Pred. No. 55;  
Matches 17; Conservative 3; Mismatches 15; Indels 4; Gaps 1;

OY 6 VHKMKKEVMPSTQSDALVK 40  
DB 565 VPIRDEVLPSTGNCFLSETNNVKEDLLQKKNRGGRPK 603

RESULT 9  
ID Q9H261 PRELIMINARY: PRT: 862 AA.  
AC Q9H261:  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE IRS-1 PH domain binding protein PHP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE-20568313; PubMed-11018022;  
RX Farhang-Fallah J., Yin X., Trentin G., Cheng A.M., Rozakis-Adcock M.,  
RT "Cloning and Characterization of PPHP, a Novel Insulin Receptor  
RT Substrate-1 Pleckstrin Homology Domain Interacting Protein."  
RL J. Biol. Chem. 275:40492-40497(2000).  
DR EMBL: AE310250; AAG45145.1; -.  
DR InterPro: IPR001487; Bromodomain.  
DR Pfam: PF00439; bromodomain; 2.  
DR PRINTS: PRO0503; BROMODOMAIN.  
DR SMART: SM00297; BROMO: 2.  
DR PROSITE: PSS0014; BROMODOMAIN\_2; 2.  
SQ SEQUENCE 862 AA; 98708 MW; 76F30382C8E41F12 CRC64;

Query Match 26.2%; Score 58; DB 4; Length 862;  
Best Local Similarity 43.6%; Pred. No. 67;  
Matches 17; Conservative 3; Mismatches 15; Indels 4; Gaps 1;

OY 6 VHKMKKEVMPSTQSDALVK 40  
DB 720 VPIRDEVLPSTGNCFLSETNNVKEDLLQKKNRGGRPK 758

RESULT 10  
ID Q8WM00 PRELIMINARY: PRT: 1821 AA.

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AC 08MW00;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE WD repeat domain 11 protein (Fragment).
GN WDR11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Scott H.S., Barras C., Miltaz L., Michaud J., Guidi S., Scamuffa N.,
RA Antonarakis S.E.;
RT "Isolation and characterization of a new chromosome 21 gene, WDR9, its
RT paralogue on chromosome 6 and their murine homologues."
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ303102; CAC83118.1; -
DR InterPro: IPR001487; Bromodomain.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00439; bromodomain; 2.
DR Pfam: PF00400; WD40; 8.
DR PRINTS: PRO0503; BROTEINBRPT.
DR PRODOM: PD000018; WD40; 1.
DR SMART: SM00320; BROMO; 2.
DR SMART: SM00320; WD40; 8.
DR PROSITE: PS00014; BROMODOMAIN_2; 2.
DR PROSITE: PS00078; WD_REPEATS_1; UNKNOWN_2.
DR PROSITE: PS00082; WD_REPEATS_2; 5.
DR PROSITE: PS0294; WD_REPEATS_REGION; 1.
KW WD repeat.
FT NON_TER
SQ SEQUENCE 1821 AA; 206646 MW; 6A132145143C8C3 CRC64;

Query Match 26.0%; Score 58; DB 4; Length 1821;
Best Local Similarity 43.6%; Pred. No. 1,4e+02;
Matches 17; Conservative 3; Mismatches 15; Indels 4; Gaps 1;

OY 6 VHKKREVMPS---IQSLDALVKEKKLGKGGPGPPPK 40
DB 1679 VHPIDVLPSSSTCNFLSTFNINVEDLQKKNRGKRPK 1717

RESULT 11
O8R134
ID 08R134; PRELIMINARY; PRT; 227 AA.
AC 08R134;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to polybromo 1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC025605; AAH25605.1; -
FT NON_TER
SQ SEQUENCE 227 AA; 24197 MW; A9C1182C840DE183 CRC64;

Query Match 26.0%; Score 57.5; DB 11; Length 227;
Best Local Similarity 43.3%; Pred. No. 20;
Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 14 MPSIQS-LDALVKEKKLGKGGPGPPPKGL 42
DB 32 LPPLGGVVDGLVSGMSQPLHNGGPPPHNL 61

```

```

RESULT 12
O9NW2
ID 09NW2; PRELIMINARY; PRT; 306 AA.
AC 09NW2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CDNA FLJ10645 fis, clone NTZRP2005767, moderately similar to G.gallus
DE Pbl gene (Polybromo 1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirooka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuho Y., Kanehori K.;
RT "NEO human cDNA sequencing project."
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=DUODENUM;
RA Strausberg R.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK001507; BAA91728.1; -
DR EMBL: BC015323; AAH15323.1; -
DR HSSP: P07155; IHMF.
DR InterPro: IPR000910; HMG_12_box.
DR Pfam: PF00505; HMG_box; 1.
DR SMART: SM00398; HMG; 1.
SQ SEQUENCE 306 AA; 33028 MW; 649E417571F59B64 CRC64;

Query Match 26.0%; Score 57.5; DB 4; Length 306;
Best Local Similarity 43.3%; Pred. No. 27;
Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 14 MPSIQS-LDALVKEKKLGKGGPGPPPKGL 42
DB 111 LPPLGGVVDGLVSGMSQPLHNGGPPPHNL 140

RESULT 13
O9H301
ID 09H301; PRELIMINARY; PRT; 1582 AA.
AC 09H301;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE BAF180.
GN BAF180.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20542072; PubMed=11078522;
RA Xue Y., Canman J.C., Lee C.S., Nle Z., Yang D., Moreno G.T.,
RA Young M.K., Salmon E.D., Wang W.;
RT "The human SWI/SNF-B chromatin-remodeling complex is related to yeast
RT Rsc and localizes at kinetochores of mitotic chromosomes."
RL Proc. Natl. Acad. Sci. U.S.A. 97:13015-13020(2000).
DR EMBL: AF197569; AAG34760.1; -
DR HSSP: P07155; IHMF.
DR InterPro: IPR001395; Aldo/ket_red.
DR InterPro: IPR001025; BAH.
DR InterPro: IPR001487; Bromodomain.
DR InterPro: IPR000910; HMG_12_box.
DR Pfam: PF00439; Bromodomain; 5.

```

DR Pfam; PF00505; HMG\_box; 1.  
 DR PRINTS; PR00503; BROMODOMAIN.  
 DR SMART; SM00439; BAH; 2.  
 DR SMART; SM00297; BROMO; 6.  
 DR SMART; SM00398; HMG; 1.  
 DR PROSITE; PS00063; ALDOXETO\_REDUCTASE\_3; UNKNOWN\_1.  
 DR PROSITE; PS00633; BROMODOMAIN\_1; 3.  
 DR PROSITE; PS50014; BROMODOMAIN\_2; 6.  
 SQ SEQUENCE 1582 AA; 181153 MW; 9862B959F36A4070 CRC64;

Query Match 26.0%; Score 57.5; DB 4; Length 1582;  
 Best Local Similarity 43.3%; Pred. No. 1.4e+02;  
 Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 14 MPSIOS-LDALVKEKKLGKGGPPPKGL 42  
 DB 1387 LPPLQGPVGLVSGMSQPLHPGPPPHHL 1416

RESULT 14  
 Q9H2T5 PRELIMINARY; PRT; 1602 AA.

AC 09H2T5;  
 DT 01-MAR-2001 (TRENBLREL. 16, Created)  
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE Polydromo-1.  
 GN PBL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Horikawa I., Barrett C.;  
 RT "cDNA Cloning of the Human Polydromo-1 Gene on Chromosome 3p21."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF225870; AAC48939.1; -.  
 DR HSSP; P07155; IHMF.  
 DR InterPro; IPR001025; BAH.  
 DR InterPro; IPR001487; Bromodomain.  
 DR InterPro; IPR000910; HMG\_12\_box.  
 DR Pfam; PF01426; BAH; 2.  
 DR Pfam; PF00439; bromodomain; 5.  
 DR Pfam; PF00505; HMG\_box; 1.  
 DR PRINTS; PR00503; BROMODOMAIN.  
 DR SMART; SM00439; BAH; 2.  
 DR SMART; SM00297; BROMO; 6.  
 DR SMART; SM00398; HMG; 1.  
 DR PROSITE; PS00633; BROMODOMAIN\_1; 3.  
 DR PROSITE; PS50014; BROMODOMAIN\_2; 6.  
 SQ SEQUENCE 1602 AA; 183689 MW; B8BA103E359A48DA CRC64;

Query Match 26.0%; Score 57.5; DB 4; Length 1602;  
 Best Local Similarity 43.3%; Pred. No. 1.5e+02;  
 Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 14 MPSIOS-LDALVKEKKLGKGGPPPKGL 42  
 DB 1407 LPPLQGPVGLVSGMSQPLHPGPPPHHL 1436

RESULT 15  
 Q9H314

ID 09H314 PRELIMINARY; PRT; 1634 AA.  
 AC 09H314;  
 DT 01-MAR-2001 (TRENBLREL. 16, Created)  
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE Polydromo-1.  
 GN PBL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Horikawa I., Barrett J.C.;  
 RT "cDNA Cloning of the Human Polydromo-1 Gene on Chromosome 3p21."  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF177387; AAC48933.1; -.  
 DR HSSP; P07155; IHMF.  
 DR InterPro; IPR001395; Aldo/ket\_red.  
 DR InterPro; IPR001025; BAH.  
 DR InterPro; IPR001487; Bromodomain.  
 DR InterPro; IPR000910; HMG\_12\_box.  
 DR Pfam; PF01426; BAH; 2.  
 DR Pfam; PF00439; bromodomain; 5.  
 DR Pfam; PF00505; HMG\_box; 1.  
 DR PRINTS; PR00503; BROMODOMAIN.  
 DR SMART; SM00439; BAH; 2.  
 DR SMART; SM00297; BROMO; 6.  
 DR SMART; SM00398; HMG; 1.  
 DR PROSITE; PS00633; ALDOXETO\_REDUCTASE\_3; UNKNOWN\_1.  
 DR PROSITE; PS00633; BROMODOMAIN\_1; 3.  
 DR PROSITE; PS50014; BROMODOMAIN\_2; 6.  
 SQ SEQUENCE 1634 AA; 187187 MW; FABIC935A9B8B4DD CRC64;

Query Match 26.0%; Score 57.5; DB 4; Length 1634;  
 Best Local Similarity 43.3%; Pred. No. 1.5e+02;  
 Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 14 MPSIOS-LDALVKEKKLGKGGPPPKGL 42  
 DB 1439 LPPLQGPVGLVSGMSQPLHPGPPPHHL 1468

Search completed: April 11, 2003, 16:14:22  
 Job time: 11.3181 secs





GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:06:33 : Search time 46.2969 Seconds  
(without alignments)  
474.899 Million cell updates/sec

Title: US-09-821-726a-18\_COPY\_21\_185  
Perfect score: 880  
Sequence: 1 DYSISVNDGNSGGSGGQSV.....ISANTILWILNISFCGIAEN 165

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
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15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
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18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	687	78.1	185	AAW99667	Human secreted pro
2	687	78.1	185	AAW99667	Human PRO1005 prot
3	687	78.1	185	AAW99667	Human signal pepti
4	687	78.1	185	AAW99667	Membrane-bound pro
5	687	78.1	185	AAW99667	Human PRO1005 (UNQ
6	687	78.1	185	AAW99667	Human PRO1005 prot
7	687	78.1	185	AAW99667	Human angiogenesis
8	687	78.1	185	AAW99667	Human PRO1005 prot
9	687	78.1	185	AAW99667	Human PRO protein,
10	687	78.1	185	AAW99667	Human secreted pro

11	687	78.1	194	AAW69974	Cancer associated
12	687	78.1	194	AAW76591	Human ovarian tumo
13	567.5	64.5	184	ABP09922	Human ORFX protein
14	186	21.1	176	AAU29228	Human PRO polypept
15	186	21.1	184	AAW66690	Membrane-bound pro
16	186	21.1	184	AAW65213	Human PRO13 (UNQ4
17	185	21.0	184	AAW23556	Human EST encoded
18	185	21.0	184	AAW4233	Human gene 14 enco
19	185	21.0	184	ABG64499	Human albumin fusl
20	185	21.0	184	ABG64500	Human albumin fusl
21	185	21.0	184	ABG64500	Human gene 14 enco
22	154.5	17.6	147	AAE04294	S cerevisiae apopt
23	94.5	10.7	695	AAW37000	Mouse distal hepal
24	87	9.9	298	AAW7250	Recombinant hepal
25	81	9.2	1051	AAW8361	Non-A, non-B hepat
26	81	9.2	1051	AAW8361	5'UTR/CORE/ENV/NS1
27	81	9.2	1051	AAW8361	Human ORFX ORF542
28	79.5	9.0	142	AAU01394	Propionibacterium
29	79.5	9.0	501	AAW01394	Novel human diagno
30	79.5	9.0	380	AAW01394	Amino acid sequenc
31	79	8.9	251	AAW06677	Arabidopsis thalia
32	78	8.9	316	AAW06675	Arabidopsis thalia
33	78	8.9	343	AAW06675	Arabidopsis thalia
34	78	8.9	349	AAW06675	Herbicidally activ
35	78	8.9	197	AAW06675	SAP(Val). synthet
36	77.5	8.8	181	AAW38086	Arabidopsis thalia
37	77	8.8	410	AAW64734	Drosophila melanog
38	77	8.8	803	AAW29030	Bacillus thuringie
39	77	8.8	803	AAW29030	Bt toxin 63B. Bac
40	77	8.8	803	AAW29521	Bt toxin 63B. Bac
41	77	8.8	803	AAW1387	Bacillus thuringie
42	77	8.8	803	AAW13913	63B protein. Bac
43	77	8.8	803	AAW13913	Ruminococcus flave
44	77	8.8	954	AAW48550	
45	77	8.8	21	AAW48550	

## ALIGNMENTS

RESULT 1	AAW99667	AAW99667 standard; protein; 185 AA.
ID	AAW99667	
AC	AAW99667	
XX	07-JUN-1999 (first entry)	
XX	Human secreted protein clone ej90_5 protein.	
XX	Human; secreted protein; nutritional; cytokine; cell proliferation;	
XX	differentiation; immune stimulating; vaccine; haematopoiesis regulation;	
KW	tissue growth; chemotactic; chemokine; haemostatic; thrombolytic;	
KW	anti-inflammatory; cadherin; tumour invasion suppressor;	
KW	tumour inhibition; gene therapy.	
XX		
XX	Homo sapiens.	
OS		
XX	WO9907840-A1.	
XX	18-FEB-1999.	
XX		
XX	06-AUG-1998; 98W0-US16318.	
XX		
XX	04-AUG-1998; 98US-0130189.	
XX	06-AUG-1997; 97US-0906708.	
XX		
XX	(GENY) GENETICS INST INC.	
XX	Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;	
XX	Merberg D, Racie LA, Steininger RJ, Treacy M;	
XX	WPI: 1999-167419/14.	

DR N-PSDB; AAX19493.  
 XX New polynucleotides encoding secreted human proteins - derived from  
 PT fetal kidney, adult testes, adult brain, adult heart, adult placenta  
 PT or adult retina cDNA libraries  
 XX  
 PS Claim 34; Page 98-99; 107pp; English.  
 XX  
 CC The present sequence represents a human secreted protein. The secreted  
 CC protein can have activities such as: nutritional activity, cytokine and  
 CC cell proliferation/differentiation activity, immune stimulating (e.g. as  
 CC vaccines) or suppressing activity, hematopoiesis regulating activity,  
 CC tissue growth activity, activin/inhibin activity, chemotactic/  
 CC chemokinetic activity, haemostatic activity and thrombolytic activity, receptor/  
 CC ligand activity, anti-inflammatory activity and tumour inhibition activity.  
 CC The secreted protein polynucleotides and proteins are predicted to have biological  
 CC activities which would make them suitable for treating, preventing or  
 CC ameliorating medical conditions in humans and animals. The  
 CC polynucleotides are also stated to be useful for gene therapy.  
 XX  
 SO Sequence 185 AA;  
 Query Match 78.1%; Score 687; DB 20; Length 185;  
 Best Local Similarity 73.3%; Pred. No. 1.4e-70;  
 Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 DYSISVNDGSGSGGQSVSVNNEHVAVYDNNNGMNSMALMDYRTGFVATRLFEKKS 60  
 DB 21 NYNINAVDNNMAGSGQSVSVNNEHVAVYDNNNGMNSMALMDYRTGFVATRLFEKKS 60  
 QY 61 CIVHKMKKEAMPISQALDALVKEKKLOGKGGPPKSLRYSVNPNVDLDRFGKSIVA 120  
 DB 81 CIVHKMKKEAMPISQALDALVKEKKLOGKGGPPKSLRYSVNPNVDLDRFGKSIVA 140  
 QY 121 MCKGIPYMAEETQGANLISYSEKISANTILMTLNTISFCGIAEN 165  
 DB 141 MCKGIPYMAEEMQEAFLFEYSGCTYTSVLTIVDISFCGDTVEN 185  
 RESULT 2  
 AAB24067  
 ID AAB24067 standard; Protein; 185 AA.  
 AC AAB24067;  
 XX  
 DT 29-JAN-2001 (first entry)  
 DE  
 XX  
 DE Human PRO1005 protein sequence SEQ ID NO:34.  
 XX  
 KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
 KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;  
 KW immunostimulant; antitumorigenic; leukaemia; lymphoid malignancy;  
 KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;  
 KW epithelial disorder; stromal disorder; blastocoealic disorder;  
 KW inflammatory disorder; immunologic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 WO2000053755-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 06-JAN-2000; 2000WO-US00376.  
 XX  
 PF 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 30-NOV-1999; 99WO-US28313.

PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
 PI Watanabe CK, Wood WI;  
 XX  
 DR WPI: 2000-572270/53.  
 DR N-PSDB: AAC58377.  
 XX  
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 PT treatment, diagnosis and prevention of cancer -  
 XX  
 PS Claim 61; Fig 22; 286pp; English.  
 XX  
 CC The present invention describes an isolated antibody that binds to  
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,  
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
 CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,  
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
 CC growth. The PRO polypeptides and nucleotides are useful in the  
 CC treatment, diagnosis and prevention of cancer. The antibodies and other  
 CC anti-tumour compounds may be used to treat various conditions, including  
 CC those characterised by overexpression and/or activation of the amplified  
 CC PRO genes. Exemplary conditions or disorders to be treated with such  
 CC antibodies and other compounds include benign or malignant tumours  
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
 CC leiomyomas, sarcomas, glioblastomas, and various head and neck tumours),  
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,  
 CC glial, astrocytal, hypothalamic and other glandular, macrophagal,  
 CC epithelial, stromal and blastocoealic disorders, and inflammatory,  
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
 CC sequences and hybridisation probes used in the isolation of the human PRO  
 CC PRO polynucleotide and AAC58396 and AAB24057 to AAB24089 represent human  
 CC the present invention.  
 CC  
 SO Sequence 185 AA;  
 Query Match 78.1%; Score 687; DB 21; Length 185;  
 Best Local Similarity 73.3%; Pred. No. 1.4e-70;  
 Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 DYSISVNDGSGSGGQSVSVNNEHVAVYDNNNGMNSMALMDYRTGFVATRLFEKKS 60  
 DB 21 NYNINAVDNNMAGSGQSVSVNNEHVAVYDNNNGMNSMALMDYRTGFVATRLFEKKS 80  
 QY 61 CIVHKMKKEAMPISQALDALVKEKKLOGKGGPPKSLRYSVNPNVDLDRFGKSIVA 120  
 DB 81 CIVHKMKKEAMPISQALDALVKEKKLOGKGGPPKSLRYSVNPNVDLDRFGKSIVA 140  
 QY 121 MCKGIPYMAEETQGANLISYSEKISANTILMTLNTISFCGIAEN 165  
 DB 141 MCKGIPYMAEEMQEAFLFEYSGCTYTSVLTIVDISFCGDTVEN 185  
 RESULT 3  
 AAY87272  
 ID AAY87272 standard; Protein; 185 AA.  
 AC AAY87272;  
 XX  
 DT 11-MAY-2000 (first entry)  
 DE  
 XX  
 DE Human signal peptide containing protein HSP-49 SEQ ID NO:49.  
 XX  
 KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;  
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;  
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;

KW reproductive disorder; developmental disorder; arteriosclerosis;  
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
KW Parkinson's disease; Huntington's disease; ovulatory defect;  
KW muscular dystrophy.  
XX  
OS Homo sapiens.  
XX  
PN WO200000610-A2.  
XX  
PD 06-JAN-2000.  
XX  
PF 25-JUN-1999; 99WO-US14484.  
XX  
PR 26-JUN-1998; 98US-0090762.  
PR 31-JUL-1998; 98US-0094983.  
PR 01-OCT-1998; 98US-0102686.  
PR 11-DEC-1998; 98US-0112129.  
XX  
PA (INCY-) INCYTE PHARM INC.  
XX  
PI Lal P, Tang YF, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
PI Bandman O;  
XX  
DR WPI: 2000-160673/14.  
DR N-PSDB: AA298157.  
XX  
PT New human signal peptide-containing proteins useful in treatment,  
PT prevention and diagnosis of e.g. cancer, inflammation and  
PT cardiovascular disease  
XX  
PS Claim 1: Page 193-194; 327pp; English.  
XX  
CC AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the  
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,  
CC neuroprotective, cardiovascular and antiasthmatic activities, and can  
CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
CC associated with decreased activity or function of HSP. Antagonists of  
CC HSP are used to treat or prevent disorders associated with increased  
CC activity or function of HSP. Such diseases include cell proliferation  
CC (including cancer), inflammation, cardiovascular, neurological,  
CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
CC asthma, Crohn's disease, microbial or other infections, congestive or  
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
CC nucleic acids can be used for the recombinant production of HSP, for  
CC detecting HSP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring), in gene therapy, as antisense,  
CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
CC or genetic variations, and for chromosomal mapping. HSP are also used to  
CC raise specific antibodies (Ab) and to screen for agonists and  
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic  
CC antagonists, in competitive drug screens, and for purification of HSP  
CC from natural sources.  
XX  
SQ Sequence 185 AA:  
XX  
Query Match 78.1%; Score 687; DB 21; Length 185;  
Best Local Similarity 73.3%; Pred. No. 1,4e-70;  
Matches 121: Conservative 22; Mismatches 22; Indels 0; Gaps 0;  
OY 1 DYSISVNDGNSGSGQSVSNNEHNVANVNNNGNNSNALMDYRTGFAVTRLEPKKS 60  
DB 21 NYININVDNNNGSGQSVSNNEHNVANVNNNGNNSIWDYCNCGAATRLFCQKKT 80  
OY 61 CTVHKKKKEKMPKSLQALDYLVEKKKLDGKGGPGPKSLKSYVNPVNDLDRFGKSLVA 120  
DB 81 CTVHKKKKEKMPKSLQALDYLVEKKKLDGKGGPGPKSLKSYVNPVNDLDRFGKSLVA 140

OY 121 MCKGIPTMAEIEQAGNLSISEKCSANILWILINISFCGIAEN 165  
DB 141 MCKGIPTMAEIEQAGNLSISEKCSANILWILINISFCGIAEN 185  
RESULT 4  
ID AAY66686  
AC AAY66686; protein: 185 AA.  
AC AAY66686;  
DT 05-APR-2000 (first entry)  
DE Membrane-bound protein PRO1005.  
XX  
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor Immunoadhesin; gene mapping.  
XX  
OS Homo sapiens.  
XX  
PN WO963088-A2.  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US12252.  
XX  
PR 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 05-JUN-1998; 98US-0088255.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 10-JUN-1998; 98US-0088828.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.

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PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090451.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 25-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091636.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 09-JUL-1998; 98US-0091982.
PR 10-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095326.
PR 10-AUG-1998; 98US-0095329.
PR 11-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 12-AUG-1998; 98US-0096146.
PR 17-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096849.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.

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PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097977.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.

XX (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
PI
XX WPI; 2000-072883/06.
XX N-PSDB; AA65023.
XX
XX Membrane-bound proteins and related nucleotide sequences -
XX
XX Claim 12; Fig 139; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIR
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
XX Sequence 185 AA:
SQ
Query Match 78.1%; Score 687; DB 21; Length 185;
Best Local Similarity 73.3%; Pred. No. 1,4e-70;
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;
QY 1 DYSISVNDGNSGSGQSVSVNNEHNVANVDNNGNSNMAIMDYRTGFAVTRLPFKKS 60
DB 21 NYNINVNDNNAAGSGQSVSVNNEHNVANVDNNGNSNMAIMDYRTGFAVTRLPFKKT 80
QY 61 CIVHKMKKPSLQALDLVKEKKLQGGKGGPPPKSLRYSVNPNKVDNLDKRGKSIVA 120
DB 81 CIVHKMKKEVMSISQSLDLVKEKKLQGGKGGPPPKGLMYSVNPKNVDLDSFGKNIAN 140
QY 121 MCKGIPTVAEELQGANLISYSEKCSANTMTLNTISFCGCIADEN 165
DB 141 MCKGIPTVAEELQGANLISYSEKCSANTMTLNTISFCGCIADEN 185

RESULT 5
AAB65209
ID AAB65209 standard; Protein; 185 AA.
XX
XX AAB65209;
AC
XX
XX 02-APR-2001 (first entry)
DT
XX
XX Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.
DE
XX

```



XX The present sequence is one of twenty eight novel PRO polypeptides. The  
 CC PRO polypeptides and their agonists, including antibodies, peptides, and  
 CC small molecule agonists, may be used to treat various tumours, e.g.,  
 CC cancers such as breast cancer, prostate cancer, ovarian cancer, colorectal  
 CC cancer, uterine cancer, lung cancer, melanoma or leukaemia. They are also  
 CC useful for treating other disorders such as neuronal, glial, astrocytal,  
 CC hypothalamic and other glandular disorders such as inflammatory, stromal and  
 CC disorders.

SO Sequence 185 AA:

Query Match 78.1% Score 687; DB 22; Length 185;  
 Best Local Similarity 73.3%; Pred. No. 1.4e-70;  
 Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

QY 1 DYSISVNDGNSGGSGQSVSVNNEHNVANVDNNNGNSMNAIMDYRTGFAVTRLEFKS 60  
 Db 21 NYININVDNNNAGSGQSVSVNNEHNVANVDNNNGNSMNAIMDYRTGFAVTRLEFKS 60  
 QY 61 CIVHKMKKEMPSTLOALDALYKKEKLOGKGGPPKSLRYSPNRPVNDLDRFGSKSYA 120  
 Db 81 CIVHKMKKEMPSTLOALDALYKKEKLOGKGGPPKSLRYSPNRPVNDLDRFGSKSYA 120  
 QY 121 MCKGIPTMAEETIGQANLISYSEKISANILIMLINSFCGGIAEN 165  
 Db 141 MCKGIPTMAEEMOEASLEFFYSGTCYTSVLMIVISFCGDTVEN 185

RESULT 7  
 ABB95492  
 ID ABB95492 standard; Protein: 185 AA.

XX ABB95492;

DT 19-JUL-2002 (first entry)

XX Human angiogenesis related protein PRO1005 SEQ ID NO: 140.

KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW antiarteriosclerotic; antiangiogenic; hypotensive; vulnary;

XX Homo sapiens.

PN WO200208284-A2.

PD 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-223695P.

XX 17-AUG-2000; 2000US-0643557.

XX 23-AUG-2000; 2000WO-US33522.

XX 24-AUG-2000; 2000WO-US33528.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000WO-US30873.

XX 10-NOV-2000; 2000WO-US30873.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000US-0747259.

XX 20-DEC-2000; 2000WO-US34956.

PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0806899.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 30-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.

PA (GETH ) GENENTECH INC.  
 PA (BAKE ) BAKER K P.  
 PA (FERR ) FERRARA N.  
 PA (GERB ) GERBER H.  
 PA (GERR ) GERRITSEN M E.  
 PA (GODD ) GODDARD A.  
 PA (GODD ) GODDARD P J.  
 PA (GURN ) GURNEY A L.  
 PA (HILL ) HILLAN K J.  
 PA (MARS ) MARSTERS S A.  
 PA (PAN ) PAN J.  
 PA (PAON ) PAONI N F.  
 PA (STEP ) STEPHAN J F.  
 PA (WATA ) WATANABE C K.  
 PA (WILL ) WILLIAMS P M.  
 PA (WOOD ) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX WPI: 2002-171999/22.  
 DR N-PDB: ABL95630.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -

PS Claim 11: Fig 140. 567pp: English.

XX The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including a  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.

SO Sequence 185 AA:

Query Match 78.1% Score 687; DB 23; Length 185;  
 Best Local Similarity 73.3%; Pred. No. 1.4e-70;  
 Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

QY 1 DYSISVNDGNSGGSGQSVSVNNEHNVANVDNNNGNSMNAIMDYRTGFAVTRLEFKS 60  
 Db 21 NYININVDNNNAGSGQSVSVNNEHNVANVDNNNGNSMNAIMDYRTGFAVTRLEFKS 60  
 QY 61 CIVHKMKKEMPSTLOALDALYKKEKLOGKGGPPKSLRYSPNRPVNDLDRFGSKSYA 120  
 Db 81 CIVHKMKKEMPSTLOALDALYKKEKLOGKGGPPKSLRYSPNRPVNDLDRFGSKSYA 120  
 QY 121 MCKGIPTMAEETIGQANLISYSEKISANILIMLINSFCGGIAEN 165

Db 141 MCRGIPYMAEEMOASLFFYSGCTTYSVLMIVDLSFGCDGVEN 185

## RESULT 8

AB884886 standard: Protein: 185 AA.

AB884886:

16-MAY-2002 (first entry)

Human PRO1005 protein sequence SPO ID NO:140.

Human: angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
angiogenic disorder; cardiac hypertrophy; arteriosclerosis; hypertension;  
age-related macular degeneration; arterial restenosis; angina;  
rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
wound healing; chromosome mapping; gene mapping.

Homo sapiens.

WO200200690-A2.

03-JAN-2002.

20-JUN-2001: 2001WO-US19692.

23-JUN-2000: 2000US-213637P.  
20-JUL-2000: 2000US-219556P.  
25-JUL-2000: 2000US-220624P.  
25-JUL-2000: 2000US-220644P.  
28-JUL-2000: 2000WO-US20710.  
02-AUG-2000: 2000US-222695P.  
17-AUG-2000: 2000US-064365P.  
23-AUG-2000: 2000WO-US23522.  
24-AUG-2000: 2000WO-US23328.  
07-SEP-2000: 2000US-230978P.  
18-SEP-2000: 2000US-0664610.  
18-SEP-2000: 2000US-0665350.  
24-OCT-2000: 2000US-242922P.  
08-NOV-2000: 2000US-0709238.  
08-NOV-2000: 2000WO-US30952.  
10-NOV-2000: 2000WO-US30873.  
01-DEC-2000: 2000WO-US32678.  
20-DEC-2000: 2000US-0747259.  
20-DEC-2000: 2000WO-US34956.  
22-JAN-2001: 2001US-0767609.  
28-FEB-2001: 2001US-0796498.  
28-FEB-2001: 2001WO-US06520.  
01-MAR-2001: 2001WO-US06666.  
09-MAR-2001: 2001US-0802706.  
14-MAR-2001: 2001US-0808689.  
22-MAR-2001: 2001US-0816744.  
05-APR-2001: 2001US-0828366.  
10-MAY-2001: 2001US-0854208.  
25-MAY-2001: 2001US-0866028.  
25-MAY-2001: 2001US-0866034.  
30-MAY-2001: 2001WO-US17092.  
30-MAY-2001: 2001US-0870574.  
01-JUN-2001: 2001WO-US17443.  
01-JUN-2001: 2001WO-US17800.

(GENTH ) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gertlissen ME, Goddard A,  
Godowski PJ, Guirney AL, Hillan KJ, Marsters SA, Pan J,  
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W.

DR WPI: 2002-090516/12.

XX N-PSDB: ABL88141.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11: Fig 140: 565pp: English.

CC ABL88072 to ABL88258 encode the PRO proteins given in AB884817 to  
CC AB885003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
CC degeneration, arteriosclerosis, hypertension, arterial restenosis,  
CC rheumatoid arthritis, angina, myocardial infarction, thrombophlebitis,  
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
CC carcinoma) and wound healing. The PRO polynucleotides have applications  
CC in molecular biology, including use as hybridisation probes, and in  
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
CC probes used in the exemplification of the present invention.

XX SO Sequence 185 AA:

Query Match 78.1%; Score 687; DB 23: Length 185;  
Best Local Similarity 73.3%; Pred. No. 1.4e-70;  
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

OY 1 DYSISVDDGNSGGSGOOSVSVNNHNANVDNNNGMSNMLMDYRTGFAVTRLEKKS 60

Db 21 NYNINVDNNDNNGSGOOSVSVNNHNANVDNNNGHDSNMSIMDGNGFAATRLFOKKT 80

OY 61 CIVHRMKKEAMPSTLOALDALVKEKKLOGKGGPPPKSLRTSYNPNRVNLDKFGKSYA 120

Db 81 CIVHMKKEWMPSTLSLDALVKEKKLOGKGGPPPKGLMYSVNPNKVDLSKFGKINIA 140

OY 121 MCKGIPYMAEIOGANLISSEKCSANITMLINISFCGIAEN 165  
141 MCRGIPYMAEEMOASLFFYSGCTTYSVLMIVDLSFGCDGVEN 185

RESULT 9

AAU83665 standard: Protein: 185 AA.

AAU83665:

08-MAY-2002 (first entry)

Human PRO protein, Seq ID No 148.

Human: secreted protein; PRO: tumour; lung cancer; colon cancer;  
breast cancer; prostate tumour; rectal tumour; liver tumour;  
pericyte cell proliferation; chondrocyte cell proliferation;  
tumour necrosis factor-alpha.

Homo sapiens.

WO200208288-A2.

31-JAN-2002.

29-JUN-2001: 2001WO-US21066.

20-JUL-2000: 2000US-219556P.  
25-JUL-2000: 2000US-220585P.  
25-JUL-2000: 2000US-220605P.  
25-JUL-2000: 2000US-220607P.  
25-JUL-2000: 2000US-220624P.  
25-JUL-2000: 2000US-220638P.  
25-JUL-2000: 2000US-220664P.

25-JUL-2000; 2000US-220666P.  
26-JUL-2000; 2000US-220893P.  
28-JUL-2000; 2000WO-US20710.  
23-AUG-2000; 2000WO-US23522.  
24-AUG-2000; 2000WO-US23522.  
15-SEP-2000; 2000US-000000P.  
10-NOV-2000; 2000WO-US30873.  
28-NOV-2000; 2000US-253646P.  
01-DEC-2000; 2000WO-US34956.  
20-DEC-2000; 2000US-0747259.  
20-DEC-2000; 2000WO-US34956.  
28-FEB-2001; 2001WO-US06520.  
10-MAY-2001; 2001US-0854280.  
25-MAY-2001; 2001WO-US17092.  
(GENE) GENENTECH INC.  
Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WL; WPI; 2002-172001/22.  
N-PSDB; ABK33609.  
One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour -  
Claim 11; Figure 148; 359pp; English.  
The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the release of tumour necrosis factor- $\alpha$  from human blood, for stimulating the release of tumour necrosis factor- $\alpha$  from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AA083592-AA083713 represent human PRO protein sequences of the invention.  
Sequence 185 AA:  
Query Match 78.1%; Score 687; DB 23; Length 185;  
Best Local Similarity 73.3%; Pred. No. 1.4e-70;  
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;  
QY 1 DYSISVNDGSGGSGGQSVSYNNHNANVANDNNNGNSNMAIMDYRTGFVTRLPFKKS 60  
DB 21 NYNINAVDNDNNAGSGGQSVSYNNHNANVANDNNNGNSNMAIMDYRTGFVTRLPFKKT 80  
QY 61 CIVHKKRKEAMPISLOADALVKEKKGKGGPPPSRLRYVNPKNVDNLDKRGKSIYA 120  
DB 81 CIVHKKRKEVMPISLOADALVKEKKGKGGPPPSRLRYVNPKNVDNLDKRGKSIYA 140  
QY 121 MCKGIPYMAEIOGANLISYSEKISANTILMILINISFCGGAEN 165  
DB 141 MCRGIPYMAEIOGANLISYSEKISANTILMILINISFCGGAEN 185  
RESULT 10  
AAB38329  
ID AAB38329 standard; Protein; 186 AA.  
XX AAB38329;  
XX  
DT 31-JAN-2001 (first entry)

XX  
DE Human secreted protein encoded by gene 9 clone HNSAD53.  
DE  
XX Immunosuppressive; antiarthritic; antineumatic; antiproliferative;  
XX cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;  
XX nontropic; antibacterial; vitricide; fungicide; ophthalmological; human;  
XX vulnerable; gene therapy; infection; secreted protein.  
XX Homo sapiens.  
XX WO200061623-A1.  
XX 19-OCT-2000.  
XX  
XX 06-APR-2000; 2000WO-US08979.  
XX  
XX 09-APR-1999; 9905-0128693.  
XX 26-APR-1999; 9905-0130991.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;  
XX Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;  
XX Young PE;  
XX WPI; 2000-647418/62.  
XX  
XX New nucleic acid molecules encoding 62 human secreted proteins for  
XX diagnosing, preventing, treating or ameliorating medical conditions and  
XX used as food additives or preservatives -  
XX  
XX Claim 11; Page 598; 716pp; English.  
XX  
XX Sequences AAB38321-B38396 represent the amino acid sequences of 62  
XX human secreted proteins encoded by the genes AAC09512-C69587. The genes  
XX and proteins are useful for preventing, ameliorating or treating medical  
XX conditions, e.g. by protein or gene therapy. The genes are isolated from  
XX a range of human tissues disclosed in the specification. The nucleic  
XX acids, proteins, antibodies and (ant)agonists are useful in the  
XX diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.  
XX rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms  
XX of the breast or liver; (c) cardiovascular disorders e.g. cardiac  
XX arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)  
XX angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)  
XX infections caused by bacteria, viruses and fungi; and (h) ocular  
XX disorders e.g. corneal infection. The polypeptides can also be used to  
XX aid wound healing and epithelial cell proliferation, to prevent skin  
XX aging due to sunburn, to maintain organs before transplantation, for  
XX supporting cell culture of primary tissues, to regenerate tissues and in  
XX chemotaxis.  
XX  
XX Sequence 186 AA:  
Query Match 78.1%; Score 687; DB 21; Length 186;  
Best Local Similarity 73.3%; Pred. No. 1.4e-70;  
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;  
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DB 21 NYNINAVDNDNNAGSGGQSVSYNNHNANVANDNNNGNSNMAIMDYRTGFVTRLPFKKT 80  
QY 61 CIVHKKRKEAMPISLOADALVKEKKGKGGPPPSRLRYVNPKNVDNLDKRGKSIYA 120  
DB 81 CIVHKKRKEVMPISLOADALVKEKKGKGGPPPSRLRYVNPKNVDNLDKRGKSIYA 140  
QY 121 MCKGIPYMAEIOGANLISYSEKISANTILMILINISFCGGAEN 165  
DB 141 MCRGIPYMAEIOGANLISYSEKISANTILMILINISFCGGAEN 185  
RESULT 11  
AAM69974  
ID AAM69974 standard; Protein; 194 AA.  
XX AAM69974;  
XX  
XX







PI Pan J, Smith V, Watanabe CK, Wood WT, Zhan ;  
XX WPI; 2001-602746/68.  
DR N-PSDB; AAS46139.  
XX  
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumours, such as prostate and breast tumours, in mammals a  
PT to screen for modulators of the compounds -  
XX  
PS Claim 11; Fig 430; 774pp; English.  
XX  
CC Sequences AAU2902A-AAU29328 represent PRO polypeptides of the invention  
CC The PRO polypeptides and their associated nucleic acids can be used to  
CC detect the presence of a tumour in a mammal by determining the level of  
CC expression of a PRO polypeptide in a test sample of cells from the animal  
CC and a control sample of normal cells, whereby a higher level of  
CC expression in the test sample indicates the presence of a tumour in the  
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
CC and rabbits but are preferably human. The polypeptides can be used to  
CC stimulate tumour necrosis factor (TNF) alpha release from human blood  
CC when contacted with it. A specific polypeptide can be used to stimulate  
CC the proliferation or differentiation of chondrocyte cells. The PRO  
CC proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide primers specific for the PRO nucleic acid  
CC can be used for genetic analysis of individuals with genetic disorders.  
XX  
SQ Sequence 176 AA:  
Query Match 21.18; Score 186; DB 22; Length 176;  
Best Local Similarity 28.08; Prev. No. 5,6e-13;  
Matches 46; Conservative 36; Mismatches 58; Indels 24; Gap 4;  
OY 11 NSGSGGQSVVNNHHNANYDNNNGMMSWALMDYRTGFAVTRLEFKKSCIVHKKKEA  
DB 23 NNGGNGQETVITIDNEKNATVNIHAGSSSTTTFYKKGYSRVLRSRACILKMDHON  
OY 71 MPST-----QALDALYKELKGGKPGGPPKSLRYSVNPNDNLDF--GKSI  
DB 83 IPIPLNLQWYIVIKQALDNMFSSNKYTW-----VKYNPLESLIKDVMFLGSP1 }  
OY 119 VAMCKGPTVMATITOGANLISYSFKCISANILMLTINISFCGCI 162  
DB 132 EKLCRHPLYKGE\FENTHWG-AGGCACAGLILGISICADI 174  
RESULT 15  
ID AAY66690 standard; protein: 184 AA.  
XX AAY66690;  
XX  
XX 05-APR-2000 (first entry)  
XX  
XX Membrane-bound protein 3/0813.  
XX  
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
XX Homo sapiens.  
XX OS  
XX MO9963088-A2.  
XX  
XX 09-DEC-1999.  
XX  
XX 02-JUN-1999; 99MO-US12252.  
XX  
XX 02-JUN-1998; 98US-0087607.  
XX 02-JUN-1998; 98US-0087609.  
XX 02-JUN-1998; 98US-0087759.  
XX 03-JUN-1998; 98US-0087827.  
XX 04-JUN-1998; 98US-0088021.

PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 05-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
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PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.

```

CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 184 AA;...
Query Match 21.1%; Score 186; DB 21; Length 184;
Best Local Similarity 28.0%; Pred. No. 6e-13;
Matches 46; Conservative 36; Mismatches 58; Indels 24; Gaps 4
QY 11 NSGSGGQSVSVNNEHNVANVDNNNGWNSMNLMDYRTGFAYTRLEKKSCIVHKMKKEA 70
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Db 31 NNGGNVQETVTIDNENKNAITVINIHAGSSCSSTTFDYKHGYIASRVLSRRACFILKMDHQN 90
   :|: \ |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 71 MPSL-----QALDALYKEKKIQCKGPGPPPKSLRYSVNPNRNVNDKF--GKSI 118
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Db 91 IPIPLNNLOWIYEKQALDNMFSENKKTW-----VKINPLESLILKDVPDFLLGPSI 139
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QY 119 VAMCGGIPTMAEEIQGANLISYSSEKCISANTIMLTNLISFCGGI 162
   :|: \ |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 140 EKLCNHIPLYKGVEVENTHNVG-AAGCAKAGHGILGISICADI 182
   :|: \ |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:08:13 : Search time 16.6884 Seconds  
(Without alignments)  
290.907 Million cell updates/sec

Title: US-09-821-726a-18\_COPY\_21\_185

Perfect score: 880  
Sequence: 1 DVSISVNDGSGSGSQGSV.....ISANLILINISFCGIAEN 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backlitest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	8.8	803	1	US-08-158-232-10
2	77	8.8	803	1	US-08-304-626-10
3	77	8.8	803	1	US-08-316-301A-12
4	77	8.8	803	2	US-08-611-928-10
5	77	8.8	803	3	US-09-173-891-10
6	77	8.8	803	4	US-09-076-137-12
7	77	8.8	803	5	PCT-US92-03624-12
8	75	8.5	674	4	US-09-199-637A-51
9	74.5	8.5	1240	3	US-08-930-966A-4
10	74	8.4	379	1	US-08-227-108-18
11	74	8.4	379	2	US-09-073-674-18
12	74	8.4	713	4	US-09-059-584-53
13	73	8.3	817	1	US-08-381-931B-2
14	72.5	8.2	655	2	US-08-492-027A-6
15	71	8.1	412	1	US-08-313-288B-18
16	71	8.1	1025	2	US-08-530-792D-23
17	70.5	8.0	718	4	US-09-346-237-10
18	70.5	8.0	746	4	US-09-134-001C-3214
19	70.5	8.0	1026	2	US-08-530-792D-22
20	70	8.0	300	4	US-09-134-001C-4457
21	69	7.8	730	1	US-07-846-181-5
22	68	7.8	730	1	US-07-845-989-5
23	68	7.7	370	4	US-09-142-551A-4
24	68	7.7	396	4	US-09-142-551A-3
25	67.5	7.7	546	2	US-08-492-027A-8
26	67.5	7.7	651	2	US-08-492-027A-1
27	67	7.6	430	2	US-08-945-848-8

28	67	7.6	2391	2	US-08-446-855A-2	Sequence 2, Appl
29	67	7.6	2391	4	US-09-150-741-2	Sequence 2, Appl
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31	66.5	7.6	334	1	US-08-241-465B-19	Sequence 19, Appl
32	66.5	7.6	334	1	US-08-241-465B-20	Sequence 20, Appl
33	66	7.5	533	1	US-08-445-586-10	Sequence 10, Appl
34	66	7.5	596	4	US-09-752-165-2	Sequence 2, Appl
35	66	7.5	978	4	US-08-897-956A-3	Sequence 2, Appl
36	65.5	7.4	542	1	US-08-701-380-2	Sequence 2, Appl
37	65.5	7.4	542	3	US-09-032-365A-13	Sequence 13, Appl
38	65.5	7.4	722	2	US-08-158-232-51	Sequence 51, Appl
39	65.5	7.4	722	2	US-08-611-928-51	Sequence 51, Appl
40	65.5	7.4	722	3	US-09-173-891-51	Sequence 51, Appl
41	65.5	7.4	747	3	US-09-035-648-18	Sequence 18, Appl
42	65.5	7.4	747	4	US-09-001-951-18	Sequence 18, Appl
43	65.5	7.4	747	4	US-08-818-829-18	Sequence 18, Appl
44	65	7.4	467	4	US-09-134-001C-3235	Sequence 3235, Ap
45	65	7.4	606	4	US-09-187-124-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-158-232-10  
: Sequence 10, Application US/08158232  
: Patent No. 5596071  
: GENERAL INFORMATION:  
: APPLICANT: Payne, Jewel  
: APPLICANT: Kennedy, M. Keith  
: APPLICANT: Randall, John Brooks  
: APPLICANT: Meier, Henry  
: APPLICANT: Wick, Heidi Jane  
: APPLICANT: Foncecrada, Luis  
: APPLICANT: Schnepf, H. Ernest  
: APPLICANT: Schwab, George E.  
: APPLICANT: Fu, Jenny  
: TITLE OF INVENTION: No. 5596071el Bacillus thuringiensis Toxins Active  
: TITLE OF INVENTION: Against Hymenopteran Pests  
: NUMBER OF SEQUENCES: 51  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: David R. Saliwanchik  
: STREET: 2421 N.W. 41st Street, Suite A-1  
: CITY: Gainesville  
: STATE: FL  
: COUNTRY: USA  
: ZIP: 32606  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentin Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/158,232  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/887,980  
: FILING DATE: 22-MAY-1992  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/797,645  
: FILING DATE: 25-NOV-1991  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/7703,977  
: FILING DATE: 22-MAY-1991  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Saliwanchik, David R.  
: REGISTRATION NUMBER: 31,794  
: REFERENCE/DOCKET NUMBER: M/SCU104.C1  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 904-375-8100  
: TELEFAX: 904-372-5800  
: INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 803 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: *Bacillus thuringiensis*  
INDIVIDUAL ISOLATE: PS63B  
IMMEDIATE SOURCE:  
CLONE: E. coli NM522(pMYC1642) NRRL B-18961  
OS-08-158-232-10

Query Match	8.8%	Score 77	DB 1	Length 803
Best Local Similarity	25.5%	Pred. No. 3.3		
Matches 41	Conservative 19	Mismatches 73	Indels 28	Gaps 9

QY 7 NDDNSGSG---SGQGSYVNNEHHVNA-VYNNNGMNSMNLW-DYRGFAVTLTLEKSC 61  
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QY 62 IVH-----KAKKEAMP-SIGALDALYKKEKLGCKRGGPPRSLSRVSMPK-VNDLdk 113  
Db 479 YNNSTGYGSESNQSLPQOKTHALPTQTNVNLGSGKLGGLASHIIPDLSPNMTIGKDT 538  
QY 114 FGKSIWAMCKGIPF-----YMAEIOGANLISYS 142  
Db 539 DSTNIVA-KGIPVEKGYASSGQKVEIIRREINAGANVOLTS 577

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TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 803 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHEetical: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Bacillus thuringiensis  
 INDIVIDUAL ISOLATE: P563B  
 IMMEDIATE SOURCE:  
 CLONE: E. COLL NM522(PMYC1642) NRRL B-18961  
 JS-08-304-626-10

Query Match	8.8%;	Score 77;	DB 1;	Length 803;
Best Local Similarity	25.5%;	Pred. No. 3.3;		
Matches	41;	Conservative	19;	Mismatches 73;
				Indels 28;
				Gaps 9;

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Oy      7  NDDGSGSG- ---SGQASVYNNEHWAN-VDDNNMNSNMMLN-DYRFGFVTRFEKSKC 61
Db      420 NDPGLSGVOLPRLMSV-VNNQRTAQYTTGSENIWTDIGRSWLTCLRGYCTTNCPPRG 478
Oy      62  IVH- ---KKMKEMP- ---SLQALDALYKREKLLQSKGCGCPPKSLRYSVPMNR-VQDLK 113
Db      479 YNNSTGYESCSNOIPGOKTHALIPFTQTNVLQSGSKGLLASHIIPDIDSPNNTIGDKPT 538
Oy      114 FGRSTVAMCKGIPT- --- ---YAEETIGCANLISYS 142
Db      539 DSTNIVA- ---KGLPVEKGYASSGQKVEIIRIMINANAVQUS 577

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US-08-316-301A-12

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APPLICATION NUMBER: 07/565,544  
FILING DATE: 10-AUG-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/0084,653  
FILING DATE: 12-AUG-1987  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/830,050  
FILING DATE: 31-JAN-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lloyd, Jeff  
REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: MA20CCCD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 803 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
INDIVIDUAL ISOLATE: PS63B  
IMMEDIATE SOURCE:  
CLONE: E. coli NM522(pMTC 1642) NRRL B-18961  
US-08-316-301A-12

Query Match  
Best Local Similarity 25.5%; Score 77; DB 1; Length 803;  
Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;

OY 7 NDDGNSGG---SGOOSVSVNNEHNAN-VNNGNWSMNAW-DYRTGFAVTRLFEKKS 61  
DB 420 NDDGLSGDVLPAPMSV-VNAQTOTAOYTDGENIMWDTGRSWLCTLRGYCTTNCFFGRGC 478  
OY 62 IVH-----KMKKEAMP--SLOALDALVKEKKILOGKGGPPPKSLRYSNPR-VNLDK 113  
DB 479 YNNSGYGESCNSQSLPGQKIHAIPTOTNNVLGOSCKLGLASHIPYDLSPNNTIGDKDT 538  
OY 114 FKSIVAMCKGIPT-----YMAEETOGANLISYS 142  
DB 539 DSTNIVA--KGIPEKGYASSGQKVEIIREWINGANVQLS 577

RESULT 4  
US-08-611-928-10  
Sequence 10, Application US/08611928  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel  
APPLICANT: Kennedy, M. Keith  
APPLICANT: Randall, John Brooks  
APPLICANT: Meier, Henry  
APPLICANT: Uick, Heidi Jane  
APPLICANT: Foncerrada, Luis  
APPLICANT: Schaeff, H. Ernest  
APPLICANT: Schwab, George E.  
APPLICANT: Fu, Jenny  
TITLE OF INVENTION: No. 5824792e1 Bacillus thuringiensis Toxins Active  
TITLE OF INVENTION: Against Hymenopteran Pests  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: David R. Salivanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL

COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/611,928  
FILING DATE: 06-MAR-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/158,232  
FILING DATE: 24-NOV-1993  
APPLICATION NUMBER: US 07/887,980  
FILING DATE: 22-MAY-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/797,645  
FILING DATE: 25-NOV-1991  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/703,977  
FILING DATE: 22-MAY-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Salivanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/SCJ104.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 803 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
INDIVIDUAL ISOLATE: PS63B  
IMMEDIATE SOURCE:  
CLONE: E. coli NM522(pMTC1642) NRRL B-18961  
US-08-611-928-10

Query Match  
Best Local Similarity 25.5%; Score 77; DB 2; Length 803;  
Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;

OY 7 NDDGNSGG---SGOOSVSVNNEHNAN-VNNGNWSMNAW-DYRTGFAVTRLFEKKS 61  
DB 420 NDDGLSGDVLPAPMSV-VNAQTOTAOYTDGENIMWDTGRSWLCTLRGYCTTNCFFGRGC 478  
OY 62 IVH-----KMKKEAMP--SLOALDALVKEKKILOGKGGPPPKSLRYSNPR-VNLDK 113  
DB 479 YNNSGYGESCNSQSLPGQKIHAIPTOTNNVLGOSCKLGLASHIPYDLSPNNTIGDKDT 538  
OY 114 FKSIVAMCKGIPT-----YMAEETOGANLISYS 142  
DB 539 DSTNIVA--KGIPEKGYASSGQKVEIIREWINGANVQLS 577

RESULT 5  
US-09-173-891-10  
Sequence 10, Application US/09173891  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel  
APPLICANT: Kennedy, M. Keith  
APPLICANT: Randall, John Brooks

APPLICANT: Meier, Henry  
APPLICANT: Vick, Heidi Jane  
APPLICANT: Poncerra, Luis  
APPLICANT: Schepf, H. Ernest  
APPLICANT: Schwab, George E.  
APPLICANT: Fu, Jenny  
TITLE OF INVENTION: No. 6077937e1 Bacillus thuringiensis Toxins Active  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESS: David R. Saliwanichik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/173,891  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/158,232  
FILING DATE:  
APPLICATION NUMBER: US 07/887,980  
FILING DATE: 22-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/797,645  
FILING DATE: 25-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/703,977  
FILING DATE: 22-MAY-1991  
APPLICATION NUMBER: US 07/703,977  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanichik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/SC104.C1  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 803 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
INDIVIDUAL ISOLATE: PS63B  
IMMEDIATE SOURCE:  
CLONE: E. coli NM522(pMVC1642) NRRL B-18961  
US-09-173-891-10  
Query Match 8.8%; Score 77; DB 3; Length 803;  
Best Local Similarity 25.5%; Pred. No. 3.3;  
Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;

DB 539 DSTNIVA--KGIPVEKGYASSGKVEILIREWINGANVOLS 577  
RESULT 6  
US-09-076-137-12  
Sequence 12, Application US/09076137B  
Patent No. 6165195  
GENERAL INFORMATION:  
APPLICANT: Schepf, Harry E.  
APPLICANT: Schwab, George E.  
APPLICANT: Payne, Jewel M.  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Poncerra, Luis  
TITLE OF INVENTION: No. 6165195e1 Nematode-Active Toxins and Genes Which Code  
TITLE OF INVENTION: Therefor  
FILE REFERENCE: MA-20CCD2  
CURRENT APPLICATION NUMBER: US/09/076,137B  
CURRENT FILING DATE: 1998-05-12  
EARLIER APPLICATION NUMBER: 08/316,301  
EARLIER FILING DATE: 1994-09-30  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: Patentn Ver. 2.1  
SEQ ID NO 12  
LENGTH: 803  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-09-076-137-12  
Query Match 8.8%; Score 77; DB 4; Length 803;  
Best Local Similarity 25.5%; Pred. No. 3.3;  
Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;  
DB 539 DSTNIVA--KGIPVEKGYASSGKVEILIREWINGANVOLS 577  
RESULT 7  
PCT-US92-03624-12  
Sequence 12, Application PC/TUS9203624  
GENERAL INFORMATION:  
APPLICANT: Schepf, Harry E.  
APPLICANT: Schwab, George E.  
APPLICANT: Payne, Jewel M.  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Poncerra, Luis  
TITLE OF INVENTION: Novel Nematode-Active Toxins and Genes  
TITLE OF INVENTION: Which Code Therefor  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESS: David R. Saliwanichik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/03624  
FILING DATE: 19920501  
CLASSIFICATION: 435



ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanichik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MA20C2C1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-372-5800  
TELEFAX: 904-375-8100  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 803 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
INDIVIDUAL ISOLATE: PS63B  
IMMEDIATE SOURCE:  
CLONE: E. coli NM522(pMYC 1642) NRRL B-18961  
PCT-US92-03624-12

Query Match 8.8%; Score 77; DB 5; Length 803;  
Best Local Similarity 25.5%; Pred. No. 3.3; Mismatches 73; Indels 28; Gaps 9;

Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;  
DB 7 NDDGNSGCG---SGQOSVSYNNEHNVAN-VDNNGNSMNAWM-DYRTGFAVTRLEFKKSC 61  
DB 420 NDRGLSGDVLPAPMSV-VNAQTQAYTDGENTWDTGRSWLCTLRGCTNCPGKDC 478  
QY 62 IVH-----KMKREAMP---SLQALDALVKKRKIQGKGGPGPPKSLRYSVNPBR-VDNLDK 113  
DB 479 YNNSGTGYSQCSQSLPGQKTHALYPTQNVNLGQSGKGLSLASHLPIDLSFNNITGDKDT 538  
QY 114 FCKSIAMCKGIPT-----YMAEIIQGANLISYS 142  
DB 539 DSTNIYA--KGIPVEKGVASSQKVEIIREWINGANVAVQLS 577

RESULT 8  
US-09-199-637A-51  
Sequence 51, Application US/09199637A  
Patent No. 6355411  
GENERAL INFORMATION:  
APPLICANT: Ausubel, Frederick  
APPLICANT: Goodman, Howard M.  
APPLICANT: Rahme, Laurence G.  
APPLICANT: Mahajan-Miklos, Shalina  
APPLICANT: Tan, Man-Wah  
APPLICANT: Cao, Hui  
APPLICANT: Denekard, Eliana  
APPLICANT: Tsongalis, John  
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID  
FILE REFERENCE: 00786/361002  
CURRENT APPLICATION NUMBER: US/09/199,637A  
CURRENT FILING DATE: 1998-11-25  
PRIOR APPLICATION NUMBER: 60/066,517  
PRIOR FILING DATE: 1997-11-25  
NUMBER OF SEQ ID NOS: 437  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 51  
LENGTH: 674  
TYPE: PROT  
ORGANISM: Pseudomonas aeruginosa  
US-09-199-637A-51

Query Match 8.5%; Score 75; DB 4; Length 674;  
Best Local Similarity 23.1%; Pred. No. 4.4;  
Matches 33; Conservative 24; Mismatches 56; Indels 30; Gaps 5;

QY 12 SGGSGQGSV-----SYNNEHNVANVDNNG--WNSMNAWM-DYRTGFAV 52

DB 418 AGSGGCKPIRIYNDYTRAGYNLTSRVNDSSVSATCNGLVONTWSSPOE-AAAFAT 476  
QY 53 TRLEFKKSCIVHKKREAMPISQALDALVKE---KKLQKGGGPGPPKSLRYSVNPBRVD 109  
DB 477 RVLEGGQOQCTCEGCKQTVTAAGVGLPLIETYYDKKLSL-----QLLSKSRPLTAE 529  
QY 110 NLDKFGKSIAMCKGIPTMAEE 132  
DB 530 NLAAGTDALPIRGVIEALRDE 552

RESULT 9  
US-08-930-996A-4  
Sequence 4, Application US/08930996A  
Patent No. 6100449  
GENERAL INFORMATION:  
APPLICANT: FLOHR, Robert  
APPLICANT: ESHED, Yuval  
APPLICANT: ORI, Naomi  
APPLICANT: PARAN, Ilan  
APPLICANT: ZAMIR, Daniel  
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE  
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND  
TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/930,996A  
FILING DATE: 09-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/05272  
FILING DATE: 15-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 113,373  
FILING DATE: 13-APR-1995  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1240 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-930-996A-4

Query Match 8.5%; Score 74.5; DB 3; Length 1240;  
Best Local Similarity 24.4%; Pred. No. 12;  
Matches 33; Conservative 19; Mismatches 50; Indels 33; Gaps 6;

QY 34 NNGNSMNAWM-----WDRYTGFAVTRLEFKKSCIVHKKREAMP---SLQALDALVKE 83  
DB 284 NQVYNEMDELNRNRYFVGQDGSKLIYV---TRKDSVALMNGNDISGNLSTEASLSLQOR 340  
QY 84 KRLQKGGPGPPKSLRYSVNPBRVNDLDFGKSIAMCKGIPTMAEIIQGANLISYS 143  
DB 341 HAFENNDPMGH-----SELEVGROIARCKGLP--LALKTLAQMRLRSKSE 384  
QY 144 ---KCSANIITWL 154  
DB 385 VERKCLIRSEIWL 399

RESULT 10

```

? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Warner-Lambert Company
? STREET: 2800 Plymouth Road
? CITY: Ann Arbor
? STATE: Michigan
? COUNTRY: U.S.A.
? ZIP: 48105
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/073,674
? FILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Crissey, Todd M.
? REGISTRATION NUMBER: 37,807
? REFERENCE/DOCKET NUMBER: 5072-DI-66-TMC
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 734 622-7530
? TELEFAX: 734 622-1553
? TELEX:
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 379 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-073-674-18

Query Match      8.4%; Score 74; DB 2; Length 379;
Best Local Similarity 23.1%; Pred No. 2.5;
Matches    51; Conservative   30; Mismatches    66; Indels    74; Gaps    13

QY      6 VNDG-----NSGSGGQGSVYNNEH-----VANVDNN-----G 36
DB      33 VEDGYILEVNRIPTYKSKNGNKGPRV-VFLDGLLASAMWISLNLAFILADG 91
QY      37 NWS-----NALMDYTGFAVTRLEPKSCITYHKKKKEAMPSLQALDAVK---KKLG 88
DB      92 YGVWLGNNGNTWRYSRNLTYSPDSVEFWAFSPDEMAKYDLPA--TIDFYKKTGGEKLY 149
QY      89 KPPG-GPPKSLRWSYNPNRVDNL-----KFGSIYAMCKGIPTMAEIOGA 136
DB      150 VCHSOGTTIGFAFSNPRLAERITFYALAPVATVTKYKSLVKNLRLEPPIWEKIIFG- 208
QY      137 NLISY-----SENC-----ISANILIINISFCG 160
DB      209 DKITYPHNFDFLATOVCSRETLNVICSNALFII----CG 245

RESULT 12
US-09-059-584-53
; Sequence 53, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario

```

COUNTRY: Canada  
ZIP: MSG 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/059,584  
FILING DATE: 14-APR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/778,570  
FILING DATE: 03-JAN-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24973  
REFERENCE/DOCKET NUMBER: 1038-794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1153  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 713 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-059-584-53

Query Match 8.4%; Score 74; DB 4; Length 713;  
Best Local Similarity 29.0%; Pred. No. 6.2;  
Matches 42; Conservative 16; Mismatches 53; Indels 34; Gaps 8;

QY 10 GNSGGSGGQSVYVNEHNV-ANVDNNNGMSNVALMDYRTGFAVTRLFEKKSCTVHKMK 67  
DB 48 GNTGGTG-----STDVNGNAGANGSGTGNAGNSGNA--NSGTGSANTPEKRYQVPTDKNE 101  
QY 68 KEAPMSLO-ALDALYKREKKLOGKGGPPKSLRYSVNPNDNDK----FGKSIAM- 121  
DB 102 KQVSSIOEPAMGYAMELKLRAHP-----LNPNKKKEAKRRLALDQKDLVAVE 150  
QY 122 --CKGIPTYMAEIOGANLISYSEK 144  
DB 151 GDLTNIPF-----DKNLIETLKK 168

RESULT 13  
US-08-381-931B-2  
Sequence 2, Application US/08381931B  
Patent No. 5714377  
GENERAL INFORMATION:  
APPLICANT: Tanner, Widmar, et al.  
TITLE OF INVENTION: Modified fungal cells and method for  
TITLE OF INVENTION: Producing recombinant products.  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sears Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,931B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32861  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 817 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-381-931B-2

Query Match 8.3%; Score 73; DB 1; Length 817;  
Best Local Similarity 23.5%; Pred. No. 10;  
Matches 27; Conservative 23; Mismatches 39; Indels 26; Gaps 5;

QY 38 NSNVALMDYRTGFAVTRLFEKKSCTVHKMKKEAPMSLOALDALYKREKKLOGKGGPPPK 97  
DB 721 SQWLSGMDYNGNTYFSSLEFKNOTL--TKRESOP---AAVSTVEETIEDG----- 768  
QY 98 SLRYSVNPNDNDKFGKSIAMCKG-----IPTYMAEIOGANLISYSEK 146  
DB 769 -----PSYEDLNEDGKKIFKDEGNELOPEVYKKMLEE-EGANILYKRAV 815

RESULT 14  
US-08-492-027A-6  
Sequence 6, Application US/08492027A  
Patent No. 5912333  
GENERAL INFORMATION:  
APPLICANT: Suzuki, Shoichi  
APPLICANT: Burnell, James N  
TITLE OF INVENTION: DNA Encoding Carbonic Anhydrase  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch and Birch  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/492,027A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr, Gerald M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 0760-206  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 655 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-492-027A-6

Query Match 8.2%; Score 72.5; DB 2; Length 655;  
Best Local Similarity 23.4%; Pred. No. 8.3;  
Matches 33; Conservative 25; Mismatches 58; Indels 25; Gaps 7;

QY 34 NGNNSNVALMDYRTGFAVTRLFEKKSCTVHKMKKEAPMSLOALDALYKREKKLOGKGP-- 91  
DB 435 SSGWPH---YDFVKGQFVT--WEPPDAILRLTS-----GFGQKRVNVYDKPELFGPLK 484  
QY 92 GGPPPKSLRYSVNPNDNDKFG-----KSIAMCKGIPTYMAEIOG-ANLISY 141

Db 485 SGQAFKTYMVFACSDSRVSPVTLGLQPGFAFTVRNIAM---VPGYDKTKYTGIGSALEY 541  
 OY 142 SEKCISANILMLINISFOCGI 162  
 Db 542 AVCALKEVELVLVIGHSCCGI 562

RESULT 15

US-08-313-288B-18  
 ; Sequence 18, Application US/08313288B

; Patent No. 5750502

; GENERAL INFORMATION:

; APPLICANT: Jessell, Thomas M. and Avihu Klar

; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A

; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/313,288B

; FILING DATE: January 5, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28, 678

; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0526

; TELEX:

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 412 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-313-288B-18

Query Match 8.1%; Score 71; DB 1; Length 412;  
 Best Local Similarity 24.1%; Pred. No. 6.4;  
 Matches 27; Conservative 14; Mismatches 25; Indels 46; Gaps 5;

OY 3 SISVNDG--NSGSGGQSVSVNEHNANVNNNGNSMNAIMDYRTGFAVTRLEFEKKS 60  
 Db 71 SLGENDGNNNGNDNGREG-----KDEDKRDGNNEDN----- 102  
 OY 61 CIYHKMKKEMPSIQALDALVKEKKIOGKGGPPPKSLRYSVNPNDNL 112  
 Db 103 ---EKLKRP-----KHKKLKOPGDGNPDPA-NRPVDPNANPNVD 138

GenCore version 5.1.4-p5-4578  
1993 - 2003 CompuGen Ltd.

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protein search, using sw model

Run on: April 11, 2003, 16:06:33 ; Search (without alignments) 474.899 Million cell updates/sec

US-09-821-726A-2  
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US-09-821-726A-2

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
 - refining chosen parameters: 908470

Total number of hits satisfactory

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Processing: Minimum Match 0%

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100	100	100

A Geneseq\_10100

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1: /SIDS2/qcgcda
2: /SIDS2/qcgcda
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A. Geneseq.-101002.*
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2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
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12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
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21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

```

## SUMMARIES

Result No.	Score	% Match	Query length	DB	ID	Description
1	103	82.4	184	23	AA099922	Human ORFX protein
2	90	72.0	185	20	AA09667	Human secreted pro
3	90	72.0	185	21	AA824067	Human PRO1005 prot
4	90	72.0	185	21	AA587272	Human signal pepti
5	90	72.0	185	21	AA56686	Membrane-bound pro
6	90	72.0	185	22	AA050957	Human PRO1005 prot
7	90	72.0	185	22	AA050957	Human angiotensin
8	90	72.0	185	23	AB054542	Human PRO1005 prot
9	90	72.0	185	23	AB084886	Human PRO protein
10	90	72.0	185	23	AA083655	Human

11	90	72.0	186	21	AA86989724
12	90	72.0	194	20	AA876591
11	90	72.0	194	20	AA876591
13	54	40.8	1194	22	AA879656
14	54	40.8	1194	22	AA879656
15	51	40.8	298	16	AA879656
16	51	40.8	298	20	AA879656
17	51	40.8	298	21	AA879656
18	51	40.8	298	21	AA879656
19	51	40.8	307	22	AA879656
20	51	40.8	307	22	AA879656
21	51	40.8	378	22	AA879656
22	51	40.8	465	22	AA879656
23	50.5	39.2	109	22	AA879656
24	49	39.2	170	11	AA879656
25	49	39.2	206	11	AA879656
26	49	39.2	214	11	AA879656
27	49	39.2	418	22	AA879656
28	49	39.2	418	22	AA879656
29	49	39.2	418	22	AA879656
30	48.5	38.8	435	12	AA879656
31	48.5	38.8	3000	22	AA879656
32	48.5	38.8	3000	22	AA879656
33	48	38.4	145	22	AA879656
34	48	38.4	147	22	AA879656
35	48	38.4	163	22	AA879656
36	48	38.4	367	22	AA879656
37	48	38.4	417	22	AA879656
38	48	38.4	417	22	AA879656
39	48	38.4	417	22	AA879656
40	48	38.4	540	21	AA879656
41	48	38.4	1044	21	AA879656
42	48	38.4	1105	21	AA879656
43	48	38.4	1189	21	AA879656
44	47	37.6	52	21	AA879656
45	47	37.6	52	21	AA879656

## ALIGNMENT'S

RESULT 1  
ARP09922  
...d. Protein; 184 AA.

ABP09922;

24-JUN-2002 (first entry)  
 AA DT  
 SFQ ID NO:19826

XX Human OREX protein sequence.  
DE  
XX Human: open reading frame: OREX; gene therapy: cancer; cirrhosis;  
KM hyperproliferative disorder; psoriasis; benign tumor; haemorrhage;  
KM degenerative disorder; osteoarthritis; neurodegenerative disorder;  
KM de novo vascular disease; diabetes mellitus; systemic erythematous;  
KM hypertension; hypothyroidism; cholesterol ester storage disease;  
KM immune deficiency; immune disorder; infectious disease;  
KM autoimmune thyroiditis;  
KM autoimmune arthritis; rheumatoid arthritis; autoimmune thyroiditis;  
KM myasthenia gravis.

XX  
OS Homo sapiens.

XX  
PN  
WO200192523-A2

XX  
PD  
06-DEC-2001.

XX  
29-MAY-2001; 2001WO-US10836.

PT 2000US-206132P  
XX 2000US-328716P  
ED 30-MAY-2000;

29-AUG-2000; 2000US-2207-20

XX  
PA (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;  
PI

CC (referred to as open reading describes substantially purified human proteins  
CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
CC proteins given in ABP00010 to ABP1500. ORFX proteins are useful for  
CC treating or preventing a pathology associated with an ORFX-associated  
CC disorder in humans, and in the manufacture of a medicament for treating a  
CC syndrome associated with ORFX associated disorder. ORFX polynucleotide  
CC sequences can be used in gene therapy. ORFX sequences can be used in the  
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
CC transplantation, cardiovascular diseases, diabetes mellitus, haemorrhage,  
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol, systemic  
CC storage diseases, various immune deficiencies and disorders, systemic  
CC diseases, autoimmune disorders such as multiple sclerosis, infectious  
CC arthritis, autoimmune inflammatory, myasthenia gravis, rheumatoid  
CC disease and autoimmune inflammatory eye disease. ORFX graft-versus-host  
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
CC bone degenerative disorders, incisions, ulcers, for treating osteoporosis,  
CC protection or regeneration and periodontal disease, and for gut  
CC repertition or regeneration and periodontal disease, and for gut  
CC systemic cytokine damage.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, and was obtained in electronic format directly from WIPO  
CC at [http://wipo.int/pub/published\\_pct-sequences](http://wipo.int/pub/published_pct-sequences).  
XX  
XX  
XX Sequence 18A.A1.

RESULT 2  
AAW99667  
ID AAW99667 standard; Protein; 185 AA  
xx  
AAC  
xx AAW99667;  
xx

PN	MO9907840-A1.	
XX		
PD	18-FEB-1999.	
XX		
PF	06-AUG-1998;	98MO-US16318
XX		
PR	04-AUG-1998;	98US-0130189
PR	06-AUG-1997;	97US-0906708.

	Best local Matches	Similarity 18: Conservative	Score 90: Pred. No. 2e-05;	DB 20: Mismatches	length 185;
Oy	1	LDPMVKRQK--GKPGAPGPKMLM	23		
Dp	97	LDALVEKKRLQGGKPGGPPGGLM	121		

29-JAN-2001 (first entry)  
Human PRO1005 protein sequ  
Human; tumour, a

PN	MO200053755-A2.	
XX		99MO-US05028
PD	14-SEP-2000.	99MO-US01252
PF		99US-0141037
XX	06-JAN-2000; 2000MO-US00376	99US-0143048
PR		99US-0145698
PR	08-MAR-1999.	99MO-US028313
PR	02-JUN-1999.	99MO-US00911
PR	23-JUN-1999.	
PR	07-JUL-1999;	
PR	26-JUL-1999;	
PR	30-NOV-1999;	
PR	20-DEC-1999;	

PR 05-JAN-2000: 2000MO-US00219.  
 XX (GENTH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
 PI Matarane CK, Wood WI;  
 XX WPI: 2000-572270/53.  
 DR N-PSDB: AAC58377.  
 XX  
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 PT treatment, diagnosis and prevention of cancer  
 XX  
 PS Claim 61: Fig 22: 286pp: English.  
 XX  
 CC The present invention describes an isolated antibody that binds to  
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,  
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
 CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,  
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
 CC growth. The PRO polypeptides and nucleotides are useful in the  
 CC treatment, diagnosis and prevention of cancer. The antibodies and other  
 CC anti-tumour compounds may be used to treat various conditions, including  
 CC those characterised by overexpression and/or activation of the amplified  
 CC PRO genes. Exemplary conditions include benign or malignant tumours  
 CC antibodies and other compounds include breast, gastric, ovarian,  
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
 CC leukemias, sarcomas, glioblastomas, and various head and neck tumours),  
 CC glioma, astrocytic, hypothalamic and other glandular, macrophagal,  
 CC epithelial, stromal and blastocoele disorders, and inflammatory,  
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
 CC primers and hybridisation probes used in the isolation of the human PRO  
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
 CC PRO polynucleotide and protein sequences given in the exemplification of  
 CC the present invention.  
 CC  
 XX  
 XX Sequence 185 AA:  
 S0  
 Query Match 72.0%; Score 90; DB 21; Length 185;  
 Best Local Similarity 72.0%; Pred. No. 2e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;  
 QY 1 LDTWYKEOK--GKPGGAPPKDLMY 23  
 ||:||||:| ||||| ||| |||  
 DB 97 LDALVKEKKLGKGGPGPPKGLMY 121  
 RESULT 4  
 AAY87272  
 ID AAY87272 standard; Protein: 185 AA.  
 XX  
 AC AAY87272;  
 XX  
 DT 11-MAY-2000 (first entry)  
 XX  
 DE Human signal peptide containing protein HSP-49 SEQ ID NO:49.  
 XX  
 XX Human: signal peptide-containing protein; HSP; diagnosis; cancer;  
 XX Inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 XX antiasthmatic; gene therapy; cell proliferation; neurologic disorder;  
 XX antileukemic; gene therapy; cell proliferation; arteriosclerosis;  
 XX reproductive disorder; developmental disorder; immunodeficiency;  
 XX asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 XX Parkinson's disease; Huntington's disease; ovulatory defect;  
 XX muscular dystrophy.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200000610-A2.

XX  
 PD 06-JAN-2000.  
 XX  
 XX 25-JUN-1999; 99WO-US14484.  
 XX  
 XX 26-JUN-1998; 98US-0090762.  
 XX 31-JUL-1998; 98US-0094983.  
 XX 01-OCT-1998; 98US-0102686.  
 XX 11-DEC-1998; 98US-0112129.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 XX Lal P, Tang YF, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
 PI Aerobion IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
 PI Bandman O;  
 XX  
 DR WPI: 2000-160673/14.  
 DR N-PSDB: AA298157.  
 XX  
 PT New human signal peptide-containing proteins useful in treatment,  
 PT prevention and diagnosis of e.g. cancer, inflammation and  
 PT cardiovascular disease  
 XX  
 PS Claim 1: Page 193-194; 327pp: English.  
 XX  
 CC AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the  
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
 CC anticancer, anti-inflammatory, antimicrobial, neurologic, hepatotropic,  
 CC neuroprotective, cardiovascular and antileukemic activities, and can  
 CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
 CC associated with decreased activity or function of HSP. Antagonists of  
 CC HSP are used to treat or prevent disorders associated with increased  
 CC activity or function of HSP. Such diseases include cell proliferation  
 CC (including cancer), inflammation, cardiovascular, neurological,  
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
 CC asthma, Crohn's disease, acquired immune deficiency syndrome, anaemia,  
 CC ischemic heart disease, microbial or other infections, congestive or  
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
 CC nucleic acids can be used for the recombinant production of HSP, for  
 CC detecting HSP in standard hybridisation and amplification assays (for  
 CC triplex-forming and monitoring), in gene therapy, as antisense,  
 CC or genetic variations, and for chromosomal mapping. HSP are also used to  
 CC raise specific antibodies (Ab) and to screen for agonists and  
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
 CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic  
 CC antagonists, in competitive drug screens, and for purification of HSP  
 CC from natural sources.  
 CC  
 XX  
 XX Sequence 185 AA:  
 S0  
 Query Match 72.0%; Score 90; DB 21; Length 185;  
 Best Local Similarity 72.0%; Pred. No. 2e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;  
 QY 1 LDTWYKEOK--GKPGGAPPKDLMY 23  
 ||:||||:| ||||| ||| |||  
 DB 97 LDALVKEKKLGKGGPGPPKGLMY 121  
 RESULT 5  
 AAY66686  
 ID AAY66686 standard; Protein: 185 AA.  
 XX  
 AC AAY66686;  
 XX  
 DT 05-APR-2000 (first entry)  
 XX  
 DE Membrane-bound protein PRO1005.  
 XX  
 XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
 XX pharmaceutical; receptor immunoadhesin; gene mapping.  
 KM

XX OS Homo sapiens.  
 XX PN WO9963088-A2.  
 XX PD 09-DEC-1999.  
 XX PF 02-JUN-1999; 99WO-US12252.  
 XX PR 02-JUN-1998; 98US-0087607.  
 PR 02-JUN-1998; 98US-0087609.  
 PR 03-JUN-1998; 98US-0087752.  
 PR 04-JUN-1998; 98US-0087827.  
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 PR 22-JUN-1998; 98US-0089952.  
 PR 22-JUN-1998; 98US-0090246.  
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 PR 23-JUN-1998; 98US-0090349.  
 PR 23-JUN-1998; 98US-0090355.  
 PR 24-JUN-1998; 98US-0090429.  
 PR 24-JUN-1998; 98US-0090431.  
 PR 24-JUN-1998; 98US-0090435.  
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 PR 24-JUN-1998; 98US-0090535.  
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 PR 24-JUN-1998; 98US-0090540.

PR 24-JUN-1998; 98US-0090557.  
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 PR 25-JUN-1998; 98US-0090688.  
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 PR 01-JUL-1998; 98US-0090863.  
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 PR 01-JUL-1998; 98US-0091360.  
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 PR 02-JUL-1998; 98US-0091646.  
 PR 02-JUL-1998; 98US-0091647.  
 PR 07-JUL-1998; 98US-0091673.  
 PR 07-JUL-1998; 98US-0091978.  
 PR 09-JUL-1998; 98US-0091982.  
 PR 10-JUL-1998; 98US-0092182.  
 PR 10-JUL-1998; 98US-0092472.  
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 PR 30-JUL-1998; 98US-0094651.  
 PR 04-AUG-1998; 98US-0095282.  
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 PR 11-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 12-AUG-1998; 98US-0096146.  
 PR 17-AUG-1998; 98US-0096329.  
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 PR 18-AUG-1998; 98US-0096895.  
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 PR 18-AUG-1998; 98US-0096960.  
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 PR 20-AUG-1998; 98US-0097141.  
 PR 24-AUG-1998; 98US-0097218.  
 PR 26-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 31-AUG-1998; 98US-0098014.  
 PR 16-SEP-1998; 98US-0098525.  
 PR 12-JAN-1999; 98US-0100634.  
 PR 99US-0115565.  
 XX



PA (GETH ) GENENTECH INC.  
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;  
 XX  
 DR WPI: 2000-072883/06.  
 XX N-PSDB: AAZ65023.  
 PT Membrane-bound proteins and related nucleotide sequences -  
 PS claim 12; Fig 139; 822pp; English.  
 XX  
 CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 CC will also be useful for the preparation of PRO polypeptides, especially  
 CC by recombinant techniques.  
 CC  
 XX  
 SQ Sequence 185 AA;  
 XX  
 Query Match 72.0%; Score 90; DB 21; Length 185;  
 Best Local Similarity 72.0%; Pred. NO. 2e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;  
 QY 1 LDTMVKRQK--GKPGGAPPKDLMY 23  
 ID 97 LDALVKEKKLQGGKPGPPKGLMY 121  
 DB  
 AAB65209 standard; Protein; 185 AA.  
 XX  
 AC AAB65209;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; cytosolic;  
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay.  
 XX  
 XX Homo sapiens.  
 OS  
 PN WO200073454-A1.  
 PD  
 XX 07-DEC-2000.  
 PD  
 XX 30-MAR-2000; 2000WO-US08439.  
 PF  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146322.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 08-OCT-1999; 99US-0158663.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Kiljavin IO, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 DR WPI: 2001-032160/04.  
 DR N-PSDB: AAF44169.  
 XX  
 PT PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -  
 PT  
 XX  
 PS Claim 12; Fig 139; 935pp; English.  
 XX  
 CC The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytosolic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 CC  
 XX  
 SQ Sequence 185 AA;  
 XX  
 Query Match 72.0%; Score 90; DB 22; Length 185;  
 Best Local Similarity 72.0%; Pred. NO. 2e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;  
 QY 1 LDTMVKRQK--GKPGGAPPKDLMY 23  
 ID 97 LDALVKEKKLQGGKPGPPKGLMY 121  
 DB  
 AAB50957 standard; Protein; 185 AA.  
 XX  
 AC AAB50957;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Human PRO1005 protein.  
 XX  
 KW Human; PRO; cytosolic; nootropic; neuroprotective; respiratory general;  
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;  
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.  
 XX  
 OS Homo sapiens.  
 PN WO200073348-A2.  
 XX

PD 07-DEC-2000.  
XX 30-MAY-2000; 2000WO-US14941.  
XX 02-JUN-1999; 99WO-US12252.  
XX 22-JUN-1999; 99US-0140650.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30999.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 03-MAR-2000; 2000US-0187202.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
PI Shelton DL, Smith V, Watanabe CK, Wood WI;  
XX MPI; 2001-016509/02.  
DR N-PSDB; AAC91559.  
XX Twenty eight nucleic acids encoding PRO polypeptides which are useful  
PT for treating various tumors, e.g. breast cancer, and other  
PI inflammatory, angiogenic and immunological disorders -  
XX Claim 31; Fig 14; 188pp; English.  
XX The present sequence is one of twenty eight novel PRO polypeptides. The  
CC PRO polypeptides and their agonists, including antibodies, peptides, and  
CC small molecule agonists, may be used to treat various tumors, e.g.,  
CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal  
CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,  
CC central nervous system cancer, melanoma or leukaemia. They are also  
CC useful for treating other disorders such as neuronal, glial, astrocytal,  
CC hypothalamic and other glandular, macrophagal, epithelial, stromal and  
CC blastocoele disorders, and inflammatory, angiogenic and immunological  
CC disorders.  
XX Sequence 185 AA:  
SQ  
Query Match 72.0%; Score 90; DB 22; Length 185;  
Best Local Similarity 72.0%; Pred. No. 2e-05;  
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;  
OY 1 LPTMYKEOK--GKPGGAPKDLAY 23  
DB 97 LDAIVKEKKLOGKPGGPPPKGLMY 121  
RESULT 8  
ID ABB95492 standard: Protein; 185 AA.  
XX ABB95492;  
AC  
XX 19-JUL-2002 (first entry)  
DT  
XX Human angiogenesis related protein PRO1005 SEQ ID NO: 140.  
DE  
XX

KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiac; cytosatic; antiangiogenic; hypotensive; vulnary;  
KW antiarteriosclerotic.  
XX Homo sapiens.  
OS  
XX WO200208284-A2.  
PN 31-JAN-2002.  
XX 09-JUL-2001; 2001WO-US21735.  
XX 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 15-SEP-2000; 2000US-000000P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001US-0802706.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854208.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 30-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.  
XX (GETH ) GENENTECH INC.  
XX (BAKE/) BAKER K P.  
XX (FERR/) FERRARA N.  
XX (GERB/) GERBER H.  
XX (GERR/) GERRITSEN M E.  
XX (GODD/) GODDARD A.  
XX (GODO/) GODOWSKI P J.  
XX (GURN/) GURNEY A L.  
XX (HILL/) HILLAN K J.  
XX (MARS/) MARSTERS S A.  
XX (PANJ/) PAN J.  
XX (PAON/) PAONT N F.  
XX (STEP/) STEPHAN J F.  
XX (WATA/) WATANABE C K.  
XX (WILL/) WILLIAMS P M.  
XX (WOOD/) WOOD W I.  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX MPI; 2002-171999/22.  
DR

DR N-PSDB: ABL95630.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 PS Claim 11; Fig 140; 567pp; English.

CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hyper trophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.

XX  
 XX  
 SQ Sequence 185 AA;

Query Match 72.0%; Score 90; DB 23; Length 185;  
 Best local Similarity 72.0%; Pred. No. 2e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKPGGAPKDLMY 23  
 II : III : I IIIII III III  
 Db 97 LDALVKEKKIKGKGPGPPKGLMY 121

RESULT 9  
 ABB84886  
 ID ABB84886 standard; Protein: 185 AA.  
 AC ABB84886;  
 XX  
 XX 16-MAY-2002 (first entry)

DE Human PRO1005 protein sequence SEQ ID NO:140.  
 XX  
 XX Human; angiogenesis; cardiact; cystostatic; antiangiogenic; hypotensive;  
 XX vulnerability; antiatherosclerotic; PRO agonist; PRO antagonist; trauma;  
 XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 XX angiotensin disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 XX age-related macular degeneration; arterial restenosis; angina;  
 XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 XX wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.  
 XX  
 XX WO200200690-A2.  
 XX  
 XX 03-JAN-2002.  
 PD  
 XX 20-JUN-2001; 2001WO-US19692.  
 PF  
 XX 23-JUN-2000; 2000US-213637P.  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.

XX (GETH ) GENENTECH INC.  
 PA  
 XX Baker KP, Ferrara N, Gerber H, Gertlsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX  
 DR WPI: 2002-090516/12.  
 DR N-PSDB: ABL88141.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 PS Claim 11; Fig 140; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiact, cystostatic,  
 CC antiangiogenic, hypotensive, vulnerability, antiatherosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.

XX  
 XX Sequence 185 AA;

Query Match 72.0%; Score 90; DB 23; Length 185;  
 Best local Similarity 72.0%; Pred. No. 2e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKPGGAPKDLMY 23  
 II : III : I IIIII III III  
 Db 97 LDALVKEKKIKGKGPGPPKGLMY 121

RESULT 10  
 AAU83665  
 ID AAU83665 standard; Protein: 185 AA.  
 XX  
 XX AAU83665;  
 AC  
 XX 08-MAY-2002 (first entry)  
 DT  
 XX Human PRO protein, Seq ID No 148.  
 DE  
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 XX breast cancer; prostate tumour; rectal tumour; liver tumour;  
 XX pericyte cell proliferation; chondrocyte cell proliferation;  
 KW tumour necrosis factor-alpha.

OS Homo sapiens.  
 XX WO200208288-A2.  
 PN  
 XX  
 XX  
 PD 31-JAN-2002.  
 PF 29-JUN-2001: 2001WO-US21066.  
 XX  
 XX 20-JUL-2000: 2000US-219556P.  
 PR 25-JUL-2000: 2000US-220585P.  
 PR 25-JUL-2000: 2000US-220605P.  
 PR 25-JUL-2000: 2000US-220607P.  
 PR 25-JUL-2000: 2000US-220624P.  
 PR 25-JUL-2000: 2000US-220638P.  
 PR 25-JUL-2000: 2000US-220664P.  
 PR 25-JUL-2000: 2000US-220666P.  
 PR 26-JUL-2000: 2000US-220893P.  
 PR 28-JUL-2000: 2000WO-US20710.  
 PR 23-AUG-2000: 2000WO-US23522.  
 PR 24-AUG-2000: 2000WO-US23328.  
 PR 15-SEP-2000: 2000US-000000P.  
 PR 10-NOV-2000: 2000WO-US30873.  
 PR 28-NOV-2000: 2000US-253646P.  
 PR 01-DEC-2000: 2000WO-US32678.  
 PR 20-DEC-2000: 2000US-0747259.  
 PR 20-DEC-2000: 2000WO-US34956.  
 PR 28-FEB-2001: 2001WO-US06520.  
 PR 10-MAY-2001: 2001US-0854280.  
 PR 25-MAY-2001: 2001WO-US17092.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AB, Smith V, Stephan JF, Watanabe CK, Wood WI,  
 XX  
 DR WPI: 2002-172001/22.  
 DR N-PSDB: ABK33609.  
 XX  
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for treating a PRO related disorder and for diagnosing tumours  
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
 PT tumour or liver tumour -  
 XX  
 PS Claim 11: Figure 148: 359pp: English.  
 XX  
 CC The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO  
 CC protein sequences of the invention.  
 XX  
 SQ Sequence 185 AA:

Query Match 72.0%; Score 90; DB 23; Length 185;  
 Best Local Similarity 72.0%; Pred. No. 2e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

OY 1 LDTWKEOK--GKPGAPPKDLMY 23  
 II :|||:| ||||| |||||  
 DB 97 LDTWKEOK--GKPGAPPKDLMY 121

RESULT 11  
 ID AAB38329 standard; Protein: 186 AA.  
 XX  
 XX  
 AC AAB38329;  
 XX  
 XX 31-JAN-2001 (first entry)  
 DT  
 XX  
 XX Human secreted protein encoded by gene 9 clone HNSAD53.  
 DE  
 XX Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;  
 KW cytostatic; cardiac; vasotropic; cerebroprotective; neuroprotective;  
 KW nocrotropic; antibacterial; virucide; fungicide; optalmallogical; human;  
 KW vulnerrary; gene therapy; infection; secreted protein.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200061623-A1.  
 XX  
 XX 19-OCT-2000.  
 PD  
 PF 06-APR-2000: 2000WO-US08979.  
 XX  
 XX 09-APR-1999: 99US-0128693.  
 PR 26-APR-1999: 99US-0130991.  
 XX  
 XX (HUMAN-) HUMAN GENOME SCI INC.  
 PA  
 XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;  
 PI Lafleur DW, Olsen HS, Edner R, Florence KA, Moore PA, Birse CE;  
 PI Young PE;  
 XX  
 DR WPI: 2000-647418/62.  
 XX  
 PT New nucleic acid molecules encoding 62 human secreted proteins for  
 PT diagnosing, preventing, treating or ameliorating medical conditions and  
 PT used as food additives or preservatives -  
 XX  
 PS Claim 11: Page 598: 716pp: English.  
 XX  
 CC Sequences AAB38321-B38396 represent the amino acid sequences of 62  
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes  
 CC and proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
 CC a range of human tissues disclosed in the specification. The nucleic  
 CC acids, proteins, antibodies and (ant)agonists are useful in the  
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.  
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms  
 CC of the breast or liver; (c) cardiovascular disorders e.g. cerebral ischemia; (e)  
 CC arrest; (d) cerebrovascular disorders e.g. Alzheimer's disease; (g)  
 CC angiogenesis; (f) nervous system disorders and fungi; and (h) ocular  
 CC infections caused by bacteria, viruses and fungi. The polypeptides can also be used to  
 CC disorders e.g. corneal infection. The polypeptides can also be used to  
 CC aid wound healing and epithelial cell proliferation, to prevent skin  
 CC aging due to sunburn, to maintain organs before transplantation, for  
 CC supporting cell culture of primary tissues, to regenerate tissues and in  
 CC chemotaxis.  
 XX  
 SQ Sequence 186 AA:

Query Match 72.0%; Score 90; DB 21; Length 186;  
 Best Local Similarity 72.0%; Pred. No. 2e-05;  
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

OY 1 LDTWKEOK--GKPGAPPKDLMY 23  
 II :|||:| ||||| |||||  
 DB 97 LDTWKEOK--GKPGAPPKDLMY 121  
 ID AAW69974 standard; Protein: 194 AA.

[illegible]

(PEKE ) PE CORP NY.  
 Venter JC, Adams M, Li PWD, Myers EW;  
 WPI: 2001-656860/75.  
 N-PSDB; ABL03749.  
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -  
 Disclosure: SEQ ID NO 5730; 21pp + Sequence Listing; English.  
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA sequences (AB057737-AB072072), and the encoded proteins  
 (AB057737-AB072072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 Sequence 1194 AA;  
 Query Match 43.2%; Score 54; DB 22; Length 1194;  
 Best Local Similarity 64.3%; Pred. No. 29;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 5 VKOKGKPGGAPP 18  
 :| | | | | | | | | |  
 Db 613 MKSPNGNGPGAPP 626

RESULT 15  
 AAR79655  
 ID AAR79655 standard; Protein; 298 AA.

AC AAR79655;  
 DT 06-DEC-1995 (first entry)  
 DE Human UBC/CDC34 protein.  
 KW Ubiquitin-conjugating enzyme; UBC/CDC34; cell cycle; cell proliferation; cancer; psoriasis; fibrosis.  
 OS Homo sapiens.  
 PN WO9518974-A.  
 PD 13-JUL-1995.  
 PF 04-JAN-1995; 95WO-US00164.  
 PR 13-SEP-1994; 94US-0305520.  
 PR 04-JAN-1994; 94US-0176937.  
 PR 23-MAY-1994; 94US-0247904.  
 PR 27-MAY-1994; 94US-0250795.  
 (MITO-) MITOTIX INC.

PI Cottarel G, Draetta G, Eckstein JW, Gyuris J, Rolfe M;  
 WPI: 1995-255137/33.  
 N-PSDB; AAQ97845.

Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle regulatory proteins - also new ubiquitin conjugating enzymes, their related nucleic acid, vectors, antibodies etc., useful for regulating e.g. cell proliferation

XX Disclosure; Page 107-108; 157pp; English.  
 PS Human UBC3/CDC34 cDNA (given in AA097845) was amplified from a HeLa  
 CC cell cDNA library. The gene was subcloned into a baculovirus or  
 CC pEX vector for expression of recombinant UBC/CDC34 in Sf9 insect  
 CC or E. coli cells for use as a component of an in vitro ubiquitin  
 CC conjugating system.  
 XX  
 SQ Sequence 298 AA;

Query Match 40.8%; Score 51; DB 16; Length 298;  
 Best Local Similarity 61.5%; Pred. No. 19;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 OY 6 KEOKGKPGGAPP 18  
 :| | | | | | | | | |  
 Db 21 EEAAGGPGGAPP 33

Search completed: April 11, 2003, 16:11:07  
 Job time : 8.45351 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:33 ; Search time 36.6069 Seconds  
(without alignments)  
928.727 Million cell updates/sec

Title: US-09-821-726a-18\_COPY\_21\_185

Perfect score: 880

Sequence: 1 DYSISVNDGNSGSGQGSV.....ISANIILNIFSGIAEN 165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	221.5	25.2	191	11	09D017
2	197	22.4	184	11	09C056
3	92	10.5	868	5	08S772
4	86	9.8	285	5	094477
5	86	9.8	574	8	09M078
6	83.5	9.5	186	5	001876
7	83.5	9.5	1297	10	094556
8	82.5	9.4	409	16	069974
9	82.5	9.4	887	16	09J212
10	81	9.2	810	3	003388
11	81	9.2	1338	5	023927
12	80.5	9.1	263	10	048991
13	80.5	9.1	642	5	017169
14	80	9.1	568	5	09N138
15	79.5	9.0	227	10	P93572
16	79.5	9.0	526	10	09LJ56

17	79.5	9.0	855	5	08SSV6	08SSV6 dictyosteli
18	79	9.0	1060	5	08SSO5	08SSO5 dictyosteli
19	79	9.0	1318	5	09SPH4	09SPH4 dictyosteli
20	78.5	8.9	887	16	09J008	09J008 neisseria m
21	77	8.8	409	5	09BKB6	09BKB6 chaetopteru
22	77	8.8	409	5	09X2F6	09X2F6 chaetopteru
23	77	8.8	410	5	09W1W2	09W1W2 drosophila
24	77	8.8	808	16	09TE37	09TE37 clostridium
25	77	8.8	1245	5	09G195	09G195 plasmodium
26	76.5	8.7	649	5	09VTK7	09VTK7 drosophila
27	76.5	8.7	764	5	09G234	09G234 plasmodium
28	76.5	8.7	1157	5	000895	000895 plasmodium
29	76.5	8.7	1298	5	09U010	09U010 plasmodium
30	76	8.6	573	4	094830	094830 homo sapien
31	76	8.6	588	5	0964F6	0964F6 plasmodium
32	75.5	8.6	241	2	033788	033788 salmonella
33	75.5	8.6	245	16	092RS8	092RS8 rhizobium m
34	75.5	8.6	362	4	09UHS5	09UHS5 homo sapien
35	75.5	8.6	443	16	09PRE4	09PRE4 staphylococ
36	75.5	8.6	608	17	08ZWK4	08ZWK4 pyrobaculum
37	75.5	8.6	995	16	08Z086	08Z086 salmonella
38	75	8.5	421	16	08YBP5	08YBP5 druceella me
39	75	8.5	434	5	08T834	08T834 dictyosteli
40	75	8.5	442	5	025830	025830 plasmodium
41	75	8.5	537	5	08T1K7	08T1K7 dictyosteli
42	75	8.5	4564	5	077075	077075 drosophila
43	74.5	8.5	1240	10	024016	024016 lycopersico
44	74.5	8.5	1266	10	09XET3	09XET3 lycopersico
45	74.5	8.5	1309	5	08T2H9	08T2H9 dictyosteli

## ALIGNMENTS

RESULT 1  
ID 09D017 PRELIMINARY: PRT: 191 AA.  
AC 09D017;  
DT 01-JUN-2001 (TREMBL:rel. 17, Created)  
DT 01-JUN-2001 (TREMBL:rel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBL:rel. 17, Last annotation update)  
DE 1190003M12R1K protein.  
GN 1190003M12R1K.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,  
RA Wystraw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL: AK004474; BAH23320.1; -;  
DR MGI: 1916138; 1190003M12R1K.

SEQUENCE 191 AA: 20772 MW: 76DDB4796AEB84D CRC64:

Query Match 25.2%; Score 221.5; DB 11; Length 191;  
Best Local Similarity 31.2%; Pred. No. 8.6e-14;  
Matches 49; Conservative 31; Mismatches 60; Indels 17; Gaps 4;

QY 13 GSGGOSVSNNHNNVANNNNNGNSMNAALMDYRTGFAVTRLFEEKSCIVHKRKEAMP 72  
DB 42 GSVGTOTTHVDALRGVSTRDINSVQSEWMDYKNDLAAKLFKMACYLAKMDRAAP 101  
QY 73 SL-----QALDALVKEKKLOGKGGPG--PPPKSLRYSVNPNRVDNDLKFGRSIYAMCKGIP 126  
DB 102 SLDDITQAL-----GKQASGHYPPTRGLTYLPSRIKNAQYGVPIKDLGRAVP 151  
QY 127 TYMA-EEIOGANLISYSEKICISANIIMILINISFCGCI 162  
DB 152 TYFARQOKEGTALTMDPDSCELOLLSFMGLSIGEI 188

RESULT 2

QY 09CQ56 PRELIMINARY: PRT: 184 AA.  
AC 09CQ56;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE 1810036H07RIK protein.  
GN 1810036H07RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=STOMACH; AND PANCREAS;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Ando S., Yamana K.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Fiedischmann W., Gasteirland T., Gissi C., Kling B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL: AK008986; BAB26008.1;  
DR EMBL: AK007451; BAB25046.1;  
DR EMBL: AK007705; BAB25041.1;  
DR MGI: 1913534; 1810036H07RIK.  
DR PRINTS: PR01559; DUFFYANTIGEN.  
SQ SEQUENCE 184 AA: 20469 MW: 612A18FABE652230 CRC64;

Query Match 22.4%; Score 197; DB 11; Length 184;  
Best Local Similarity 29.4%; Pred. No. 2e-11;  
Matches 45; Conservative 37; Mismatches 67; Indels 4; Gaps 3;

QY 12 SGGGOSVSNNHNNVANNNNNGNSMNAALMDYRTGFAVTRLFEEKSCIVHKRKEAMP 71  
DB 32 NGGNTQETVITDNOONTATINIHSGSSSTTIPYKKGITASRLSRACVITMDHKAT 91  
QY 72 PSLOALDALVKEKKLOGKGGPGPPKSLRYSVNPNRVDNDL-KFGSIYAMCKGIP 129  
DB 152 PSLOALDALVKEKKLOGKGGPGPPKSLRYSVNPNRVDNDL-KFGSIYAMCKGIP 129

DB 92 PALDKLQRFLEKQTM-NAIDSPETWVRNPLKSLITKVWDFLFGSP1RQLOCKHMPLYE 150  
QY 130 AEIOGANLISYSEKICISANIIMILINISFCGCI 162  
DB 151 GEVATRPKEVS-IGACAKYGLLIGVSTICGCI 182

RESULT 3

QY 08SX72 PRELIMINARY: PRT: 868 AA.  
AC 08SX72;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE ID30050p.  
GN CG9381.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
RA Patel S., Phouenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Ceiniker S.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY094811; AAM11164.1;  
SQ SEQUENCE 868 AA: 92619 MW: E6FFE05B4392EE3B CRC64;

Query Match 10.5%; Score 92; DB 5; Length 868;  
Best Local Similarity 23.8%; Pred. No. 2.5;  
Matches 30; Conservative 15; Mismatches 45; Indels 36; Gaps 3;

QY 5 SYNDGSGGSGGOSVSNNHNNVANNNNNGNSMNAALMDYRTGFAVTRLFEEKSCIVH 64  
DB 86 NVNLINGSGNNNNNGNNNNNGNNNNNGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 122  
QY 65 KMKKEAMPSSLOALDALVKEKKLOGKGGPGPPKSLRYSVNPNRVDNDLKFGRKSIV-AMCK 123  
DB 123 --NKDANPNCHS-----QGCGGNSPGLGHHNGVNGNNGNNGNNGNNGNNTN 170  
QY 124 GIPYIM 129  
DB 171 GPPDYM 176

RESULT 4

QY 094477 PRELIMINARY: PRT: 285 AA.  
AC 094477;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ORFvegl58 (Fragment).  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RA Loomis W.F.;  
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U66524; AAB06787.1;  
DR Interpro: IPR001849; PH.  
DR Pfam: PR00169; PH; 1.  
DR SMART: SM00233; PH; 1.  
FT NON\_TER 1  
SQ SEQUENCE 285 AA: 31010 MW: A1AFA742F99AAE36 CRC64;



[REDACTED]

34 NNGWNSWNL-----WDYRTGFAVTRLFEKKSCIVHKMKKEAMP---SL

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      | : || |
24 NNNNNNNNNAL-----WDIRIGFAVIRLFEKKSCTVIHKKKKEAMP-----SL

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      | : || |
24 NNNNNNNNNAL-----WDIRIGFAVIRLFEKKSCTVIHKKKKEAMP-----SL

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Db 293 NENYEMNDLRNIFVOGDIGKIIIVT---TRKDSVALMNGNEOISMGNLSTEASWSLFKR 349

QY 84 KRIQGGPGGPPPKSLRYSVNPNRVNDLDFKGSIVAMCKGIPYMAEEIOGANLISYE 143

Db 350 HAFENMDPMKHP-----ELEEVGRIOIAKCKGLP--LAKLTLAGLRRKSE 393

QY 144 ----KCSANILMIL 154

Db 394 IDEMKCLIRSEIMEL 408

RESULT 8

069974 PRELIMINARY; PRT; 409 AA.

AC 069974: STRAIN-A3(2) / M145; Created

DT 01-AUG-1998 (TREMBlrel. 07, last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)

DE Putative secreted protein.

GN SC05798 OR SC4H2.19C.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.

OX NCBI\_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2) / M145;

RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,

RA Rahlbrowisch E., Rajandream M.A., Rutherford K., Ruter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,

RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2)";

RL Nature 417:141-147(2002).

DR EMBL: AL022268; CAA18335.1; -

SQ SEQUENCE 409 AA; 42955 MW; F99AEF3D5FE14E5B CRC64;

Query Match 9.4%; Score 82.5; DB 16; Length 409;

Best Local Similarity 21.1%; Pred. No. 8.3;

Matches 39; Conservative 21; Mismatches 74; Indels 51; Gaps 7;

QY 3 SISVNDGSGGSGQSVSVNHNHNAVNDN--NNGMNSMN-----AL 43

Db 54 SASAADGNGGIRIPDDIKDKLEHGIDVDKMGKMKMNDMDLREAOFPVPIIEGL 113

QY 44 WPIRTGFATRLFEKKSCIVHKMKKREAMPISLALDALVREKKLOG-KGPGPPKSLRYS 102

Db 114 WD-----PRMRDAEPPDDEVDENDISGGOGVTPPEPAPVEAE 151

QY 103 VNPENRV-DNLDFKGSIVAMCKGIPYMAEEIOG-----ANLISSEKISANIL--WT 153

Db 152 AVPAKYHDNAATGAKLLFDSPKSGMVCATVYVXDPAHPKSGMVTAGHCVAAGSGGWY 211

QY 154 LNISE 158

Db 212 RNIAF 216

RESULT 9

09J212 PRELIMINARY; PRT; 887 AA.

AC 09J212: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)

DE Pyruvate dehydrogenase, E1 component.

GN NMB1341.

OS Neisseria meningitidis (serogroup B).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_TaxID=491;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-MC58 / SEROGROUP B;

RX MEDLINE=2015755; PubMed=10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

RA Nelson W.C., Gwynn M.L., Deboy R., Peterson J.D., Dougherty B.A.,

RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Venter J.C.,

RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,

RA Cotton M.D., Ullrich V., Masignani V., Pizzo V., Grandi G., Sun L.,

RA Gill J., Scarlato V., Masignani V., Pizzo V., Grandi G., Sun L.,

RA Smith H.O., Fraser C.M., Moxon E.R., Rappaport J., Venter J.C.;

RT "Complete genome sequence of Neisseria meningitidis serogroup B strain

RT MC58";

RL Science 287:1809-1815(2000).

DR EMBL: AE002462; AAF41716.1; -

DR TIGR; NMB1341; -

DR InterPro; IPR004660; ACEE.

DR InterPro; IPR000360; Transketolase.

DR Pfam; PF00456; Transketolase; 1.

DR TIGRFAMs; TIGR00759; acee; 1.

RW Complete proteome.

SQ SEQUENCE 887 AA; 99562 MW; BA7BA93E38C5206F CRC64;

Query Match 9.4%; Score 82.5; DB 16; Length 887;

Best Local Similarity 24.1%; Pred. No. 21;

Matches 41; Conservative 24; Mismatches 60; Indels 45; Gaps 9;

QY 9 DGNSSGSGGQSVSVNHNHNAVNDNNGMN-----SMNALMDYRTGFATRLFEK-KSCIV 63

Db 264 DDPVGNCK--IIQLEGNFEGA-----GNVYKVLWGRMD-----RLAKKDKDGL 309

QY 64 HKMKKRAM-----PSLQALDALVREKKLOG-KGPGPPKSLRY 101

Db 310 RQRMEECLDGDYQYKSKSGKAYVREHFNTPELKALVADMTDEQJMALNRGCHDPOKY-Y 368

QY 102 SVNPNRVNDLDFKGSIVAMCKGIPY-MAEEIOGANLISSEKISANI 150

Db 369 NAYDRAANHAD--GKPTVILARTIKGYMGASGEQONVAHOKMKKASL 416

RESULT 10

003388 PRELIMINARY; PRT; 810 AA.

AC 003388: 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)

DE D8035.28P.

GN YDR485C OR D8035.28.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,

RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,

RA Hunticke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,

RA Moseedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,

RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,

RA Winant A., Yelton M., Botstein D., Davis R.W.;

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Dietrich F.S.;

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Jia Y., Cherry J.M.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: U33050; AAB64928.1; -  
 SQ S0002893; YDRA85C.  
 SEQUENCE 810 AA; 92247 MW; D49FECADD9C0093 CRC64;

Query Match  
 Best Local Similarity 9.2%; Score 81; DB 3; Length 810;  
 Matches 26; Conservative 25; Mismatches 39; Indels 20; Gaps 5;

OY 5 SVNDGSGGSGGQSVNNEHNANVNDNN---GNMSMALMDYRTGFAVTRLEKSC 61  
 DB 364 SIKNDGDVNLGENSSSVHOKRIETSTDTVEGESSPA-----ASRVN---- 411  
 OY 62 IVHAKMKKAMPISQALDALVKEKKLOGKGGPPKSLRYSVNPVRDNL 111  
 DB 412 --DELKPTALPDV-TLDAIAINKOSTVDEAPNSQPKNI--ITTEOKITNV 456

## RESULT 11

OY 023927 PRELIMINARY; PRT: 1338 AA.  
 AC 023927;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX-2;  
 RA Adler Kristin.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U64830; AAB04999.1; -  
 DR HSP; P08631; IAD5.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR004040; STY\_pkinase.  
 DR InterPro: IPR001245; TYR\_pkinase.  
 DR Pfam: PF00069; pkinase; 2.  
 DR ProDom: PD000001; Euk\_pkinase; 2.  
 DR SMART; SM00221; STYK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 2.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 KW ATP-binding; kinase; transferase; tyrosine-protein kinase.  
 SQ SEQUENCE 1338 AA; 149926 MW; D257958DD71C02 CRC64;

Query Match  
 Best Local Similarity 9.2%; Score 81; DB 5; Length 1338;  
 Matches 42; Conservative 23; Mismatches 42; Indels 78; Gaps 8;

OY 7 NDDGNSG-----GSGQGSVSVNNEHNANVNDNNGNMNLMDYRTGF 50  
 DB 465 NNINNSGIRKSADDTVTLSPRLSSGSSSTSSNPHN-PNHHQKGLNN----- 512  
 OY 51 AVTRLEFKSCIVHAKMKKAMPISQALDALVKEKKLOGKGGPPKSLRYSVNPVRDNL 110  
 DB 513 --KLEKLTSC--TRKEITELIEKKSLEKONLIDEG-----YSENADSPEN 555  
 OY 111 LDKRGKSVANCKGIPYMAEIQCANLISYEKCI-----SANTILWILNISC 160  
 DB 556 L-----SEEIIOKIN-----EKTELENLITLSNSNSWLSNGSSSTS 592  
 OY 161 GIAEN 165  
 DB 593 TISGN 597

## RESULT 12

ID 048991 PRELIMINARY; PRT: 263 AA.  
 AC 048991;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 OS NBS-LRR type resistance protein (Fragment).  
 GN R11.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Euphorbiaceae; Oryzaeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN 111

RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPONBARE.  
 RX MEDLINE=98081880; PubMed=9419382;  
 RA Leister D., Kurth U., Laurie D.A., Yano M., Sasaki T., Devos K.,  
 RT "Rapid reorganization of resistance gene homologues in cereal  
 genomes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:370-375(1998).  
 DR EMBL: AF032698; AAB96995.1; -  
 DR InterPro: IPR000767; Disease-resist.  
 DR InterPro: IPR002182; NB-ARC.  
 DR Pfam: PF00931; NB-ARC; 1.  
 DR PRINTS: PR00364; DISEASERSIST.  
 FT NON\_TER 1  
 FT NON\_TER 263  
 SQ SEQUENCE 263 AA; 30261 MW; 476A54B153B105BC CRC64;

Query Match  
 Best Local Similarity 9.1%; Score 80.5; DB 10; Length 263;  
 Matches 26; Conservative 25; Mismatches 50; Indels 19; Gaps 4;

OY 15 SGQGSVSVNNEHNANVNDNNGNMNLMDYRTGFAVTRLEKSCIV-----HKMK 68  
 DB 59 SPHERLAKRIKHKVLLVLDLNNRRCMD-----LICEPMNTALCMIVTTRSERVAK 114  
 OY 69 --EAMPISQALDALVKEKKLOGKGGPPKSLRYSVNPVRDNLDKFGKSVANCKGIP 126  
 DB 115 LVOTMPNPTSLNCLSSSEWS-----LFQVAFVYDNGMTPNLQETGMSIVKCKGLP 167

## RESULT 13

ID 017169 PRELIMINARY; PRT: 642 AA.  
 AC 017169;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE Hypothetical 68.1 kDa protein.  
 GN B0454.8.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN 111

RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=9906113; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN 121

RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Geisel C., Beck C., Gibson A.;  
 RL "The sequence of C. elegans cosmid B0454.";  
 RN Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RT "Direct Submission.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.



GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 ; Search time 9.69005 Seconds  
(without alignments)  
706.250 Million cell updates/sec

Title: US-09-821-726a-18\_COPY\_21\_185  
Perfect score: 880  
Sequence: 1 DYSISVNDGNSGGSGQSV.....ISANILWILNISFCGIAEN 165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	687	78.1	199	1	Q9ns71 homo sapien
2	593.5	67.4	184	1	Q9cr36 mus musculu
3	94.5	10.7	79	1	P32770 saccharomyc
4	87	9.9	695	1	P51141 mus musculu
5	87	9.9	695	1	DV11_MOUSE
6	83	9.4	296	1	DV11_RAT
7	78	8.9	349	1	DP5D_CLOPA
8	77	8.8	803	1	CDAA_BACTU
9	77	8.8	954	1	XYNA_RUMFL
10	76	8.6	345	1	TL29_LYCES
11	76	8.6	1597	1	RRL1_YEAST
12	75	8.5	442	1	CSP_PLATW
13	74.5	8.5	728	1	KDGI_ARATH
14	74	8.4	1146	1	MMCL_MYCTU
15	74	8.4	1282	1	TP2M_DICDI
16	73.5	8.4	219	1	FLRZ_BACSU
17	73.5	8.4	1195	1	YK76_YEAST
18	73	8.3	414	1	SPYA_PELCA
19	73	8.3	472	1	ME11_CABEL
20	73	8.3	535	1	ARSB_FELCA
21	73	8.3	817	1	PMT1_YEAST
22	73	8.3	1025	1	LCAP_HUMAN
23	72.5	8.2	341	1	ARGC_METJA
24	72.5	8.2	476	1	HM1N_BOMBO
25	72.5	8.2	1341	1	YL78_YEAST
26	72	8.2	417	1	KCRU_CHICK
27	71.5	8.1	211	1	ADAA_BACSU
28	71.5	8.1	536	1	PYRG_CHILMU
29	71.5	8.1	819	1	SWE1_YEAST
30	71.5	8.1	905	1	GYRA_RICCN
31	71	8.1	1025	1	CSP_PLAFA
32	71	8.1	1025	1	LCAP_RAT
33	70.5	8.0	348	1	SXL_CERCA

34	70.5	8.0	818	1	CTNB_URECA	P35224 urechis cau
35	70.5	8.0	1914	1	KMLS_HUMAN	Q15746 homo sapien
36	70	8.0	309	1	P2A_BRANA	P23778 brassica na
37	70	8.0	329	1	MKR2_CRILLO	P49136 cricetus
38	70	8.0	385	1	MKR2_MOUSE	P49136 mus musculu
39	70	8.0	400	1	MKR2_HUMAN	P49137 homo sapien
40	70	8.0	404	1	FTRL_YEAST	P40088 saccharomyc
41	70	8.0	419	1	KCRS_RABIT	Q77814 oryctolag
42	70	8.0	937	1	CD47_HUMAN	Q9un72 homo sapien
43	70	8.0	1342	1	RPOB_ECOLI	P00575 escherichia
44	70	8.0	1742	1	MY5C_HUMAN	Q9nqx4 homo sapien
45	69.5	7.9	398	1	LIPG_HUMAN	P07098 homo sapien

## ALIGNMENTS

## RESULT 1

CLIP\_HUMAN

STANDARD: PRT; 199 AA.

AC Q9ns71; 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE CALL protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN 11

RP SEQUENCE FROM N.A.

RC TISSUE=Stomach;

RA MEDLINE=20296773; PubMed=10835488;

RT Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;

Jpn. J. Cancer Res. 91:459-463(2000).

"Isolation of two novel genes, down-regulated in gastric cancer."

-1- TISSUE SPECIFICITY: Expressed in stomach. No expression is

detected in cancer tissue or gastric cancer cell lines.

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CC EMBL: AB039886; BAA92433.1; -

DR MIM: 606402; -

CC EMBL: AB039886; BAA92433.1; -

DR MIM: 606402; -

CC EMBL: AB039886; BAA92433.1; -

DR MIM: 606402; -

CC EMBL: AB039886; BAA92433.1; -

DR MIM: 606402; -

CC EMBL: AB039886; BAA92433.1; -

DR MIM: 606402; -

```

DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CAIL protein homolog.
GN CAIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach; and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Welt C., Whitaker C., Wilming L.,
RA Wyshaw-Boriss A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
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CC -----
DR EMBL: AK008990; BAB26010.1; -
DR EMBL: AK008622; BAB25784.1; -
DR EMBL: AK008641; BAB25801.1; -
DR EMBL: AK008647; BAB25805.1; -
DR EMBL: AK008722; BAB25856.1; -
DR EMBL: AK008745; BAB25872.1; -
DR EMBL: AK008933; BAB25875.1; -
DR EMBL: AK008956; BAB25988.1; -
DR EMBL: AK009145; BAB26103.1; -
DR EMBL: AK019050; BAB31525.1; -
DR MGD: MGI:1913533; 2200002K21R1K.
FT CONFLICT 113 113 P -> L (IN REF. 1; BAB26103).
SQ SEQUENCE 184 AA; 20134 MW; 2889820404FF8B CRC64;
Query Match 67.4%; Score 593.5; DB 1; Length 184;
Best Local Similarity 65.9%; Pred. No. 7.2e-50;
Matches 108; Conservative 22; Mismatches 31; Indels 3; Gaps 2;
QY 2 YSISVN-DGNGSGGSGGSGSVNNEHNANVDNNNGNSMNAIMDYRTGPAVTRLEFKS 60
DB 21 YVNIINGNDGNDVSGGSGSVSINGVNVANINDNNGMSIMDYENFATRLFSKKS 80
QY 61 CIVHKKRKAEMPSLDALDAIVKREKLOGGPGPKSLRYSVNPRNVNDLDFGSGIYA 120
DB 81 CIVHNNKNDAMPSLDLDITMVEKQ--GKPGGAPPKDLIMYSVNPTRVDLNTFGPKIAG 138
QY 121 MCKGIPYMAEITOGANLISSEKISANIILMIILNISFGGIAE 164
DB 139 MCKGIPYMAEITPGNPQPLYSKKCYTADIIILMRSFGGTSVE 182

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RESULT 3
ID NRPI_YEAST STANDARD; PRT; 719 AA.
AC P32770; O12228;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Asparagine-rich protein (ARP protein).
DE NRPI OR ARP1 OR ARP OR YDL167C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AH22;
RX MEDLINE=93247548; PubMed=8483449;
RA Wehner E.P., Rao E., Brendel M.,
RA "Molecular structure and genetic regulation of SFA, a gene
RA responsible for resistance to formaldehyde in Saccharomyces
RA cerevisiae, and characterization of its protein product.";
RL Mol. Gen. Genet. 237:351-358(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX Polh T.M.;
RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RT -1- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS.
RT -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
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CC -----
DR EMBL: X68020; CAA48159.1; -
DR EMBL: Z67750; CAA91579.1; -
DR EMBL: Z74215; CAA98741.1; -
DR PTR: S31139; S31139.
DR SGD: S0002326; NRPI.
DR InterPro: IPR000504; RNA_rec-mot.
DR InterPro: IPR001876; Znf_RanGDP.
DR Pfam: PF00076; rrm; 1.
DR Pfam: PF00641; zf-RanBP; 2.
DR SMART: SM00360; RRM; 1.
DR SMART: SM00547; Znf_RBZ; 2.
DR PROSITE: PS0102; RRM; 1.
DR PROSITE: PS0030; RRM_RNP_1; FALSE_NEG.
DR PROSITE: PS01358; ZF_RANBP2_1; 2.
DR PROSITE: PS0199; ZF_RANBP2_2; 2.
KW Nuclear protein; zinc-finger; RNA-binding; Repeat.
FT DOMAIN 226 322
FT ZN_FING 355 384
FT ZN_FING 581 610
FT DOMAIN 490 564
FT CONFLICT 493 493 ASN-RICH.
SQ SEQUENCE 719 AA; 79299 MW; ADA9BC09F58269 CRC64;
Query Match 10.7%; Score 94.5; DB 1; Length 719;
Best Local Similarity 24.8%; Pred. No. 0.25;
Matches 39; Conservative 18; Mismatches 63; Indels 37; Gaps 5;
QY 2 YSISVNDGNGSGGSGGSGSVNNEHN-----VANVDNNNGNSMNAIM 44
DB 508 YVNIINGNDGNDGNSNNNNNNNNNNHHNGSINSNTNNNNNNNNNNNS 567
QY 45 DYRTGPAVTRL-----FEKSKCIYHKKKKKAEM-----PSLDALDAIVKREK 90
DB 568 NIGMGCGSGNMFRAGDMKSTCTYHNFAKNVYCLRCGGPKSISDASFTNHYIDSTFG 627

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Oy 91 PGPPPKSLRYSVNPN-----RVNDLDFGKSIYAM 121  
 Db 628 PASRTPSNNNISVNTNGSGNACRTGNDKKGDISLM 664

## RESULT 4

ID DVL1\_MOUSE STANDARD: PRT: 695 AA.

AC P51141: 060868; (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)  
 DE (DSH homolog 1).  
 GN DVL1 OR DVL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=95046919; PubMed=7958461;  
 RA Sussman D.J., Klingensmith J., Salinas P., Adams P.S., Nusse R.,  
 RA Perrimon N.;  
 RT "Isolation and characterization of a mouse homolog of the Drosophila  
 RT segment polarity gene dishevelled.";  
 RL Dev. Biol. 166:73-86(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/c;  
 RX MEDLINE=96632916; PubMed=9132266;  
 RA Lijam N., Sussman D.J.;  
 RT "Organization and promoter analysis of the mouse dishevelled-1 gene.";  
 RL Genome Res. 5:116-124(1995).  
 RN [3]  
 RP KNOCK-OUT.  
 RX MEDLINE=97442352; PubMed=9298901;  
 RA Lijam N., Paylor R., McDonald M.P., Crawley J.N., Deng C.-X.,  
 RA Herrup K., Stevens K.E., Maccaferri G., McBain C.J., Sussman D.J.,  
 RA Wynshaw-Boris A.;  
 RT "Social interaction and sensorimotor gating abnormalities in mice  
 RT lacking Dvl1.";  
 RL Cell 90:895-905(1997).  
 CC -i- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY  
 CC MEDIATED BY MULTIPLE WNT GENES. DVL1 DEFICIENT MICE DISPLAY  
 CC ABNORMALITIES IN SOCIAL BEHAVIORS AND SENSORIMOTOR GATING.  
 CC -i- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -i- TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE BRAIN, TESTIS AND  
 CC KIDNEY. LOWER LEVELS IN THE OVARY, BREAST, MUSCLE, LIVER AND SMALL  
 CC INTESTINE. AND VERY LOW LEVELS ARE SEEN IN THE SPLEEN AND THYMUS.  
 CC A MODERATE LEVEL EXPRESSION IS SEEN IN THE HEART.  
 CC DEVELOPMENTAL STAGE: IS EXPRESSED THROUGHOUT THE EMBRYONIC CENTRAL  
 CC NERVOUS SYSTEM FROM PRE-SOMITE STAGES AND IN NEURON-RICH AREAS OF  
 CC THE BRAIN THROUGHOUT POSTNATAL DEVELOPMENT, AS WELL AS IN MANY  
 CC OTHER TISSUES.  
 CC -i- SIMILARITY: CONTAINS 1 DEP DOMAIN.  
 CC -i- SIMILARITY: BELONGS TO THE DSH FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: 010115; AAA82175.1; -  
 CC EMBL: 028138; AAA74049.1; -  
 CC HSSP: 012923; 3PDZ.  
 CC MGD: MGI:94941; DVL1.  
 CC InterPro: IPR000591; DEP.

DR InterPro: IPR001158; DIX.  
 DR InterPro: IPR003351; Dishevelled.  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ; 1.  
 DR Pfam: PF00610; DEP; 1.  
 DR Pfam: PF00778; DIX; 1.  
 DR Pfam: PF02377; Dishevelled; 1.  
 DR Prodom: PD003639; DIX; 1.  
 DR SMART: SM00021; DAX; 1.  
 DR SMART: SM00049; DEP; 1.  
 DR SMART: SM00228; PDZ; 1.  
 DR PROSITE: PS50186; DEP; 1.  
 DR PROSITE: PS50106; PDZ; 1.  
 KW Developmental protein.  
 FT DOMAIN 251 323 PDZ.  
 FT DOMAIN 425 489 DEP.  
 FT DOMAIN 390 393 POLY-SER.  
 FT CONFLICT 122 125 MISSING (IN REF. 2).  
 FT CONFLICT 211 211 T -> N (IN REF. 2).  
 SQ SEQUENCE 695 AA; 75350 MW; A9FA49F95CF75F2 CRC64;

Query Match 9.9%; Score 87; DB 1; Length 695;  
 Best Local Similarity 26.8%; Pred. No. 1.2;  
 Matches 30; Conservative 15; Mismatches 49; Indels 18; Gaps 5;

Oy 12 SGSGGGSVSVNNEHNVANDNNNGNSMALDYRTGFVTRLEFKKSCIVHKKEAM 71  
 Db 596 AGSGSGSES-----DHTVPSGSGSTGW-----WER-----FVSQLSKSS--PSSQASAVA 638  
 Oy 72 PSIQALDAIVKERRKLOGKGGPPPKSLRYSVNPNRVNDLDFGKSIYAMCK 123  
 Db 639 PGLPLPLPLTKAVAVVGGPPGPPVRELA-AVPELITGSPQSKAMGNCE 689

## RESULT 5

ID DVL1\_RAT STANDARD: PRT: 695 AA.

AC Q9WVB9: Q9WVB8; Q9W0C5;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)  
 DE (DSH homolog 1).  
 GN DVL1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar Kyoto;  
 RX MEDLINE=21254118; PubMed=11354832;  
 RA de Lange R.P.J., Burr K., Clark J.S., Negrin C.D., Brosnan M.J.,  
 RA St Clair D.M., Dominiczak A.F., Shaw D.J.;  
 RT "Mapping and sequencing rat dishevelled-1: a candidate gene for  
 RT cerebral ischemic insult in a rat model of stroke.";  
 RL Neurogenetics 3:99-106(2001).  
 CC -i- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY  
 CC MEDIATED BY MULTIPLE WNT GENES.  
 CC -i- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -i- SIMILARITY: BELONGS TO THE DSH FAMILY.  
 CC -i- SIMILARITY: CONTAINS 1 DEP DOMAIN.  
 CC -i- SIMILARITY: CONTAINS 1 PDZ/DSH DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: AF143545; AAD33896.2; -

DR EMBL: AF143546; AAC33897.2; -  
 DR EMBL: AF143548; AAD41492.2; -  
 DR EMBL: AF143547; AAD41492.2; JOINED.  
 DR EMBL: AF143550; AAD41493.1; -  
 DR EMBL: AF143549; AAD41493.1; JOINED.  
 DR InterPro: IPR000591; DEP.  
 DR InterPro: IPR001158; DIX.  
 DR InterPro: IPR003351; Dishevelled.  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ; 1.  
 DR Pfam: PF00610; DEP; 1.  
 DR Pfam: PF00778; DIX; 1.  
 DR Pfam: PF02377; Dishevelled; 1.  
 DR ProDom: PD003639; DIX; 1.  
 DR SMART: SM00021; DAX; 1.  
 DR SMART: SM00049; DEP; 1.  
 DR PROSITE: PS50186; DEP; 1.  
 DR PROSITE: PS50106; PDZ; PARTIAL.  
 KW Developmental protein.  
 FT DOMAIN 251 323 PDZ.  
 FT DOMAIN 425 499 DEP.  
 SO SEQUENCE 695 AA; 75447 MW; EEC4AA99A117D22A CRC64;

Query Match 9.9%; Score 87; DB 1; Length 695;  
 Best Local Similarity 26.8%; Pred. No. 1.2;  
 Matches 30; Conservative 15; Mismatches 49; Indels 18; Gaps 5;

QY 12 SGSSGQSVNNEHNVANDNNNGNSWMLMDYRTGFAVTRLEFEKSCIVHKKKKEAM 71  
 Db 596 AGSSGSS-----DHYPSSSSGSTGW-----WER-----PVSQLSRGS--PRSCASAVA 638  
 QY 72 PSIALDALVKEKKLQCKPGGPGPKSLRYSVNPNVDNLDKFGKSIYAMCK 123  
 Db 639 GGLPPLPLTKAVAVVGGPPGPPVRELA-AVPELTLGSRGSPQKAMGNPCE 689

RESULT 6  
 DPSD\_CLOPA STANDARD; PRT; 296 AA.

AC 046192;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65).  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 6013;  
 RA Meyer J.;  
 Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Phosphatidyl-L-serine -  
 phosphatidylethanolamine + CO(2).  
 CC -1- Cofactor: Pyruvoyl group (By similarity).  
 CC -1- PATHWAY: Aminophospholipid biosynthesis.  
 CC -1- SIMILARITY: TO THE C-TERMINAL OF YEAST PSD2.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: Z28353; CAAB2212.1; -  
 DR InterPro: IPR003817; PS\_Decarboxylase.  
 DR InterPro: IPR005221; PS\_Decarb.  
 DR Pfam: PF02666; PS\_Decarboxylase; 1.  
 DR TIGRFAMs: TIGR00163; PS\_Decarb; 1.  
 KW Phospholipid biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen.

FT SITE 255 256 CLEAVAGE (NONHYDOLYTIC)  
 FT (BY SIMILARITY).  
 FT MOD\_RES 256 256 CONVERTED TO A PYRUVYL GROUP  
 FT (BY SIMILARITY).  
 SO SEQUENCE 296 AA; 34243 MW; A131FA6D2FB0472A CRC64;

Query Match 9.4%; Score 83; DB 1; Length 296;  
 Best Local Similarity 27.3%; Pred. No. 1;  
 Matches 36; Conservative 18; Mismatches 46; Indels 32; Gaps 6;

QY 20 VSVNNEHNVANDNNNGNSWMLMDYRTGFAVTRLEFEKSCIVHKKKKEAMPSLQALDA 79  
 Db 116 IIVYNNIMNNMNIIOVGIT--YKLNLDLQNDISIKVEKGCILARLPDYHFRHFLDN 173  
 QY 80 LVKEKKLQCKPGGPGPKSLRYSVNPNVDNLDKFGKSIYAMCK 123  
 Db 174 GICESTIKITGN-----YYSVNPALINKINLNFQCKRMSFNSDNGKILYVEIG 225

QY 120 AMCKG--IPTYM 129  
 Db 226 ATCVSGSIQTYM 237

RESULT 7  
 TL29\_ARATH STANDARD; PRT; 349 AA.

AC P82281; Q9M0S6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative L-ascorbate peroxidase, chloroplast precursor (EC 1.11.1.11)  
 DE (Thylakoid lumenal 29 kDa protein) (TL29) (P29).  
 GN ARAF09010 OR F2J3.40.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv Columbia;  
 RA MEDLINE=20083488; PubMed=10617198;  
 RA Mayer K.F.X., Schnell C., Wambutt R., Murphy G., Volckaert G.,  
 RA Pohl T., Duesterhoeft A., Stiekema W., Ertlan K.-D., Terryn N.,  
 RA Harris B., Ansoorge W., Brandt P., Griwall L.A., Rieger M.,  
 RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,  
 RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,  
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,  
 RA Vos P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,  
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,  
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,  
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,  
 RA Weltzenegger T., Bothe G., Ransperger U., Hilbert H., Braun M.,  
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirksen W.,  
 RA Boonjman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,  
 RA Bernreiser S., Hempel S., Feldpausch M., Lambert H., Van den Daele H.,  
 RA de Keyser A., Buysaert C., Gielen J., Villalroel R., De Clercq R.,  
 RA Van Montagu M., Rogers J., Cronin A., Quail R., Bray-Allen S.,  
 RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K.,  
 RA Pettelt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,  
 RA Botrova D., Bloeker H., Scharte M., Grimm M., Loehner T.-H.,  
 RA Gabel S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,  
 RA Dose C., Fuchs M., Fairman B., Graeberth K., Dauner D., Herzl A.,  
 RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,  
 RA Massenet O., Ouglet F., Clabaud G., Muendlein A., Felber R.,  
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,  
 RA Chedror F., Cooke R., Berger C., Montfort A., Casachubta E.,  
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,  
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,  
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Biele C.,  
 RA Frishman D., Haase D., Lemcke K., Meves H.-W., Stocker S.,  
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,  
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,



```

OS Bacillus thuringiensis.
CC Bacillia:Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN RP
  SEQUENCE FROM N.A.
  STRAIN=NRRL B-18246 / P663B:
  Schmeff H.E., Schwab G.E., Payne J.M., Narva K.E., Foncecrada L.;
  RA "Novel nematode-active toxins and genes which code therefor.";
  RL Patent number W09219739, 09-DEC-1992.
CC CC
  -1- FUNCTION: ENDOTOXIN WITH NEMATOCIDAL ACTIVITY.
  -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
  SERIATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
  OF THE SPORE COAT.
CC CC
  -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
  N-TERMINUS.
CC CC
  -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC CC
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  or send an email to license@isb.slb.ch).
CC CC
  EMBL: L07023; AAA22356.1; -.
  DR InterPro: IPR001178; Endotoxin.
  DR Pfam: PF00555; endotoxin; 1.
  KW Toxin; Sporulation.
  SQ SEQUENCE 803 AA; 88142 MW; 680E57C6A246A826 CRC64;

Query Match 8.8%; Score 77; DB 1; Length 803;
Best local Similarity 25.5%; Pred. No. 13;
Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;

OY 7 NDDGNSGC-----SCQGSYSVNNHNVAN-VYNNNGMSMWNLW-DYRTGFAYVTLFEKSKC 61
    || || || || || || || || || || || || || || || || || || || || || ||
DB 420 NDPGLSGDVOLPAPMSV-VNAQOTOTAYTDGENTIMWTDGHSWLCTLRGCTTCFCFGRC 478
OY 62 IVH-----KMKKEAMP--SLQALDALVKEKKLOGKGGGPPPSLRYSVNPN-VYNLKK 113
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 479 YNNSGSGESCNOSLPQKIHALPYQTVNLQSGGLGLASHIPYDLSPNNTIGDKDT 538
OY 114 FGSIVAMCKGIP-----YMERIOGANLISYS 142
    : ||| |||| : : : : : : : : : : : : : : : : : : : : : :
DB 539 DSTNIVA--KGIPYBKGYASGQVVEILREINANVQOLS 577

RESULF 9
XNNA_RUMFL STANDARD; PRT; 954 AA.
ID XNNA_RUMFL
AC P29126;
DC 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bifunctional endo-1,4-beta-xylanase xyla precursor (EC 3.2.1.8).
GN XNNA.
OS Ruminococcus flavefaciens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
OC Ruminococcus.
OX NCBI_TaxID=1265;
RN RX
  (1)
  RP SEQUENCE FROM N.A.
  RC STRAIN=17;
  RA MEDLINE=92261318; PubMed=1564021;
  RA Zhang J.-X., Flint H.J.;
  RT "A bifunctional xylanase encoded by the xyna gene of the rumen
  RT cellulolytic bacterium Ruminococcus flavefaciens 17 comprises two
  RT dissimilar domains linked by an asparagine/glutamine-rich sequence."
  RT Mol. Microbiol. 6:1013-1023(1992).
  RL -1- FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XYL0-OLIGOSACCHARIDES
  CC AND DOMAIN 2 MORE XYLOSE.
  CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

```

CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO CELLULOSE FAMILY  
 CC G (FAMILY 11 OF GLYCOSYL HYDROLASES).  
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION: BELONGS TO CELLULOSE FAMILY  
 CC F (FAMILY 10 OF GLYCOSYL HYDROLASES).  
 CC  
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 CC  
 CC EMBL: Z11127; CAAT7476.1;  
 CC PIR: S18043; S18043.  
 CC DR PIR: S20907; S20907.  
 CC DR HSP: P48793; 1XND.  
 CC DR InterPro: IPR001137; GH\_11.  
 CC DR Pfam: PF00333; Glyco\_hydro\_10.  
 CC DR Pfam: PF00457; Glyco\_hydro\_11.  
 CC DR PRINTS: PR00134; GLHYDRLASE10.  
 CC DR PRINTS: PR00591; GLYCOSYL\_HYDROL\_F10; 1.  
 CC DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11; 1.  
 CC DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F12; 1.  
 CC KW Xylan degradation; Hydrolase; Glycosidase; Multifunctional enzyme;  
 CC Repeat; Signal.  
 CC FT SIGNAL 1 27  
 CC FT CHAIN 1 27 OR 28, OR 29 (POTENTIAL).  
 CC FT DOMAIN 28 954 BIFUNCTIONAL\_ENO-1,4-BETA-XYLANASE XYLA.  
 CC FT DOMAIN 244 244 XYLANASE DOMAIN 1.  
 CC FT DOMAIN 245 622 ASN/GIN/TRP-RICH (LINKER).  
 CC FT DOMAIN 623 954 XYLANASE DOMAIN 2.  
 CC FT ACT\_SITE 122 122 NUCLEOPHILE (BY SIMILARITY).  
 CC FT ACT\_SITE 223 223 PROTON DONOR (BY SIMILARITY).  
 CC FT ACT\_SITE 774 774 PROTON DONOR (BY SIMILARITY).  
 CC FT ACT\_SITE 884 884 NUCLEOPHILE (BY SIMILARITY).  
 CC SEQUENCE 954 AA: 11362 MW: 10356756 Da B526ED C6C64;  
 CC  
 CC Query Match 8.6%; Score 77; DB 1; Length 954;  
 CC Best Local Similarity 39.1%; Pred. No. 17;  
 CC Matches 18; Conservative 6; Mismatches 18; Indels 4; Gaps 2;  
 CC  
 CC Oy 3 SISVNDGSGSGGQSVNNEHNAVYNNNGNSW---NALMD 45  
 CC Db 235 SVSVTGGSSDNGGQONNDNMNQON-NNOQNNNDNMNQONNDNM 279  
 CC  
 CC RESULT 10  
 CC TL29\_LYCES STANDARD: PRT: 345 AA.  
 CC AC 09THX6:  
 CC DT 16-OCT-2001 (Rel. 40, Created)  
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 CC DE Putative L-ascorbate peroxidase, chloroplast precursor (EC 1.11.1.11)  
 CC DE (Thylakoid lumenal 29 kDa protein) (TL29) (P29).  
 CC GN CLEB399.  
 CC OS Lycopersicon esculentum (Tomato).  
 CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC OC Asteridae; Magnoliophyta; eudicotyledons; core eudicots;  
 CC OC NCBI\_TaxID=4081;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A. AND SUBCELLULAR LOCATION.  
 CC RX MEDLINE=20487156; PubMed=11034343;  
 CC RA Kieselbach T., Bystedt M., Hynds P., Robinson C., Schroeder W.P.;  
 CC RT "A peroxidase homologue and novel plastocyanin located by proteomics  
 CC RT to the Arabidopsis chloroplast thylakoid lumen.";  
 CC FEBS Lett. 480:271-276(2000).  
 CC -1- FUNCTION: PLAYS A KEY ROLE IN HYDROGEN PEROXIDE REMOVAL IN

CC THE CHLOROPLASTS AND CYTOSOL OF HIGHER PLANTS.  
 CC -1- CATALYTIC ACTIVITY: L-ascorbate + H(2)O(2) = dehydroascorbate + 2  
 CC H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.  
 CC -1- SIMILARITY: TO ASCORBATE PEROXIDASES.  
 CC  
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 CC  
 CC EMBL: A1251882; CAB64343.1;  
 CC DR HSP: P48534; 1APX.  
 CC DR InterPro: IPR002016; Peroxidase.  
 CC DR Pfam: PF00141; Peroxidase; 1.  
 CC KW Oxidoreductase; Peroxidase; Hydrogen peroxide; Chloroplast;  
 CC Transmembrane; Thylakoid.  
 CC FT TRANSIT 1 2  
 CC FT CHAIN 79 345 THYLAKOID (BY SIMILARITY).  
 CC SEQUENCE 345 AA: 37749 MW: 6810485 Da B526ED C6C64;  
 CC  
 CC Query Match 8.6%; Score 76; DB 1; Length 345;  
 CC Best Local Similarity 28.6%; Pred. No. 5.9;  
 CC Matches 32; Conservative 16; Mismatches 42; Indels 22; Gaps 4;  
 CC  
 CC Oy 65 KMKREMPISQAL---DALYKREKLDGKPGPPKSLRYSNPRVDN-----LD 112  
 CC Db 103 KANPDILPELTLALNDATLTKATKGTGPN---SIRFSSEISRPENKGDALNLE 158  
 CC  
 CC Oy 113 KFGKSVAMKGIPTVMAEIEGAMISYSEKISANILITILISFGGIGNE 164  
 CC Db 159 ESKKVIDIDSKGP-----ISYADLIQFAQSNKSFISAIISKOGNVE 204  
 CC  
 CC RESULT 11  
 CC RL1\_YEAST STANDARD: PRT: 1597 AA.  
 CC AC P53552:  
 CC DT 01-OCT-1996 (Rel. 34, Created)  
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 CC DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE RL1 protein (THO2 protein)  
 CC GN RL1 OR THO2 OR YNL139C OR N1209 OR N1835.  
 CC OS Saccharomyces cerevisiae (Baker's yeast).  
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 CC OX NCBI\_TaxID=4932;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX STRAIN=YM256;  
 CC RA West R.W., Kruger B., Thomas S.;  
 CC RT Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RX STRAIN=5288C;  
 CC RA MEDLINE=96109932; PubMed=8619318;  
 CC RA Mallet L., Bussereau F., Jacquet M.;  
 CC RT "A 43.5 kb segment of yeast chromosome XIV, which contains MEA2,  
 CC RT MEK2, CAP5/RV2, NAM9, FKBP1/RBP1, MCM22 and CPT1, predicts an  
 CC RT adenoviral deaminase gene and 14 new open reading frames.";  
 CC RT Yeast 11:1195-1209(1995).  
 CC RN [3]  
 CC RP CHARACTERIZATION.  
 CC RX MEDLINE=98372750; PubMed=9707445;  
 CC RA Pirval J.I., Aguilera A.;  
 CC RT "A novel yeast gene, THO2, is involved in RNA pol II transcription and  
 CC RT provides new evidence for transcriptional elongation-associated  
 CC RT recombination.";  
 CC EMBO J. 17:4859-4872(1998).

CC -1- FUNCTION: PILOTROPIC REGULATORY PROTEIN INVOLVED IN POST-  
 CC TRANSCRIPTION INITIATION CONTROL. INVOLVED IN RNA POLYMERASE II  
 CC TRANSCRIPTION.  
 CC -1- SIMILARITY: TO S.POMBE SPAC22F3.14C.  
 CC  
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 CC  
 CC EMBL: U22361; AAA93160.1; -  
 CC EMBL: Z46843; CAA6686.1; -  
 CC EMBL: Z71416; CAA96023.1; -  
 CC SGD: S0005083; RLRI.  
 CC Transcription regulation.  
 CC  
 CC SEQUENCE 1597 AA; 183930 MW; 5F1993C3726F298 CRC64;  
 SQ  
 Query Match 8.6%; Score 76; DB 1; Length 1597;  
 Best Local Similarity 22.6%; Pred. No. 39;  
 Matches 43; Conservative 32; Mismatches 61; Indels 54; Gaps 10;  
 OY 28 VANVDNNGNSWNL--W-DY--RTGFAVTRL-----FEKKSCT 62  
 DB 554 VADIQNHGSESLHTIDKIDYRKIFPATSLONNPATSEVYELMKFPPEKRYPI 613  
 OY 63 VHKM-----KKEAMPSLOAL--DALVKEKKLGCKPGCPGPKSLRYS 102  
 DB 614 YNEWMKRLSODILPLKYSFNKAREKSLTKALSIDTAKESRPAKLSTNPLASLIVA 673  
 OY 103 VNPBRVNDLKFSGSIYAMCKGIPTVMAEIEOGANL--ISYSEKCIJAN--TLWLNI 156  
 DB 674 V--KQIENYKVSLEYVTTTKYFNDAVDLQFVLLRLTYNRPAAVDFGVQNMVQRL 731  
 OY 157 S-FCGIGAEIEN 165  
 DB 732 SIFAGLAKN 741  
 RESULT 12  
 CSP\_PLAFW STANDARD: PRT: 442 AA.  
 ID CSP\_PLAFW STANDARD: PRT: 442 AA.  
 AC P08307;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Circumsporozoite protein precursor (CS).  
 OS Plasmodium falciparum (isolate Welmcome).  
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 CC NCBI\_TaxID=5848;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87115616; PubMed=3543671;  
 RA Lockyer M.J., Schwartz R.T.;  
 RT "Strain variation in the circumsporozoite protein gene of Plasmodium  
 RT falciparum.";  
 RT Mol. Biochem. Parasitol. 22:101-108(1987).  
 CC -1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT  
 CC SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE  
 CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE  
 CC VERTEBRATE HOST). THE C-TERMINAL REGION IS PROBABLY USED FOR  
 CC MISCELLANEOUS. THE C-TERMINAL REGION IS PROBABLY USED FOR  
 CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES  
 CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.  
 CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.  
 CC  
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 CC  
 CC EMBL: M15505; AAA29554.1; -  
 CC PIR: A54529; A54529.  
 CC DR InterPro: IPR003067; Circumsporozoite.  
 CC DR InterPro: IPR000884; TSP1.  
 CC DR Pfam: PF00090; TSP1.1; TSP1.  
 CC DR PRINTS: PR01303; CIRCUMSPOROITE.  
 CC SMART: SM00209; TSP1; 1.  
 CC Malaria; Sporozoite; Repeat; Signal.  
 CC FT SIGNAL 1 16  
 CC FT CHAIN 17 442 CIRCUMSPOROZOITE PROTEIN.  
 CC FT DOMAIN 130 320 47 X 4 AA tandem repeats of N-A-N-P.  
 CC SEQUENCE 442 AA; 47402 MW; BD57A9A152B85E03 CRC64;  
 SQ  
 Query Match 8.5%; Score 75; DB 1; Length 442;  
 Best Local Similarity 28.2%; Pred. No. 10;  
 Matches 31; Conservative 13; Mismatches 34; Indels 32; Gaps 5;  
 OY 3 SISVNDGNSGSGGQSVSNNEHNVAVDNNNGNSWNLMDYRTGFAVTRLFEKKSCT 62  
 DB 71 SLGENDDD-----NDNGNNNNNGNNNGDNG-----REG-----KDEDKRDGN 108  
 OY 63 VHKMKEAMPSLOALDALVKEKKLGCKPGGPKSLRYSVNPBRVNDL 112  
 DB 109 NEDNKKLRP-----KHKKLKQPGDGNPDPA-NPNVDPAVNPVND 148  
 RESULT 13  
 KDOI\_ARATH STANDARD: PRT: 728 AA.  
 ID KDOI\_ARATH STANDARD: PRT: 728 AA.  
 AC Q39017; Q9SD92;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Diacylglycerol kinase 1 (EC 2.7.1.107) (Diglyceride kinase 1)  
 DE (DGK 1) (DAG kinase 1).  
 GN DGK1 OR AT5G07920 OR F13G24.120 OR MXM12.16.  
 OS Arabidopsis thaliana (mouse-ear cress).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC euroids II; Brassicales; Brassicaceae; Arabidopsia.  
 CC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=96189276; PubMed=8605313;  
 RA Katagiri T., Mizoguchi T., Shinozaki K.;  
 RT "Molecular cloning of a cDNA encoding diacylglycerol kinase (DGK) in  
 RT Arabidopsis thaliana.";  
 RT Plant Mol. Biol. 30:647-653(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016721; PubMed=11130714;  
 RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,  
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,  
 RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,  
 RA Nakazaki M., Nartuo K., Okumura S., Shino S., Takeuchi G., Wada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,  
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,  
 RA Haberman K., Murray J., Johnson D., Rohlfing T., Nelson J.,  
 RA Stoneking T., Peplin K., Spielh J., Courtney L., Courtney M., Dante M.,  
 RA Belter E., Cordum H., Cordes M., Muraki A., Lamat E., Latreille P.,  
 RA Du H., Edwards J., Fryman J., Haakensen B., Jambor E., Latreille P.,  
 RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strommatt C.,  
 RA Wanner-McPherson C., Wollem A., Yeakum M., Bell M., Dedina N.,  
 RA Kirschner L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,  
 RA Kitzhoff K., Toth K., King L., Bahret A., Miller B., Marra M.,  
 RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,  
 RA Volckert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,  
 RA Enliar K.-D., Terry N., Hartley N., Bent E., Johnson S.,

Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,  
 Ramsberger U., Wedler H., Balke K., Wedler E., Peters S.,  
 van Staveren M., Dirks W., Moolman P., Klein Lankhorst R.,  
 RA Weitsengger T., Both G., Rose G., Hauf J., Berneiser S., Hempel S.,  
 RA Feldpausch M., Lamberth S., Villarroel R., Gelen J., Ardiles W.,  
 RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,  
 RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.,  
 RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis  
 thaliana.";  
 RL Nature 408:823-826(2000).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. Columbia;  
 RX MEDLINE=97471969; PubMed=9330910;  
 RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,  
 RA Miyajima N., Tabata S.,  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence  
 features of the 1.6 Mb regions covered by twenty physically assigned  
 pl clones.";  
 RL DNA Res. 4:215-230(1997).  
 CC -1- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-  
 diacylglycerol 3-phosphate.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: DETECTED IN ROOTS, SHOOTS, AND LEAVES.  
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE  
 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG  
 BINDING DOMAINS.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: D63787; BAA09856.1; -  
 DR EMBL: AL133421; CAB62604.1; -  
 DR EMBL: AB005249; BAB09956.1; -  
 DR InterPro: IPR000756; DAGKA.  
 DR InterPro: IPR001206; DAGKC.  
 DR InterPro: IPR002219; DAG-PE-bind.  
 DR InterPro: IPR003622; DAG\_Kin\_cat.  
 DR Pfam: PF00609; DAGKA; 1.  
 DR Pfam: PF00781; DAGKC; 1.  
 DR ProDom: PD002939; DAGKA; 1.  
 DR ProDom: PD005043; DAG\_Kin\_cat; 1.  
 DR SMART: SM00109; C1; 2.  
 DR SMART: SM00045; DAGKA; 1.  
 DR SMART: SM00046; DAGKC; 1.  
 DR PROSITE: PS00479; DAG-PE\_BIND\_DOM\_1; FALSE\_NEG.  
 DR PROSITE: PS00081; DAG-PE\_BIND\_DOM\_2; 2.  
 KW Transferase; Kinase; Phorbol-ester binding; Transmembrane; Repeat.  
 FT TRANSMEM 27 48  
 FT DOMAIN 95 137 PHORBOL-ESTER AND DAG BINDING 1.  
 FT DOMAIN 169 212 PHORBOL-ESTER AND DAG BINDING 2.  
 FT DOMAIN 359 480 CATALYTIC (POTENTIAL).  
 FT DOMAIN 507 664 CATALYTIC (POTENTIAL).  
 FT CONFLICT 509 509 N -> T (IN REF. 1).  
 SQ SEQUENCE 728 AA; 79983 MW; 9E3190721C083DE9 CRC64;

Query Match 8 5%; Score 74.5; DB 1; Length 728;  
 Best Local Similarity 25.7%; Pred. No. 21;  
 Matches 43; Conservative 22; Mismatches 67; Indels 35; Gaps 8;

OY 8 DDGSGSGSGQGVY-----SVNNEH-----NVAVDNNNGMSMAIMDYRGFAV 52  
 Db 273 DGGSGSGSGNDESTESTADGTPVNGAHVLENSISVWNGSDSSGDSNGKLEKPSVR 332  
 OY 53 TRLEFKKS--CLVHKMKKA--MPSLDALDLVKEKKLOGKGGPPPKSLRYSVNPBV 108  
 Db 333 TGSFOKEYHNRSLKRYELADLP--DARPLLVFNKSSGAGRGDSLRLHLHLNPVY 391

OY 109 DMLDKF-GKSI-----VAMCKGIPY--YMAEIOGANLIS 140  
 Db 392 FELSSVGGPEVGLFLPKRVHFRVAVCGGDTAGTADALEKONFIS 438

RESULT 14  
 MIMC\_MYCTU  
 ID MIMC\_MYCTU STANDARD; PRT; 1146 AA.  
 AC Q50585;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative membrane protein mmp12.  
 GN Mmp12 OR RV1522C OR MT1573 OR MTCY1965.06.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteriales (class); Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares R., Sultston J.E., Taylor K.,  
 RA Whitehead S., Whittam J., Whitehead S., Barrett B.G.,  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmolava M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weisman J., Kouri H., Gill J., Mikula A.,  
 RA Bishai W.,  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE MMP12 FAMILY.  
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DR EMBL: Z77826; CAB01394.1; -  
 DR EMBL: AE007024; AAK45840.1; -  
 DR TIGR: MT1573; -  
 DR TubercuList; RV1522C; -  
 DR InterPro: IPR004707; Act1.  
 DR InterPro: IPR000731; HMGCR/patch\_57M.  
 DR InterPro: IPR004869; MMP1.  
 DR Pfam: PF03176; MMP1; 2.  
 DR PROSITE: PS50156; SSD; 1.  
 DR TIGRfams: TIGR00833; act1; 1.  
 KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 25 45  
 FT TRANSMEM 206 226  
 FT TRANSMEM 254 274  
 FT TRANSMEM 350 350  
 FT TRANSMEM 382 402  
 FT TRANSMEM 826 846  
 FT TRANSMEM POTENTIAL.  
 FT TRANSMEM POTENTIAL.  
 FT TRANSMEM POTENTIAL.  
 FT TRANSMEM POTENTIAL.  
 FT TRANSMEM POTENTIAL.  
 FT TRANSMEM POTENTIAL.

FT TRANSMEM 850 870 POTENTIAL.  
 FT TRANSMEM 883 903 POTENTIAL.  
 FT TRANSMEM 928 948 POTENTIAL.  
 FT TRANSMEM 949 969 POTENTIAL.  
 SQ SEQUENCE 1146 AA: 122429 MW: AC03075641C5CB09 CRC64;  
 Query Match 8.4%: Score 74; DB 1; Length 1146;  
 Best Local Similarity 20.8%: Pred. No. 40;  
 Matches 41: Conservative 26; Mismatches 66; Indels 64; Gaps 6;  
 9 DGNNGSGGCOOS--VSVNEHNVANVNDNNNGNSMNALMDYRTGFAVTRLPFKKSCIVAK 65  
 514 DQLTGGAHQDLALAQITNEINGAVASSGIVNTLQAMMDLMGDKTITPLENASOYGR 573  
 66 MK-----KEAMPSLQAL-----DALV 81  
 574 MRALGDNLSGTVTDAEQIATWASPVNVALNSSPVCNSDPACRTSRALAIYQAOQDGLL 633  
 82 KKK-----LQKRGPGGPPPSLRKSVNPNRYDNLDFGKKSIVAMCK---GIPTWAEEL 133  
 634 RSTRALAVTQ-----QTOEYQTLARTVSTLDGQIKQVSTLKAVDGHPTKLAQMQ 684  
 134 QGANLISYSEKICISANI 150  
 685 QGANALADGSAALAGV 701

RESULT 15  
 TP2M\_DICDI STANDARD; PRT: 1282 AA.  
 ID TP2M\_DICDI  
 AC P90520:  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE DNA topoisomerase II, mitochondrial precursor (EC 5.99.1.3).  
 GN TOPB OR TOPA.  
 OS Dictyostelium discoideum (Slime mold).  
 OX Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
 NX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX3;  
 RX MEDLINE=97320633; PubMed=9177484;  
 RA Komori K., Kuroe K., Yanagisawa K., Tanaka Y.;  
 RT Cloning and characterization of the gene encoding a mitochondrially  
 RT localized DNA topoisomerase II in Dictyostelium discoideum. Western  
 RT blot analysis.\*;  
 RL Biochim. Biophys. Acta 1352:63-72(1997).  
 CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT  
 CC BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II  
 CC MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining  
 CC of double-stranded DNA.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- DEVELOPMENTAL STAGE: PRESENT IN GROWTH PHASE AND DURING  
 CC DEVELOPMENT, ALTHOUGH LEVELS DECLINED AS DEVELOPMENT PROCEEDED.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: D82024: BAA11510.1: -;  
 DR HSSP: P06786; IBGM.  
 DR DICTYDB: DD05117; TOPB.  
 DR INTERPRO: IPR003594; ATPbind\_ATPase.  
 DR INTERPRO: IPR001241; DNA\_topoisomII.  
 DR INTERPRO: IPR002205; DNA\_topoisomIV.

DR Pfam: PF00204; DNA\_gyraseB; 1.  
 DR Pfam: PF00521; DNA\_topoisomIV; 1.  
 DR Pfam: PF02518; HATPase\_C; 1.  
 DR PRINTS: PR00418; TP12FAMILY.  
 DR PRODOM: PD000616; DNA\_topoisomII; 1.  
 DR ProDom: PD000742; DNA\_topoisomIV; 1.  
 DR SMART: SM00387; HATPase\_C; 1.  
 DR SMART: SM00433; TOP2C; 1.  
 DR SMART: SM00434; TOP4C; 1.  
 DR PROSITE: PS00177; TOPOISOMERASE\_II; 1.  
 KW Isomerase; Topoisomerase; DNA-binding; ATP-binding;  
 KW Mitochondrion; Transil peptide.  
 FT TRANSIT 1 35  
 FT CHAIN 36 1282 MITOCHONDRION (POTENTIAL).  
 FT NP\_BIND 253 258 ATP (POTENTIAL).  
 FT ACT\_SITE 899 899 DNA\_CLEAVAGE (BY SIMILARITY).  
 FT DOMAIN 147 154 POLY-THR.  
 FT DOMAIN 1252 1256 POLY-SER.  
 FT DOMAIN 1260 1265 POLY-SER.  
 SQ SEQUENCE 1282 AA: 145866 MW: 7E21DEBF3D069951 CRC64;

Query Match 8.4%: Score 74; DB 1; Length 1282;  
 Best Local Similarity 21.7%: Pred. No. 46;  
 Matches 31: Conservative 25; Mismatches 39; Indels 48; Gaps 6;

QY 17 QQSVSVNNEHNVANVNDNNNGNSMNALMDYRTGFAVTRLPFKKSCIVAKMKKAMPST-- 74  
 DB 130 KKTIELNDNNNEKVES-----TTTTTTKTNKKPLIYIPKATYIPGLK 175  
 QY 75 -----QALDALYKKEKLLQCKGPGGPPPSLRKSVNPNRYDNLDFGKKSIVAMCKGIPT 127  
 DB 176 IYDEILVNADNNKRRDSKM-----SFIKVEINFN-----ENSISIMNDKGIPV 219  
 QY 128 -----VYAEETOGANLISYS 142  
 DB 220 VMHQTENCYVEEYMG-NLMSG 241

Search completed: April 11, 2003, 16:12:02  
 Job time : 12.8567 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:53 ; Search time 17.7651 Seconds

(without alignments)  
892.885 Million cell updates/sec

Title: US-09-821-726A-18\_COPY\_21\_185

Perfect score: 880

Sequence: 1 DYSISVNDGSGSGGQOSV.....ISANILWILINISFCGIAEN 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94.5	10.7	719	2 T30577	ARPI protein - yea
2	83.5	9.5	186	2 S71629	hypothetical prote
3	83	9.4	296	2 S38907	probable phosphati
4	82.5	9.4	409	2 T35118	pyruvate dehydroge
5	82.5	9.4	887	2 E81094	hypothetical prote
6	81	9.2	810	2 S69652	hypothetical prote
7	81	9.2	1338	2 T18287	protein-tyrosine k
8	80.5	9.1	263	2 T02227	NBS-LRR type resis
9	80.5	9.1	642	2 G68087	protein B0454.8 [1
10	80	9.1	568	2 JC7210	molluscan shell ma
11	79.5	9.0	227	2 T07755	disease resistance
12	78.5	8.9	887	2 E81847	pyruvate dehydroge
13	78	8.9	192	2 T02628	hypothetical prote
14	78	8.9	349	2 A85091	hypothetical prote
15	77	8.8	808	2 B97303	hypothetical prote
16	77	8.8	954	1 S20907	endo-1,4-beta-xyla
17	77	8.8	1245	1 D71613	GAF domain protein
18	76.5	8.7	764	2 H71607	hypothetical prote
19	76	8.6	1597	2 S51144	Ribi protein - yea
20	75.5	8.6	443	2 B99552	conserved hypothet
21	75	8.5	421	2 A43627	maltoase-binding pe
22	75	8.5	442	2 A54529	citruamporozolite p
23	74.5	8.5	728	2 S71467	diacylglycerol kin
24	74.5	8.5	1240	2 T06404	resistance complex
25	74.5	8.5	2010	2 B71616	phosphatase (acid
26	74	8.4	244	2 A86873	transcription regu
27	74	8.4	883	2 T49781	related to mutanas
28	74	8.4	1146	2 B70723	probable mmp12 pr
29	74	8.4	1168	2 T15890	hypothetical prote

30	74	8.4	1282	2 T30577	DNA topoisomerase
31	74	8.4	2150	2 S71629	sensory transducti
32	73.5	8.4	219	2 B41886	flagellar membrane
33	73.5	8.4	1195	2 S38174	probable purine nu
34	73	8.3	414	2 S43253	alanine-glyoxylate
35	73	8.3	472	2 T24316	hypothetical prote
36	73	8.3	535	1 A44475	N-acetylglactosam
37	73	8.3	817	2 A47716	dolichyl-phosphate
38	73	8.3	1006	2 A59384	oxylactinase/insuli
39	73	8.3	1025	2 A59383	oxylactinase/insuli
40	72.5	8.2	286	2 F90006	hypothetical prote
41	72.5	8.2	375	1 G64436	N-acetyl-gamma-glu
42	72.5	8.2	476	2 B41792	homeotic protein 1
43	72.5	8.2	653	2 T02080	probable carbonate
44	72.5	8.2	753	2 D83081	probable outer mem
45	72.5	8.2	1341	2 S50366	probable membrane

## ALIGNMENTS

```
RESULT 1
S61046
ARPI protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D1478; protein YDL167c
C:Species: Saccharomyces cerevisiae
C:Date: 15-Feb-1996 #sequence, revision 01-Mar-1996 #text-change 29-Oct-1999
C:Accession: S61046; S31139; S67719
R:Pohl, T.M.
Submitted to the EMBL Data Library, November 1995
A:Reference number: S61010
A:Accession: S61046
A:Molecule type: DNA
A:Residues: 1-719 <POH>
A:Cross-references: EMBL:267750; NID:g1061256; PIDN:CAA91579.1; PID:g1061272
R:Wehner, E.P.; Rao, E.; Brendel, M.
Mol. Gen. Genet. 237, 351-358, 1993
A:Title: Molecular structure and genetic regulation of SFA, a gene responsible for re
A:Reference number: S31138; MID:93247548; PMID:8483449
A:Accession: S31139
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-492; N:494-719 <MEH>
A:Cross-references: EMBL:X68020; NID:g577609; PIDN:CAA48159.1; PID:g288590
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pohl, T.M.
Submitted to the Protein Sequence Database, July 1996
A:Reference number: S67708
A:Accession: S67719
A:Molecule type: DNA
A:Residues: 1-719 <POH>
A:Cross-references: EMBL:274215; NID:g1431265; PIDN:CAA98741.1; PID:e253076; PID:g143
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:NRP1; ARPI
A:Cross-references: MIPS:YDL167c; SGD:S0002326
A:Map position: 4L

Query Match      10.7%; Score 94.5; DB 2; Length 719;
Best local Similarity 24.8%; Pred. No. 0.34;
Matches 39; Conservative 18; Mismatches 63; Indels 37; Gaps 5;

QY 2 YSISVNDGSGSGGQOSVSNNEHN-----VAAYDNNNGNNSWALW 44
DB 508 YNINNNINGNGNGNNGNNSNNNNNNHHNHSINSNSNTNNNNNNNGNNSNCNS 567
QY 45 DYRTGFAVTRL-----FEKKSCIVHKMKKEAM-----PSLOALDLVKEKKLOGK--G 90
DB 568 NIGMGCGSNMPPRRADMKSTCTYHFAKNVYCLRGCGKKSISGDASEFNHYIDSSTFG 627
QY 91 PGGPPEKSLRYSVNP-----RVNDLDFKGSIVAM 121
DB 628 PASRTPSNNNISVNTNGSGNAGRTDGNKGRDISLM 664
```

## RESULT 2

T30918

hypothetical protein D1007.14 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999

C:Accession: T30918

R:Davidson, S.; Rohlfing, T.

Submitted to the EMBL Data Library, August 1999

A:Description: The sequence of *C. elegans* cosmid D1007.

A:Reference number: Z20934

A:Accession: T30918

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-186 &lt;DAV&gt;

A:Cross-references: EMBL:AF003151; PIDN:AMB54231.1

A:Experimental source: strain Bristol N2; clone D1007

C:Genetics:

A:Map position: 1

A:Introns: 15/2; 68/2; 87/2

A:Note: D1007.14

A:Note: D1007.14

Query Match 9.5%; Score 83.5; DB 2; Length 186; Best Local Similarity 39.5%; Pred. No. 0.75; Matches 17; Conservative 8; Mismatches 15; Indels 3; Gaps 1;

7 NDDGNSGGSGGQSVSVNNEHNVANVDNNNGW---NSMNLMDY 46

34 NNGAGSGSGWGNANNNNNNNNGGNNNGWGNNDWSSNYN 76

## RESULT 3

S38907

probable phosphatidylserine decarboxylase (EC 4.1.1.65) precursor - *Clostridium pasteurianum*C:Species: *Clostridium pasteurianum*

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 28-Jul-2000

C:Accession: S38907

R:Meyer, J.

Submitted to the EMBL Data Library, November 1993

A:Description: Sequence of 6764 bp EcoRI-Sau3A fragment of *Clostridium pasteurianum* gene

ly M62754).

A:Reference number: S38903

A:Accession: S38907

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-296 &lt;MEY&gt;

A:Cross-references: EMBL:Z28353; NID:9431946; PIDN:CAAB2212.1; PID:9431951

C:Superfamily: Escherichia coli phosphatidylserine decarboxylase

C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 9.4%; Score 83; DB 2; Length 296; Best Local Similarity 27.3%; Pred. No. 1.5; Matches 36; Conservative 18; Mismatches 46; Indels 3; Gaps 6;

20 VSVNNEHNVANVDNNNGSNMNLMDYRTGFAVTRLFEEKSCIVHKMKKEAMPSLOALDA 79

116 IIVVNNIMNMNIIQYKLT--YKLNLDLQNDISIKTEKGTICIAIACPTDHRFHLN 173

80 LVREKKLQKGPGRPPKSLKYSVP---NRVDNL-----DKFGK---STV 119

174 GICSTIKIKGN-----YYSVPDIALINKINLFCQKREMSIFNSDNFGKILYEIG 225

120 AMCKG--IPTYM 129

226 ATCVGSIIQTYM 237

## RESULT 4

T35118

probable secreted protein - *Streptomyces coelicolor*C:Species: *Streptomyces coelicolor*

C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 08-Sep-2000

C:Accession: T35118

R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

Submitted to the EMBL Data Library, March 1998

A:Reference number: Z21568

A:Accession: T35118

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-409 &lt;SEE&gt;

A:Cross-references: EMBL:AL022268; PIDN:CAI18335.1; GSPDB:GN00070; SCOPDB:SC4H2.19C

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOPDB:SC4H2.19C

C:Superfamily: Streptomyces coelicolor probable secreted protein SC4H2.19C

Query Match 9.4%; Score 82.5; DB 2; Length 409; Best Local Similarity 21.1%; Pred. No. 2.6; Matches 39; Conservative 21; Mismatches 74; Indels 51; Gaps 7;

3 SISVNDGNSGGSGGQSVSVNNEHNVANVDN--NNGNNSWN-----AL 43

54 SASAADGNGGIRIPDDIKDKLKEHGIDVDDMKGNAMKMDLREADPVPNLEGL 113

44 WDYRTGFAVTRLFEEKSCIVHKMKKEAMPSLOALDALYKCKLQK-KPGGPPKSLKYS 102

114 WD-----PDRMRDAEPPDOEVDENDISGQGVTPDEPAPVNAE 151

103 VNPBRV-DNLDPFGKSIYAMCKGIPTYMAEEIOG-----ANLISYSEKISANIL--WI 153

152 AVPAKYHDNMAATAGKLLFPDPSKSNVCSATYVKKDPAHFGKSNMVTAGCHVAGKSGCY 211

154 LNISF 158

212 RNIAF 216

## RESULT 5

E81094

pyruvate dehydrogenase, E1 component NMB1341 [imported] - *Neisseria meningitidis* (strC:Species: *Neisseria meningitidis*

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

C:Accession: E81094

R:Teitelin, H.; Saunders, N.J.; Haldenberger, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizzato, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.

A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: E81094

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-887 &lt;TEF&gt;

A:Cross-references: GB:AE002482; GB:AE002098; NID:97226577; PIDN:AAI1716.1; PID:97222

A:Experimental source: serogroup B, strain MC58

C:Genetics:

C:Superfamily: pyruvate dehydrogenase (lipoamide); thiamin pyrophosphate-binding doma

Query Match 9.4%; Score 82.5; DB 2; Length 887; Best Local Similarity 24.1%; Pred. No. 7.2; Matches 41; Conservative 24; Mismatches 60; Indels 45; Gaps 9;

9 DGNSGGSGGQSVSVNNEHNVANVDNNNGN---SMNLMDYRTGFAVTRLFEEK-KSCIV 63

264 DGPYRGNGK--IIQLEEGNFGA---GMNVYKVIWGRWD-----RLAKRKDGIL 309

64 HKMKKEAM-----PSLOALDALYKCKLQK-KPGGPPKSLKYS 101

310 RQRMEECLDGDGYQYKSKDAVYREHFNPELAKALVADMDDEQALNLRGCHDPQKY-Y 368

102 SVNPNRVNDLDPFGKSIYAMCKGIPTY-MAEIOGANLISSEKISANI 150

369 NAYDRAANHAD--GKPTVIAKTIKYGCMGASGCGONVAAHQAQKWDKASL 416





RESULT 10  
JC7210  
molluscan shell matrix protein N66 - Pinctada maxima  
C:Species: Pinctada maxima  
C:Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jun-2000  
C:Accession: JC7210  
R:Kono, M.; Hayashi, N.; Samata, T.  
Biochem. Biophys. Res. Commun. 269, 213-218, 2000  
A:Title: Molecular mechanism of the nacreous layer formation in Pinctada maxima.  
A:Reference number: JC7210; MUID:20160475; PMID:10694502  
A:Accession: JC7210  
A:Molecule type: mRNA  
A:Residues: 1-568 <CON>  
A:Cross-references: DBJ:AB032612  
C:Comment: This protein is rich in asparagine and glycine residues, it serves as a protein  
ayers. It is also important in calcification.  
C:Keywords: matrix protein

Query Match 9.1%; Score 80; DB 2; Length 568;  
Best Local Similarity 26.8%; Pred. No. 7.2;  
Matches 30; Conservative 18; Mismatches 38; Indels 26; Gaps 6;  
OY 9 DGNSSGSGQGSVSNNEHNVAVDNNNGNSMNA-----LMDYRTGFAVTRLEKK-- 59  
DB 392 NGNNGNG-----NGNNGNDGNGDNGYNGDNGSDGRLRWDLAN--VRRHAEHYH 442  
OY 60 ---SCIVHKMKKAMPSSQALDALYKERRKLOGKGGPPPKSLRYSNPRV 108  
DB 443 FSGGCIYKAKKLS-----RLCEAYRHKKVREFKRG-EEKGLDVIDTPMV 489

RESULT 11  
T07755  
disease resistance protein homolog 11 - potato (fragment)  
C:Species: Solanum tuberosum (potato)  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 03-Nov-2000  
C:Accession: T07755  
R:Leister, D.; Ballvora, A.; Salamini, F.; Gebhardt, C.  
Nature Genet. 14, 421-429, 1996  
A:Title: A PCR based approach for isolating pathogen resistance genes from potato with F  
A:Reference number: Z16117; MUID:97099453; PMID:8944022  
A:Accession: T07755  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-227 <LEI>  
A:Cross-references: EMBL:U60069; NID:g1708709; PIDD:AA049588.1; PID:g1708710  
A:Experimental source: diploid F1 hybrid of H79.1506/1 and H80.696/4 heterozygous for th  
C:Genetics:  
A:Map position: 11  
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 9.0%; Score 79.5; DB 2; Length 227;  
Best Local Similarity 28.1%; Pred. No. 2.4;  
Matches 41; Conservative 16; Mismatches 46; Indels 43; Gaps 8;  
OY 26 HNVAVDNNNGNSMNAALMDYRTGFAVTRLEFKKSCIVHKMKKEAMP----- 72  
DB 70 HDVNV-DNYNQM-----YDLRNVF-VQGGFGSK--IIVTTKRESVALMGNDQISMDNL 119  
OY 73 SLQALDALYKERRKLOGKGGPPPKSLRYSNPRVNDLDFKSGIVAMCKGIPTTYMAEE 132  
DB 120 STEASMSLFKRHAFENMPDMPGHP-----ELEEVGKQIAACKGKLP--LALK 163  
OY 133 ICGANLISYSE---KCSANLILWL 154  
DB 164 TLAGMLRKSSEVEEMKRILRSEIMEL 189

RESULT 12  
E81847  
pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) E1 component NMA1554 [imported] - Neisseria

C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: E81847  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo  
; Holroyd, S.; Jorgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rejz  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: E81847  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-887 <PAR>  
A:Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDD:CA894781.1; PID:g738  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: aceD; NMA1554  
C:Superfamily: pyruvate dehydrogenase (lipoamide); thiamin pyrophosphate-binding doma  
C:Keywords: oxidoreductase

Query Match 8.9%; Score 78.5; DB 2; Length 887;  
Best Local Similarity 23.5%; Pred. No. 18;  
Matches 40; Conservative 24; Mismatches 61; Indels 45; Gaps 9;  
OY 9 DGNSSGSGQGSVSNNEHNVAVDNNNGNSMNA-----LMDYRTGFAVTRLEKK--KSCIV 63  
DB 264 DGPYKGNCK--IIDLKGNFAGA-----GNNVYKVTWGRWD-----RLAKDKDGL 309  
OY 64 HKMKKEAM-----PSQALDALYKERRKLOGKGGPPPKSLRY 101  
DB 310 RQMEBCLDGDTQYKYKSDGAVYREHFNTPKLTLLVADMTQEQALNALNRGGHDPOK-V 368  
OY 102 SVNPNRVNDLDFKSGIVAMCKGIPTTY--MAEIQGANLISYSEKCSANI 150  
DB 369 NAYDRAANHAD--GKPTVILAKTIKYGCGASGEQNAHQKKMDKASL 416

RESULT 13  
T02628  
hypothetical protein Atg262950 [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein T19L18.24  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 16-Feb-2001  
C:Accession: T02628; G84654  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke  
submitted to the EMBL data library, August 1998  
A:Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.  
A:Reference number: Z14681  
A:Accession: T02628  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-192 <ROU>  
A:Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413717  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon  
euss, D.; Nleman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617157  
A:Accession: G84654  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-192 <STO>  
A:Cross-references: GB:AE002093; NID:g3413717; PIDD:AA031240.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: T19L18.24; Atg262950  
A:Map position: 2  
A:Introns: 28/3; 55/3; 72/2; 98/2; 117/3

Query Match 8.9%; Score 78; DB 2; Length 192;  
Best Local Similarity 24.7%; Pred. No. 2.8;  
Matches 39; Conservative 29; Mismatches 64; Indels 26; Gaps 7;

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Oy  49  GFAVTRLEEK--KSCIYHKMKKEMPS-----LQALDALYKEKKILOGKPGGCPPEKSLR  100
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  379  GLRIEALTEIKLVKKAVIDSIDSLMDNPATLVNGDTASINAVIK-----PDNATNNGLT  430
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy  101  KSVAPNRVDNDLDRGKSLVAMCRGIPPYMAEIOGA-----NLISYSKCI  146
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  431  WTSSDNKLIISVDNSGK-ITGINKGIATITAAISNDGSKKACCTITVNDPNPNNIIVTFKDSNL  489
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy  147  SANILILILN  155
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  490  EAEVRKCIIN  498
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

QY 9 DGSNGSGGQSY-----SVNENHVANVDNNNGWNSW-----NALMDYRT 48  
|| : : : || : : : || : : :  
Db 324 DGSEAGTDCGLRVEAIRIKLVNMPGVSIETYSHVQN-----GWQNVWSDDGEAGTDGR- 378



Mon Apr 14 14:02:08 2003

us-09-821-726a-18\_copy\_21\_185.rapb

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: April 11, 2003, 16:11:18 ; Search time 16.4192 Seconds  
(without alignments)  
614.367 Million cell updates/sec

Title: US-09-821-726a-18\_COPY\_21\_185  
Perfect score: 880  
Sequence: 1 DYSISVNDGNGSGGQOSV.....ISANILMLNISFGGIAEN 165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEM\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppaa/PC1\_NEM\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEM\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppaa/US07\_NEM\_PUB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppaa/US10\_NEM\_PUB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppaa/US06\_NEM\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	687	78.1	185	US-09-992-598-211	Sequence 211, App
2	687	78.1	185	US-09-989-293A-211	Sequence 211, App
3	687	78.1	185	US-09-989-735-211	Sequence 211, App
4	687	78.1	185	US-09-990-444-211	Sequence 211, App
5	687	78.1	185	US-10-001-054-14	Sequence 14, App
6	687	78.1	185	US-09-989-730-211	Sequence 211, App
7	687	78.1	185	US-09-990-436-211	Sequence 211, App
8	687	78.1	185	US-09-991-181-211	Sequence 211, App
9	687	78.1	185	US-09-993-687-211	Sequence 211, App
10	687	78.1	185	US-09-989-734-211	Sequence 211, App
11	687	78.1	185	US-09-993-653-211	Sequence 211, App
12	687	78.1	185	US-09-990-438-211	Sequence 211, App
13	687	78.1	185	US-09-990-562-211	Sequence 211, App
14	687	78.1	185	US-09-997-428-211	Sequence 211, App
15	687	78.1	185	US-09-997-666-211	Sequence 211, App
16	687	78.1	185	US-10-227-884-148	Sequence 148, App
17	687	78.1	185	US-09-990-711-211	Sequence 211, App
18	687	78.1	185	US-10-230-163-148	Sequence 148, App
19	687	78.1	185	US-10-230-163-148	Sequence 148, App

20	687	78.1	185	US-09-989-726-211	Sequence 211, App
21	687	78.1	185	US-09-746-783-146	Sequence 146, App
22	687	78.1	185	US-09-990-437-211	Sequence 211, App
23	687	78.1	185	US-09-998-156-211	Sequence 211, App
24	687	78.1	185	US-10-218-631-148	Sequence 148, App
25	687	78.1	185	US-10-230-338-148	Sequence 148, App
26	687	78.1	185	US-09-991-157-211	Sequence 211, App
27	687	78.1	185	US-09-991-172-211	Sequence 211, App
28	687	78.1	185	US-09-997-514-211	Sequence 211, App
29	687	78.1	185	US-09-997-573-211	Sequence 211, App
30	687	78.1	185	US-10-050-704-105	Sequence 105, App
31	687	78.1	185	US-10-230-414-148	Sequence 148, App
32	687	78.1	185	US-09-990-443-211	Sequence 211, App
33	687	78.1	185	US-09-990-726-211	Sequence 211, App
34	687	78.1	185	US-09-997-559-211	Sequence 211, App
35	687	78.1	185	US-09-997-601-211	Sequence 211, App
36	687	78.1	185	US-09-989-729A-211	Sequence 211, App
37	687	78.1	185	US-09-990-440-211	Sequence 211, App
38	687	78.1	185	US-09-991-854-211	Sequence 211, App
39	687	78.1	185	US-09-997-349-211	Sequence 211, App
40	687	78.1	185	US-09-997-440-211	Sequence 211, App
41	687	78.1	185	US-09-997-628-211	Sequence 211, App
42	687	78.1	185	US-09-997-683-211	Sequence 211, App
43	687	78.1	185	US-09-989-722-211	Sequence 211, App
44	687	78.1	185	US-09-989-723-211	Sequence 211, App
45	687	78.1	185	US-09-989-729-211	Sequence 211, App

ALIGNMENTS

RESULT 1  
US-09-992-598-211  
Sequence 211, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paonli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
CURRENT APPLICATION NUMBER: US/09/992,598  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13





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1 PRIOR FILING DATE: 1998-07-02
2 PRIOR APPLICATION NUMBER: 60/091544
3 PRIOR FILING DATE: 1998-07-01
4 PRIOR APPLICATION NUMBER: 60/091519
5 PRIOR FILING DATE: 1998-07-02
6 PRIOR APPLICATION NUMBER: 60/091626
7 PRIOR FILING DATE: 1998-07-02
8 PRIOR APPLICATION NUMBER: 60/091633
9 PRIOR FILING DATE: 1998-07-02
10 PRIOR APPLICATION NUMBER: 60/091978
11 PRIOR FILING DATE: 1998-07-07
12 PRIOR APPLICATION NUMBER: 60/091982
13 PRIOR FILING DATE: 1998-07-07
14 PRIOR APPLICATION NUMBER: 60/092182
15 PRIOR FILING DATE: 1998-07-09

Query Match 78.1%; Score 687; DB 9; Length 185;
Best Local Similarity 73.3%; Pred. No. 3,6e-65;
Matches 121; Conservatival 22; Mismatches 22; Indels 0; Gaps

QY 1 DVSIVNDGNSGGGSGOOSVSVNNEHNVANVDNNNGNSWNAIMDYGFAVTRLEFKS 60
DB 21 NNVINVDNNNAGSGOOSVSVNNEHNVANVDNNNGMSWMSIMWYGNFAATRFQKRT 80
QY 61 CIVHMKKKEPSTLQALDALYKEKKLQKGGPGGPPKSLRYSVNPNRYDNDLKEFSKIVA 120
DB 81 CIVHMKKEVMPSTQSLDALYKEKKLQKGGPGGPPKSLRYSVNPNRYDNDLKEFSKIVA 140
QY 121 MCKGIPYMAEFIOGANLISYSEKCSANIIMILNISFCGIAEN 165
DB 141 MCKGIPYMAEKEASLFEYSGTCYTTSLMIVDISFCGDTVEN 185

RESULT 3
US-09-989-735-211
Sequence 211, Application US/09989735
Publication No. US20020135299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guney, Austin E.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301PC61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186

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1	PRIOR APPLICATION NUMBER: 60/0655311
2	PRIOR FILING DATE: 1997-11-13
3	PRIOR APPLICATION NUMBER: 60/066770
4	PRIOR FILING DATE: 1997-11-24
5	PRIOR APPLICATION NUMBER: 60/075945
6	PRIOR FILING DATE: 1998-02-25
7	PRIOR APPLICATION NUMBER: 60/078910
8	PRIOR FILING DATE: 1998-03-20
9	PRIOR APPLICATION NUMBER: 60/083322
10	PRIOR FILING DATE: 1998-04-28
11	PRIOR APPLICATION NUMBER: 60/084600
12	PRIOR FILING DATE: 1998-05-07
13	PRIOR APPLICATION NUMBER: 60/087106
14	PRIOR FILING DATE: 1998-05-28
15	PRIOR APPLICATION NUMBER: 60/087607
16	PRIOR FILING DATE: 1998-06-02
17	PRIOR APPLICATION NUMBER: 60/087609
18	PRIOR FILING DATE: 1998-06-02
19	PRIOR APPLICATION NUMBER: 60/087759
20	PRIOR FILING DATE: 1998-06-02
21	PRIOR APPLICATION NUMBER: 60/087827
22	PRIOR FILING DATE: 1998-06-03
23	PRIOR APPLICATION NUMBER: 60/088021
24	PRIOR FILING DATE: 1998-06-04
25	PRIOR APPLICATION NUMBER: 60/088025
26	PRIOR FILING DATE: 1998-06-04
27	PRIOR APPLICATION NUMBER: 60/088026
28	PRIOR FILING DATE: 1998-06-04
29	PRIOR APPLICATION NUMBER: 60/088028
30	PRIOR FILING DATE: 1998-06-04
31	PRIOR APPLICATION NUMBER: 60/088029
32	PRIOR FILING DATE: 1998-06-04
33	PRIOR APPLICATION NUMBER: 60/088030
34	PRIOR FILING DATE: 1998-06-04
35	PRIOR APPLICATION NUMBER: 60/088033
36	PRIOR FILING DATE: 1998-06-04
37	PRIOR APPLICATION NUMBER: 60/088326
38	PRIOR FILING DATE: 1998-06-04
39	PRIOR APPLICATION NUMBER: 60/088167
40	PRIOR FILING DATE: 1998-06-05
41	PRIOR APPLICATION NUMBER: 60/088202
42	PRIOR FILING DATE: 1998-06-05
43	PRIOR APPLICATION NUMBER: 60/088212
44	PRIOR FILING DATE: 1998-06-05
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PRIOR APPLICATION NUMBER: 60/092182
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Query Match 78.1%; Score 687; DB 9; Length 185;
Best Local Similarity 73.3%; Pred. No. 3, 6e-65;
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

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Db 21 NVNIVNNDNNAGSGQSVSYVNEHNVANVONNNGMNSNALMDYRTGFAVTRLEPKKT 80
QY 61 CIVHMKKEAMPSLOALDALVKEKLGKPGGPPKSLRYSVNPNKVDLDFKGSIVA 120
Db 81 CIVHMKKEAMPSLOALDALVKEKLGKPGGPPKSLRYSVNPNKVDLDFKGSIVA 140
QY 121 MCKGPTMAEFIGANLISYSEKCSANILMTLNTSFCGGIEN 165
Db 141 MCKGPTMAEFIGANLISYSEKCSANILMTLNTSFCGGIEN 185

RESULT 4
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Sequence 211, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
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19 Query Match          78.1%; Score 687; DB 9; Length 185;
20 Best Local Similarity 73.3%; Pred. No. 3; Gaps 65;
21 Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps
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35 RESULT 5
36 US-10-001-054-14
37 Sequence 14, Application US/10001054
38 Publication No. US20020192209A1
39 GENERAL INFORMATION:
40 APPLICANT: Genentech, Inc.
41 APPLICANT: Baker, Kevin
42 APPLICANT: Goddard, Audrey
43 APPLICANT: Guernsey, Austin
44 APPLICANT: Heberfl, Carolyn
45 APPLICANT: Henzeli, William
46 APPLICANT: Kabakoff, Rhona
47 APPLICANT: Shelton, David
48 APPLICANT: Smith, Victoria
49 APPLICANT: Watanabe, Colin
50 APPLICANT: Wood, William
51 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
52 FILE REFERENCE: P3034RI.PCT
53 CURRENT APPLICATION NUMBER: US/10/001,054
54 CURRENT FILING DATE: 2001-11-30
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 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match	78.1%	Score 687;	DB 9;	Length 185;
Best Local Similarity	73.3%	Pred. No. 3.6e-05;		
Matches 121; Conservative	22;	Mismatches 22;	Indels 0;	Gaps 0;

[illegible]

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RESULT 7
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? Sequence 211, Application US/05990436
? Publication No. US20020198148A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi J.
? APPLICANT: Baker, Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan L.
? APPLICANT: Ferrara, Napoleone
? APPLICANT: Fong, Sherman
? APPLICANT: Gerber, Hapspeter
? APPLICANT: Gerritsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Kljavin, Ivar J.
? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Colin K.
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE REFERENCE: P2730P1C14
? CURRENT APPLICATION NUMBER: US/09/990,436
? PRIOR APPLICATION NUMBER: 60/049787
? PRIOR FILING DATE: 1997-06-16
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/065186

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Page 11

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3	PRIOR APPLICATION NUMBER: 60/089532
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5	PRIOR APPLICATION NUMBER: 60/089538
6	PRIOR FILING DATE: 1998-06-17
7	PRIOR APPLICATION NUMBER: 60/089598
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10	PRIOR FILING DATE: 1998-06-17
11	PRIOR APPLICATION NUMBER: 60/089600
12	PRIOR FILING DATE: 1998-06-18
13	PRIOR APPLICATION NUMBER: 60/089601
14	PRIOR FILING DATE: 1998-06-18
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75	PRIOR APPLICATION NUMBER: 60/091360

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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 78.1% Score 687; DB 9; Length 185;  
 Best Local Similarity 73.3%; Pred. No. 3, 6e-65;  
 Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

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 Db 21 NNNINVDNNDNNGSGQSVSVNNEHNANVDNNGMNSMNLMDYRGTGFAVTRLEPKKS 80  
 QY 61 CIVHMKRKAEMPSLQALALYKELKLGKPGPPKSLRSVNDNRVNDLDFEKSIVA 120  
 Db 81 CIVHMKRKAEMPSLQALALYKELKLGKPGPPKSLRSVNDNRVNDLDFEKSIVA 140  
 QY 121 MCKGIPTMAEIOGANTISYSEKISANILILNISFCGIAEN 165  
 Db 141 MCKGIPTMAEIOGANTISYSEKISANILILNISFCGIAEN 185

RESULT 8  
 US-09-991-181-211  
 Sequence 211, Application US/09991181  
 Publication No. US20020197615A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerlitsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C53  
 CURRENT APPLICATION NUMBER: US/09/991.181  
 PRIOR FILING DATE: 2001-11-16  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186  
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72	PRIOR FILING DATE: 1998-06-26
73	PRIOR APPLICATION NUMBER: 60/090863



Query Match	78.18;	Score 687;	DB 9;	Length 185;
Best Local Similarity	73.38;	Pred. No. 3.6e-05;		
Matches 121; Conservative	22;	Mismatches 22;	Indels 0;	Gaps 0

RESULT 11  
US-09-997

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PRIOR FILING DATE: 1998-06-24	Publication No. US20030008297A1
PRIOR APPLICATION NUMBER: 60/090435	GENERAL INFORMATION:
PRIOR FILING DATE: 1998-06-24	APPLICANT: Ashkenazi, Avi J.
PRIOR APPLICATION NUMBER: 60/090444	APPLICANT: Baker, Kevin P.
PRIOR FILING DATE: 1998-06-24	APPLICANT: Botstein, David
PRIOR APPLICATION NUMBER: 60/090445	APPLICANT: Desnoyers, Luc
PRIOR FILING DATE: 1998-06-24	APPLICANT: Eaton, Dan L.
PRIOR APPLICATION NUMBER: 60/090472	APPLICANT: Ferrara, Napoleone
PRIOR FILING DATE: 1998-06-24	APPLICANT: Fong, Sherman
PRIOR APPLICATION NUMBER: 60/090535	APPLICANT: Gerber, Hanspeter
PRIOR FILING DATE: 1998-06-24	APPLICANT: Gerlitsen, Mary E.
PRIOR APPLICATION NUMBER: 60/090540	APPLICANT: Goddard, Audrey
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PRIOR APPLICATION NUMBER: 60/090542	APPLICANT: Grimaldi, J. Christopher
PRIOR FILING DATE: 1998-06-24	APPLICANT: Gurney, Austin L.
PRIOR APPLICATION NUMBER: 60/090557	APPLICANT: Kijavlin, Ivar J.
PRIOR FILING DATE: 1998-06-24	APPLICANT: Napier, Mary A.
PRIOR APPLICATION NUMBER: 60/090676	APPLICANT: Pan, James
PRIOR FILING DATE: 1998-06-25	APPLICANT: Paoni, Nicholas F.
PRIOR APPLICATION NUMBER: 60/090678	APPLICANT: Roy, Margaret Ann
PRIOR FILING DATE: 1998-06-25	APPLICANT: Stewart, Timothy A.
PRIOR APPLICATION NUMBER: 60/090690	APPLICANT: Tumas, Daniel
PRIOR FILING DATE: 1998-06-25	APPLICANT: Watanabe, Colin K.
PRIOR APPLICATION NUMBER: 60/090694	APPLICANT: Williams, P. Mickey
PRIOR FILING DATE: 1998-06-25	APPLICANT: Wood, William I.
PRIOR APPLICATION NUMBER: 60/090695	APPLICANT: Zhang, Zemin
PRIOR FILING DATE: 1998-06-25	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
PRIOR APPLICATION NUMBER: 60/090696	TITLE OF INVENTION: Acids Encoding the Same
PRIOR FILING DATE: 1998-06-25	FILE REFERENCE: P2730P1C38
PRIOR APPLICATION NUMBER: 60/090862	CURRENT APPLICATION NUMBER: US/09/997,653
PRIOR FILING DATE: 1998-06-26	CURRENT FILING DATE: 2001-11-15
	PRIOR APPLICATION NUMBER: 60/049787

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[illegible]

PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 78.1%; Score 687; DB 9; Length 185;  
Best Local Similarity 73.3%; Pred No. 3; 6e-65;  
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

QY 1 DYSISVNDGSGGSGGQSVSYNNEHNVANVDNNNGSNMNLMDYRTGFAVTRLEKKS 60  
DB 21 NYNINVDNNNAGSGGQSVSYNNEHNVANVDNNNGSNMNLMDYRTGFAVTRLEKKT 80  
QY 61 CIVHMKREAMPISLOALVALVEKKLGGKGGPPPKSLRYSYNPKRVNLDKFGSIVA 120  
DB 81 CIVHMKREAMPISLOALVALVEKKLGGKGGPPPKSLRYSYNPKRVNLDKFGSIVAN 140  
QY 121 MCKGIPTVMAEIOGANTISYSEKISANIILWILNISFCGIAEN 165  
DB 141 MCRGIPVMAEIOGANTISYSEKISANIILWILNISFCGIAEN 185

RESULT 12  
US-09-993-667-211  
Sequence 211, Application US/09993667  
Publication No. US20030022187A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC4  
CURRENT APPLICATION NUMBER: US/09/993,667  
CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
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PRIOR FILING DATE: 1998-06-02  
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PRIOR FILING DATE: 1998-06-03  
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PRIOR FILING DATE: 1998-06-04  
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PRIOR FILING DATE: 1998-06-04  
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PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105

Query Match	78.1%;	Score 687;	DB 9;	Length 165;
Best Local Similarity	73.3%;	Pred. No. 3.6e-65;		
Matches 121; Conservative	22;	Mismatches 22;	Indels 0;	Gaps 0

RESULT 13  
US-09-990-438-211

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US-09-990,438, 211, Application No. US20030027754A1
Sequence 211, Application No.099990438
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerbel, Hanspeter
APPLICANT: Gertlsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC3
CURRENT APPLICATION NUMBER: US/09/990,438

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us-09-821-726a-18\_copy\_21\_185.rapp

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3 PRIOR FILING DATE: 1997-06-16  
4 PRIOR APPLICATION NUMBER: 60/062250  
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7 PRIOR FILING DATE: 1997-11-12  
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8	PRIOR FILING DATE: 1997-11-12
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1 PRIOR APPLICATION NUMBER: 60/090696  
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 19 PRIOR APPLICATION NUMBER: 60/091978  
 20 PRIOR FILING DATE: 1998-07-07  
 21 PRIOR APPLICATION NUMBER: 60/091982  
 22 PRIOR FILING DATE: 1998-07-07  
 23 PRIOR APPLICATION NUMBER: 60/092182  
 24 PRIOR FILING DATE: 1998-07-09

Query Match	78.1%	Score 687;	DB 9;	Length 185;
Best Local Similarity	73.3%	Pred. No. 3.6e-65;		
Matches 121; Conservative	22;	Mismatches 22;	Indels 0;	Gaps 0

QY	1	DYSLSTVNDGNSGGSGQGSYVNNEHHVAVDNNNGNSNNMLMDYTGPAVTRLPFEKS	60
Db	21	NYNINVDNDNNNGSGQGSYVNNEHHVAVDNNNGDMSNSTLMDYGNGLAARLRLPQKT	80
QY	61	CIYHKMKKEKMPQLDALDYVEKKIQGKGPGGPEKSLRYSVNPNVDMLDKFGKSIVA	120
Db	81	CIYHKMKKEKMPSTQSDALDYVEKKIQGKGPGGPPGLWYVSNPNKVDLDLSFKFGKNIAN	140
QY	121	MCKGIPTYMAEETQGANLISYSEKISANTLMTLINTISFCGGIAEN	165
Db	141	MCKGIPTYMAEEMQASLFLFYSGTCYTTSTVMTLVDSIFCCDYEEN	185

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PRIORITY APPLICATION NUMBER: 60/090429
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RESULT 15
US-09-997-428-211
; Sequence 211, Application US/09997428
; Publication No. US20030027162A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

```

[illegible]

; PRIOR FILING DATE: 1998-06-25  
 ; PRIOR APPLICATION NUMBER: 60/090696  
 ; PRIOR FILING DATE: 1998-06-25  
 ; PRIOR APPLICATION NUMBER: 60/090862  
 ; PRIOR FILING DATE: 1998-06-26  
 ; PRIOR APPLICATION NUMBER: 60/090863  
 ; PRIOR FILING DATE: 1998-06-26  
 ; PRIOR APPLICATION NUMBER: 60/091360  
 ; PRIOR FILING DATE: 1998-07-01  
 ; PRIOR APPLICATION NUMBER: 60/091478  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091544  
 ; PRIOR FILING DATE: 1998-07-01  
 ; PRIOR APPLICATION NUMBER: 60/091519  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091626  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091633  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091978  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

Query Match 78.1%; Score 687; DB 9; Length 185;

Best Local Similarity 73.3%; Pred. No. 3.6e-65;

Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

OY 1 DYSISVNDGSGSGGQSVSVNHNANVNDNNNGNSMNLMDYRTGFAVTRLEPKS 60  
 Db 21 NYNINVDNDNNAGSGQSVSVNHNANVNDNNNGNSMNLMDYRTGFAVTRLEPKS 80  
 OY 61 CIVHKMKKEAMPISQALDALYKKEKKGPGPGPPKSLRYSVNPBNRYDNLDPKFGKSIYA 120  
 Db 81 CIVHKMKKEVVPISQSLDALYKKEKKGPGPGPPKGLMYSVNPNKYVDLSEKFGKNIAN 140  
 OY 121 MCKGIPITYMAEIOGANLISYSEKICISANIITLILNISFCGIAEN 165  
 Db 141 MCRGIPITYMAEIOGANLISYSEKICISANIITLILNISFCGIAEN 185

Search completed: April 11, 2003, 16:17:46  
 Job time : 17.4192 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:06:33 ; Search time 11.7847 Seconds

(without alignments)  
474.899 Million cell updates/sec

Title: US-09-821-726A-13\_COPY\_78\_119

Perfect score: 221

Sequence: 1 KKTCTVHKMKKEVMPISQSL.....LVKEKKLQKGPGRPKGL 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the entry being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	216	97.7	185	20	AAW99667
2	216	97.7	185	21	AAW99667
3	216	97.7	185	21	AAW99667
4	216	97.7	185	21	AAW99667
5	216	97.7	185	22	AAW99667
6	216	97.7	185	22	AAW99667
7	216	97.7	185	23	AAW99667
8	216	97.7	185	23	AAW99667
9	216	97.7	185	23	AAW99667
10	216	97.7	185	23	AAW99667

11	216	97.7	194	19	AAW69974	Cancer associated
12	216	97.7	194	20	AAW76591	Human ovarian tumor
13	137	62.0	184	23	ABP09922	Human ORFX protein
14	62.5	28.3	103	21	AAW41048	Human ORFX ORF812
15	62.5	28.3	103	21	ABP35077	Human ORF4050 prot
16	62.5	28.3	103	21	AAW03592	Human DNA modifica
17	62.5	28.3	103	21	AAW94309	Human protein sequ
18	59.5	26.9	269	20	AAW43915	Human protein kina
19	59.5	26.9	269	20	AAW43915	Human protein kina
20	59.5	26.9	321	22	AAW98442	Novel human kinase
21	59.5	26.9	540	22	ABG22922	Novel human kinase
22	59.5	26.9	696	21	AAW19564	Protein kinase C-I
23	59.5	26.9	697	22	AAW82018	Human protein sequ
24	59.5	26.9	697	22	AAW78746	Human protein sequ
25	59.5	26.9	730	22	AAW79730	Human protein sequ
26	59.5	26.9	555	22	AAW16208	Human novel secret
27	58	26.2	555	22	AAW16621	Human novel secret
28	58	26.2	707	23	AAW91371	Human novel secret
29	58	26.2	862	23	AAW73697	Human bromodomain-
30	58	26.2	862	23	AAW73380	Human pleckstrin h
31	58	26.2	898	23	AAW73379	Human pleckstrin h
32	58	26.2	898	23	AAW73366	Human pleckstrin h
33	58	26.2	1039	23	AAW73398	Human pleckstrin h
34	58	26.2	1041	23	AAW73383	Human pleckstrin h
35	58	26.2	1416	22	ABW50153	Human transcriptio
36	57.5	26.0	306	22	AAW93026	Human protein sequ
37	57.5	26.0	1633	23	AAW78407	Amino acid sequenc
38	57	25.8	108	22	AAW08592	Human polypeptide
39	57	25.8	467	20	AAW81634	GABA-gated chlorid
40	57	25.8	496	20	AAW81633	GABA-gated chlorid
41	56.5	25.6	127	22	AAW07630	Human polypeptide
42	56.5	25.6	464	22	ABW61748	Drosophila melanog
43	56	25.3	222	22	ABW70836	Human polypeptide
44	55.5	25.1	128	22	AAW03204	Human polypeptide
45	55.5	25.1	147	22	AAW06887	Human polypeptide

## ALIGNMENTS

RESULT 1	
AAW99667	
ID	AAW99667 standard; Protein: 185 AA.
AC	AAW99667;
DT	07-JUN-1999 (first entry)
XX	
DE	Human secreted protein clone eJ90_5 protein.
XX	
KW	Human; secreted protein; nutritional; cytokine; cell proliferation;
KW	tissue growth; chemotactic; chemokine; haematopoiesis regulation;
KW	anti-inflammatory; cadherin; tumour invasion suppressor;
KW	tumour inhibition; gene therapy.
XX	
OS	Homo sapiens.
PN	WO9907840-A1.
PN	18-FEB-1999.
PD	
XX	
PE	06-AUG-1998; 98WO-US16318.
XX	
PR	04-AUG-1998; 98US-0130189.
PR	06-AUG-1997; 97US-0906708.
XX	
PA	(GENY ) GENETICS INST INC.
XX	
PI	Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;
PI	Merberg D, Racie LA, Steindler RJ, Treacy M;
XX	
DR	WPI; 1999-167419/14.

DR N-PSDB: AAX19493.  
XX New polynucleotides encoding secreted human proteins - derived from  
PT fetal kidney, adult testes, adult brain, adult heart, adult placenta  
PT or adult retina cDNA libraries  
XX  
XX Claim 34; Page 98-99; 107pp; English.  
XX  
CC The present sequence represents a human secreted protein. The secreted  
CC protein can have activities such as: nutritional activity, cytokine and  
CC cell proliferation/differentiation activity, immune stimulating (e.g. as  
CC vaccines) or suppressing activity, haematopoiesis regulating activity,  
CC tissue growth activity, activating/inhibiting activity, chemotactic/  
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/  
CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion  
CC suppressor activity, and tumour inhibition activity. The secreted  
CC protein polynucleotides and proteins are predicted to have biological  
CC activities which would make them suitable for treating, preventing or  
CC ameliorating medical conditions in humans and animals. The  
CC polynucleotides are also stated to be useful for gene therapy.  
XX  
SQ Sequence 185 AA:  
Query Match 97.7%; Score 216; DB 20; Length 185;  
Best Local Similarity 97.6%; Pred. No. 2.4e-19;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 KKTCTVHKMKKEVMPSTQSDALVKEKKLOGKPGGPPKGL 42  
DB 78 KKTCTVHKMKKEVMPSTQSDALVKEKKLOGKPGGPPKGL 119  
RESULT 2  
AAB24067  
ID AAB24067 standard; protein; 185 AA.  
XX  
AC AAB24067;  
XX  
DT 29-JAN-2001 (first entry)  
DE Human PRO1005 protein sequence SEQ ID NO:34.  
XX  
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
KW neurotropic; neuroprotective; anti-inflammatory; immunosuppressive;  
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
KW hypothalamic disorder; glandular disorder; macrophagal disorder;  
KW epithelial disorder; stromal disorder; blastocoelec disorder;  
KW inflammatory disorder; immunologic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200053755-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 06-JAN-2000; 2000WO-US00376.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 26-JUL-1999; 99US-0145698.  
PR 30-NOV-1999; 99WO-US28313.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
PI Watanabe CK, Wood WI;  
XX

DR WPI: 2000-572270/53.  
DR N-PSDB: AAC583377.  
XX  
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
PT treatment, diagnosis and prevention of cancer -  
PT  
XX  
XX Claim 61; Fig 22; 286pp; English.  
XX  
XX  
CC The present invention describes an isolated antibody that binds to  
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,  
CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,  
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
CC growth. The PRO polypeptides and nucleotides are useful in the  
CC treatment, diagnosis and prevention of cancer. The antibodies and other  
CC anti-tumour compounds maybe used to treat various conditions, including  
CC those characterised by overexpression and/or activation of the amplified  
CC PRO genes. Exemplary conditions or disorders to be treated with such  
CC antibodies and other compounds include benign or malignant tumours  
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),  
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,  
CC glial, astrocytal, hypothalamic and other glandular, macrophagal,  
CC epithelial, stromal and blastocoelec disorders, and inflammatory,  
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
CC primers and hybridisation probes used in the isolation of the human PRO  
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
CC PRO polynucleotide and protein sequences given in the exemplification of  
CC the present invention.  
XX  
SQ Sequence 185 AA:  
Query Match 97.7%; Score 216; DB 21; Length 185;  
Best Local Similarity 97.6%; Pred. No. 2.4e-19;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 KKTCTVHKMKKEVMPSTQSDALVKEKKLOGKPGGPPKGL 42  
DB 78 KKTCTVHKMKKEVMPSTQSDALVKEKKLOGKPGGPPKGL 119  
RESULT 3  
AAY87272  
ID AAY87272 standard; protein; 185 AA.  
XX  
XX AAY87272;  
XX  
XX 11-MAY-2000 (first entry)  
DE Human signal peptide containing protein HSP-49 SEQ ID NO:49.  
XX  
XX Human signal peptide containing protein: HSP; diagnosis; cancer;  
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
KW antimicrobial; neuroprotective; cardiovascular; hepatotropic;  
KW antiastrumatic; gene therapy; cell proliferation; neurological disorder;  
KW reproductive disorder; developmental disorder; arteriosclerosis;  
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
KW Parkinson's disease; Huntington's diseases; ovulatory defect;  
KW muscular dystrophy.  
XX  
OS Homo sapiens.  
XX  
PN WO200000610-A2.  
XX  
PD 06-JAN-2000.  
XX  
PF 25-JUN-1999; 99WO-US14484.  
XX  
PI 26-JUN-1998; 98US-0090762.  
PI 31-JUL-1998; 98US-0094983.  
XX

PR 01-OCT-1998; 98US-0102686.  
PR 11-DEC-1998; 98US-0112129.  
XX  
PA (INCY-) INCYTE PHARM INC.  
PI Lal P, Tang YT, Goryone GA, Corley NC, Guegler KJ, Baughn MR;  
PI Axelblom IE, Au-Young J, Yae H, Patterson C, Reddy R, Hillman JL;  
PI Bandman O;  
XX  
XX WPI: 2000-160673/14.  
DR N-PSDB; AA298157.  
PT  
PT New human signal peptide-containing proteins useful in treatment,  
PT prevention and diagnosis of e.g. cancer, inflammation and  
PT cardiovascular disease  
XX  
XX  
XX Claim 1; Page 193-194; 327pp; English.  
XX  
XX AA298109 to AA298242 encode AAY67224 to AAY87357 which represent the  
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,  
CC neuroprotective, cardiovascular and antiaesthetic activities, and can  
CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
CC associated with decreased activity or function of HSP. Antagonists of  
CC HSP are used to treat or prevent disorders associated with increased  
CC activity or function of HSP. Such diseases include cell proliferation  
CC (including cancer), inflammation, cardiovascular, neurological,  
CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
CC asthma, Crohn's disease, microbial or other infections, congestive or  
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
CC nucleic acids can be used for the recombinant production of HSP, for  
CC detecting HSP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring), in gene therapy, as antisense,  
CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
CC or genetic variations, and for chromosomal mapping. HSP are also used to  
CC raise specific antibodies (Ab) and to screen for agonists and  
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic  
CC antagonists, in competitive drug screens, and for purification of HSP  
CC from natural sources.  
XX  
XX Sequence 185 AA:  
SO  
Query Match 97.7%; Score 216; DB 21; Length 185;  
Best local Similarity 97.6%; Pred. No. 2,4e-19;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 KKTCTVHKMKKMPKSIOSLALVEKKKLOGKPGGPPKGL 42  
DB 78 KKTCTVHKMKKMPKSIOSLALVEKKKLOGKPGGPPKGL 119  
RESULT 4  
AAY66686  
ID AAY66686 standard: protein; 185 AA.  
XX  
XX AAY66686;  
AC  
XX  
XX 05-APR-2000 (first entry)  
DT  
XX  
XX Membrane-bound protein PRO1005.  
DE  
XX  
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO963088-A2.  
PN  
XX  
XX 09-DEC-1999.  
PD  
XX

PF 02-JUN-1999; 99WO-US12252.  
XX  
XX 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
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PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
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PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
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PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
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PR 22-JUN-1998; 98US-0090254.  
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PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
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PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
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 PR 26-JUN-1998; 98US-0090863.  
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 PR 10-JUL-1998; 98US-0092182.  
 PR 20-JUL-1998; 98US-0092472.  
 PR 30-JUL-1998; 98US-0093339.  
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 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096940.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.  
 PA (GETH ) GENENTECH INC.  
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,  
 PI Wood WI, Yuan J;  
 XX MPI; 2000-072883/06.  
 DR N-PSDB; AAZ65023.

XX Membrane-bound proteins and related nucleotide sequences  
 PT Claim 12; Fig 139; 822pp; English.  
 XX  
 PS The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 CC will also be useful for the preparation of PRO polypeptides, especially  
 CC by recombinant techniques.  
 XX  
 SQ Sequence 185 AA;  
 Query Match 97.7%; Score 216; DB 21; Length 185;  
 Best Local Similarity 97.6%; Pred. No. 2.4e-19;  
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPKGL 42  
 DB 78 KKTCTVHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPKGL 119  
 RESULT 5  
 AAB65209  
 ID AAB65209 standard; Protein: 185 AA.  
 XX  
 AC AAB65209;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; cytosolic;  
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay.  
 OS Homo sapiens.  
 OS  
 PN WO200073454-A1.  
 PD 07-DEC-2000.  
 XX  
 PF 30-MAR-2000; 2000MO-US08439.  
 XX  
 PR 02-JUN-1999; 99MO-US11252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99MO-US21090.  
 PR 15-SEP-1999; 99MO-US21547.  
 PR 08-OCT-1999; 99US-0158663.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 01-DEC-1999; 99MO-US28301.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 05-JAN-2000; 2000MO-US00219.  
 PR 06-JAN-2000; 2000MO-US00376.  
 PR 11-FEB-2000; 2000MO-US00365.  
 PR 18-FEB-2000; 2000MO-US04341.  
 PR 22-FEB-2000; 2000MO-US04414.  
 PR 24-FEB-2000; 2000MO-US04914.



24-FEB-2000: 2000WO-US05004.  
PR 02-MAR-2000: 2000WO-US05841.  
PR 15-MAR-2000: 2000WO-US06884.  
PR 20-MAR-2000: 2000WO-US07377.  
XX  
XX  
PA (GENTH ) GENENTECH INC.  
PI Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gertlsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Kljavin LJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
XX WPI: 2001-032160/04.  
DR N-PSDB: AAF44169.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
XX  
XX  
PS Claim 12: Fig 139; 935pp; English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
XX Sequence 185 AA;  
SQ  
Query Match 97.7%; Score 216; DB 22: Length 185;  
Best Local Similarity 97.6%; Pred. No. 2.4e-19;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KKTCTVHKMKKRVMPSTIOSLDAVKEKKLOGKGGPPPKGL 42  
DB 78 KKTCTVHKMKKRVMPSTIOSLDAVKEKKLOGKGGPPPKGL 119  
RESULT 6  
AAB50957  
ID AAB50957 standard; Protein: 185 AA.  
XX  
XX AAB50957;  
XX  
XX 21-MAR-2001 (first entry)  
XX  
XX Human PRO1005 protein.  
DE  
XX  
XX Human; PRO: cytostatic; neuroprotective; respiratory general;  
KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;  
KW PRO agonist; cancer; inflammatory disorder; immunological disorder.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO20007348-A2.  
XX  
XX  
XX 07-DEC-2000.  
XX  
XX 30-MAY-2000: 2000WO-US14941.  
XX  
XX 02-JUN-1999; 99WO-US12252.  
PR 22-JUN-1999; 99US-0140650.  
PR 23-JUN-1999; 99US-0141037.  
XX

20-JUL-1999; 99US-0144758.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US30095.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30999.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 03-MAR-2000; 2000WO-US187202.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
PI Shelton DL, Smith V, Watanabe CK, Wood WI;  
PI  
XX  
XX WPI: 2001-016509/02.  
DR N-PSDB: AAC91559.  
XX  
XX Twenty eight nucleic acids encoding PRO polypeptides which are useful  
PT for treating various tumors, e.g. breast cancer, and other  
PT inflammatory, angiogenic and immunological disorders -  
XX  
XX  
PS Claim 31: Fig 14; 188pp; English.  
XX  
XX The present sequence is one of twenty eight novel PRO polypeptides. The  
CC PRO polypeptides and their agonists, including antibodies, peptides, and  
CC small molecule agonists, may be used to treat various tumors, e.g.,  
CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal  
CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,  
CC central nervous system cancer, melanoma or leukemia. They are also  
CC useful for treating other disorders such as neuronal, glial, astrocyt,  
CC hypothalamic and other glandular, macrophegal, epithelial, stromal and  
CC blastocoele disorders, and inflammatory, angiogenic and immunological  
CC disorders.  
XX  
XX Sequence 185 AA;  
SQ  
Query Match 97.7%; Score 216; DB 22: Length 185;  
Best Local Similarity 97.6%; Pred. No. 2.4e-19;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KKTCTVHKMKKRVMPSTIOSLDAVKEKKLOGKGGPPPKGL 42  
DB 78 KKTCTVHKMKKRVMPSTIOSLDAVKEKKLOGKGGPPPKGL 119  
RESULT 7  
AAB95492  
ID AAB95492 standard; Protein: 185 AA.  
XX  
XX AAB95492;  
XX  
XX 19-JUL-2002 (first entry)  
XX  
XX Human angiogenesis related protein PRO1005 SEQ ID NO: 140.  
DE  
XX  
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnary;  
KW antiarteriosclerotic.  
XX  
XX Homo sapiens.  
OS  
XX

PN WO200208284-A2.  
XX  
PD 31-JAN-2002.  
XX  
XX 09-JUL-2001; 2001WO-US21735.  
XX 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23352.  
PR 24-AUG-2000; 2000WO-US23338.  
PR 07-SEP-2000; 2000US-230978P.  
PR 15-SEP-2000; 2000US-000000P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30873.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.  
XX  
XX (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANS/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
XX  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
XX WPI; 2002-171999/22.  
DR N-PSDB; ABL95630.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PI useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PI infarction), endothelial or angiogenic disorders in a mammal -  
XX  
XX  
PS Claim 11; Fig 140; 567pp; English.

XX The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a PRO protein of the invention.  
XX  
XX Sequence 185 AA;  
XX  
Query Match 97.7%; Score 216; DB 23; Length 185;  
Best local Similarity 97.6%; Pred. No. 2, 4e-19;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLGKGPGGPPKGL 42  
DB 78 KKTCTVHKMKKEVMPSTQSLDALVKEKKLGKGPGGPPKGL 119  
RESULT 8  
AB84886  
ID AB84886 standard; Protein; 185 AA.  
XX  
XX AB84886;  
AC  
XX  
XX  
DT 16-MAY-2002 (first entry)  
XX  
XX Human PRO1005 protein sequence SEQ ID NO:140.  
DE  
XX  
XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;  
KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping.  
XX  
OS Homo sapiens.  
XX  
XX WO200200690-A2.  
PN  
XX  
XX 03-JAN-2002.  
PD  
XX  
PF 20-JUN-2001; 2001WO-US19692.  
XX  
XX 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23352.  
PR 24-AUG-2000; 2000WO-US23338.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30873.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001US-0870974.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001US-0871743.  
 PR 01-JUN-2001; 2001US-08717800.  
 PR XX  
 PA (GETH ) GENENTECH INC.  
 PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 PI XX  
 DR WPI: 2002-090516/12.  
 DR N-PSDB: ABL88141.  
 DR XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 PT XX  
 PS Claim 11; Fig 140; 565pp; English.  
 PS XX  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.  
 CC XX  
 SQ Sequence 185 AA;  
 SQ XX  
 Query Match 97.7%; Score 216; DB 23; Length 185;  
 Best Local Similarity 97.6%; Pred. No. 2.4e-19;  
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 KKTCTVHHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPKGL 42  
 DB 78 KKTCTVHHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPKGL 119  
 RESULT 9  
 AAB83665  
 ID AAB83665 standard; Protein; 185 AA.  
 AC AAB83665;  
 AC XX  
 DT 08-MAY-2002 (first entry)  
 DT XX  
 DE Human PRO protein, Seq ID No 148.  
 DE XX  
 KM Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KM breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KM pericyte cell proliferation; chondrocyte cell proliferation;  
 KM tumour necrosis factor-alpha.  
 KM XX  
 OS Homo sapiens.  
 OS XX  
 PN WO200208288-A2.  
 PN XX  
 PD 31-JAN-2002.  
 PD XX  
 XX

PF 29-JUN-2001; 2001US-0821066.  
 PF XX  
 XX 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220585P.  
 PR 25-JUL-2000; 2000US-220605P.  
 PR 25-JUL-2000; 2000US-220607P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220638P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 25-JUL-2000; 2000US-220666P.  
 PR 26-JUL-2000; 2000US-220893P.  
 PR 28-JUL-2000; 2000US-220710P.  
 PR 23-AUG-2000; 2000US-220711P.  
 PR 24-AUG-2000; 2000US-220712P.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 10-NOV-2000; 2000US-0530873.  
 PR 28-NOV-2000; 2000US-253646P.  
 PR 01-DEC-2000; 2000US-0532678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0506520.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0854280.  
 PR XX  
 PA (GETH ) GENENTECH INC.  
 PA XX  
 PI Baker KP, Desnoyers L, Gertlisen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
 PI XX  
 DR WPI: 2002-172001/22.  
 DR N-PSDB: ABB33609.  
 DR XX  
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for treating a PRO related disorder and for diagnosing tumours,  
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
 PT tumour or liver tumour -  
 PT XX  
 PS Claim 11; Figure 148; 359pp; English.  
 PS XX  
 CC The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. AAB83592-AAB83713 represent human PRO  
 CC protein sequences of the invention.  
 CC XX  
 SQ Sequence 185 AA;  
 SQ XX  
 Query Match 97.7%; Score 216; DB 23; Length 185;  
 Best Local Similarity 97.6%; Pred. No. 2.4e-19;  
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 KKTCTVHHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPKGL 42  
 DB 78 KKTCTVHHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPKGL 119  
 RESULT 10  
 AAB38329  
 ID AAB38329 standard; Protein; 186 AA.  
 AC AAB38329;  
 AC XX  
 XX

DT 31-JAN-2001 (first entry)  
XX Human secreted protein encoded by gene 9 clone HNSAD53.  
DE  
XX Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;  
XX cytostatic; cardiast; vasotropic; cerebroprotective; neuroprotective;  
XX neurotropic; antibacterial; virucide; fungicide; opthalmological; human;  
XX vulterary; gene therapy; infection; secreted protein.  
OS Homo sapiens.  
XX  
XX WO200061623-A1.  
XX  
XX 19-OCT-2000.  
XX  
XX 06-APR-2000; 2000WO-US08979.  
XX  
XX 09-APR-1999; 99US-0128693.  
XX 26-APR-1999; 99US-0130991.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;  
XX Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;  
XX Young PE;  
XX WPI: 2000-647418/62.  
XX  
XX New nucleic acid molecules encoding 62 human secreted proteins for  
XX diagnosing, preventing, treating or ameliorating medical conditions and  
XX used as food additives or preservatives -  
XX  
XX Claim 11; Page 598; 716pp; English.  
XX  
XX Sequences AAB8321-B38396 represent the amino acid sequences of 62  
XX human secreted proteins encoded by the genes AAC69512-C69587. The genes  
XX and proteins are useful for preventing, ameliorating or treating medical  
XX conditions, e.g. by protein or gene therapy. The genes are isolated from  
XX a range of human tissues disclosed in the specification. The nucleic  
XX acids, proteins, antibodies and (ant)agonists are useful in the  
XX diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.  
XX rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms  
XX of the breast or liver; (c) cardiovascular disorders e.g. cardiac  
XX arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)  
XX angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)  
XX infections caused by bacteria, viruses and fungi; and (h) ocular  
XX disorders e.g. corneal infection. The polypeptides can also be used to  
XX aid wound healing and epithelial cell proliferation, to prevent skin  
XX aging due to sunburn, to maintain organs before transplantation, for  
XX supporting cell culture of primary tissues, to regenerate tissues and in  
XX chemotaxis.  
XX  
XX Sequence 186 AA:  
SO  
Query Match 97.7%; Score 216; DB 21; Length 186;  
Best Local Similarity 97.6%; Pred. No. 2.4e-19;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KKTCTVHKMKKEVMPISQSLDALVKEKKIQGKGPGGPPPKGL 42  
Db 78 KKTCTVHKMKKEVMPISQSLDALVKEKKIQGKGPGGPPPKGL 119  
RESULT 11  
AAW69974 standard; Protein; 194 AA.  
ID AAW69974:  
XX AAW69974:  
XX  
XX 16-NOV-1998 (first entry)  
XX  
XX Cancer associated protein.  
DE  
XX

KW Cancer; PCR; Northern blotting; ribonuclease protection assay;  
KW diagnosis; metastatic cancer.  
XX  
XX Synthetic.  
XX  
XX WO9837187-A1.  
XX  
XX 27-AUG-1998.  
XX  
XX 18-FEB-1998; 98MO-JP00667.  
XX  
XX 21-FEB-1997; 97JP-0052508.  
XX  
XX (TAKI ) TAKARA SHUZO CO LTD.  
XX  
XX Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;  
XX WPI: 1998-467552/40.  
XX  
XX Detection of cancer cells in tissue samples - by changes in mRNA  
XX expression compared to normal tissue of specific cancer-associated  
XX gene sequences  
XX  
XX Claim 14; Page 64-65; 92pp; Japanese.  
XX  
XX The cancer associated proteins AAW69974-W69976 where used in the method  
XX of the invention to detect cancer cells in tissue samples or biological  
XX fluids. They are detected by monitoring the change in mRNA expression  
XX as compared to normal tissue of one or more cancer-associated genes  
XX whose cDNA stringently hybridises to cancer associated gene nucleic acid  
XX fragments. The change in expression may be an increase or a decrease  
XX compared to normal tissue. The mRNA expression may be determined by  
XX PCR, Northern blotting or ribonuclease protection assay, or by  
XX determining the change in the amount of protein encoded by the gene(s) as  
XX compared to normal tissue, for example by using a labelled antibody  
XX recognising the protein. Detection of cancer cells for cancer diagnosis,  
XX including detection of metastatic cancer cells in tissues other than the  
XX primary tumour site.  
XX  
XX Sequence 194 AA:  
SO  
Query Match 97.7%; Score 216; DB 19; Length 194;  
Best Local Similarity 97.6%; Pred. No. 2.5e-19;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KKTCTVHKMKKEVMPISQSLDALVKEKKIQGKGPGGPPPKGL 42  
Db 87 KKTCTVHKMKKEVMPISQSLDALVKEKKIQGKGPGGPPPKGL 128  
RESULT 12  
AAW76591 standard; Protein; 194 AA.  
ID AAW76591:  
XX AAW76591:  
XX  
XX 10-APR-2000 (first entry)  
XX  
XX Human ovarian tumor EST fragment encoded protein 87.  
XX  
XX Expressed sequence tag; EST; human; ovarian tumor; anticancer;  
XX gene therapy; treatment.  
XX  
XX Homo sapiens.  
XX  
XX DE19817557-A1.  
XX  
XX 21-OCT-1999.  
XX  
XX 09-APR-1998; 98DE-1017557.  
XX  
XX 09-APR-1998; 98DE-1017557.  
XX  
XX

PA (META-) METAGEN GES. GENOMFORSCHUNG MBH.  
XX  
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;  
XX WPI: 1999-591920/51.  
XX N-PSDB: AAZ77487.  
XX  
XX New nucleic acid sequences expressed in ovarian, and some other, cancer  
PT tissues, and derived polypeptides, for treatment of ovarian cancer and  
PT identification of therapeutic agents -  
XX  
PS Claim 25; Page 279; 310pp; German.  
XX  
XX This invention describes novel nucleic acid (cDNA) sequences (A) which  
CC have anticancer activity and are highly expressed in ovarian tumor  
CC tissue (and some also in testis and breast cancer tissue). The products  
CC of the invention can be used for gene therapy. (A) are used (1) for  
CC recombinant expression of polypeptides (B) and (1) to isolate complete  
CC genes. (B) are used (1) to identify agents suitable for treatment of  
CC ovarian cancer; (11) directly for treating this form of cancer  
CC (including expression from gene therapy vectors) and (11) for generation  
CC of specific antibodies. (A) are identified by assembling ESTs (expressed  
CC sequence tags) from a particular tissue type before comparison of  
CC expression patterns. This allows a significantly longer fragment of the  
CC gene to be revealed, so should reduce the number of failures associated  
CC with the fact that ESTs from different libraries may represent different  
CC parts of the same unknown gene, distorting the estimated frequency of  
CC occurrence in a particular tissue. AAY76505-Y76638 represent protein  
CC fragments encoded by the human ovarian tumor cDNA library derived EST  
CC fragments represented in AAZ77450-777572.  
XX  
SQ Sequence 194 AA:  
XX  
XX Query Match 97.7%; Score 216; DB 20; Length 194;  
XX Best Local Similarity 97.6%; Pred. No. 2.5e-19;  
XX Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 KKTCTVHKMKKEVMPISQSLDALVKEKKLOGKGGPPKGL 42  
DB 87 KKTCTVHKMKKEVMPISQSLDALVKEKKLOGKGGPPKGL 128  
RESULT 13  
ABP09922  
ID ABP09922 standard; Protein: 184 AA.  
XX  
XX AC ABP09922;  
XX  
XX 24-JUN-2002 (first entry)  
DE  
XX  
XX Human ORFX protein sequence SEQ ID NO:19826.  
XX  
XX Human: open reading frame; ORFX: gene therapy; cancer; cirrhosis;  
KM hyperproliferative disorder; psoriasis; benign tumor; haemorrhage;  
KM degenerative disorder; osteoarthritis; neurodegenerative disorder;  
KM cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
KM hypertension; hypothyroidism; cholesterol ester storage disease;  
KM immune deficiency; immune disorder; infectious disease;  
KM autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
KM myasthenia gravis.  
XX  
XX Homo sapiens.  
XX  
XX WO200192523-A2.  
XX  
XX PD 06-DEC-2001.  
XX  
XX PF 29-MAY-2001; 2001WO-0510836.  
XX  
XX PR 30-MAY-2000; 2000US-206132P.  
XX  
XX PR 29-AUG-2000; 2000US-228716P.  
XX  
XX (CURA-) CURAGEN CORP.

XX  
XX Shimkets RA, Leach MD;  
XX WPI: 2002-106308/14.  
XX N-PSDB: ABN25674.  
XX  
XX Novel human polypeptides and polynucleotides useful for diagnosing,  
PT preventing and treating cardiovascular disease, neurodegenerative,  
PT hyperproliferative disorders and autoimmune disorders -  
XX  
PS Disclosure; SEQ ID 19826; 1037pp; English.  
XX  
XX The present invention describes substantially purified human proteins  
CC (referred to as open reading frame, ORFX, where x is 1-11491 (see Table 1  
CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
CC treating or preventing a pathology associated with an ORFX-associated  
CC disorder in humans, and in the manufacture of a medicament for treating a  
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
CC sequences can be used in gene therapy. ORFX sequences can be used in the  
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,  
CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
CC storage disease, various immune deficiencies and disorders, infectious  
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
CC bone degenerative disorders, or periodontal disease, and for gut  
CC protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissues and conditions resulting from  
CC systemic cytokine damage.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 184 AA:  
XX  
XX Query Match 62.0%; Score 137; DB 23; Length 184;  
XX Best Local Similarity 64.3%; Pred. No. 2.1e-09;  
XX Matches 27; Conservative 5; Mismatches 8; Indels 2; Gaps 1;  
OY 1 KKTCTVHKMKKEVMPISQSLDALVKEKKLOGKGGPPKGL 42  
DB 78 KKTCTVHKMKKEVMPISQSLDALVKEKKLOGKGGPPKGL 117  
RESULT 14  
AAB41048  
ID AAB41048 standard; Protein: 103 AA.  
XX  
XX AC AAB41048;  
XX  
XX 08-FEB-2001 (first entry)  
DE  
XX  
XX Human ORFX ORF812 polypeptide sequence SEQ ID NO:1624.  
XX  
XX Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;  
KM vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
KM anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiant;  
KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KM hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KM antiviral; antibacterial; antifungal; antineumatic; antithyroid;  
KM antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KM neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KM cholesterol ester storage; systemic lupus erythematosus; infection;  
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KM thrombosis; contraceptive.

XX OS Homo sapiens.  
 XX W0200058473-A2.  
 XX PD 05-OCT-2000.  
 XX PF 31-MAR-2000; 2000OWO-US08621.  
 XX PR 31-MAR-1999; 990US-0127607.  
 XX PR 02-APR-1999; 990US-0127636.  
 XX PR 05-APR-1999; 990US-0127728.  
 XX PR 30-MAR-2000; 2000OUS-0540763.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Shinkets RA, Leach M;  
 XX DR WPI: 2000-602362/57.  
 XX DR N-PSDB; AAC75257.  
 XX PT Novel nucleic acids and peptides derived from open reading frame X,  
 XX PT useful for treating e.g. cancers, proliferative disorders,  
 XX PT neurodegenerative disorders and cardiovascular disease -  
 XX PS Claim 11; Page 1306; 5507pp; English.  
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;  
 CC antiproliferative; antiparasitism; neutrotropic; neuroprotective;  
 CC osteoplastic; anticonvulsant; antiallergic; immunosuppressive;  
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic;  
 CC antidiabetic; hypotensive; dermatologic; immunosuppressive;  
 CC antiinflammatory; antibacterial; antiviral; antifungal; antineumatic;  
 CC antihypertoid; and antianemic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORFX-associated disorder. The  
 CC nucleic acids can be used to express ORFX proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat cancers,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antinflammatory disease, to enhance  
 CC coagulation; to inhibit thrombosis; and as a contraceptive.  
 XX SQ Sequence 103 AA;  
 XX  
 XX Query Match 28.3%; Score 62.5; DB 21; Length 103;  
 XX Best Local Similarity 37.8%; Pred. No. 2.8;  
 XX Matches 14; Conservative 7; Mismatches 15; Indels 1; Gaps 1;  
 QY 4 CIVHKKEVMPISQIDALVKEKKLOGKPGGPRPK 40  
 Db 39 CLGAKNKQSL-QLSLADSRPLKRSKSGKRGPRPK 74  
 ID ABB35077 standard; Protein: 103 AA.  
 AC ABB35077;  
 XX 08-JUL-2002 (first entry)  
 XX DE Human ORF4050 protein, SEQ ID NO:8100.  
 XX KW Human; ORF: open reading frame; ORFX: drug screening; diagnosis;  
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;  
 KW immune modulation; haematopoiesis regulation; tissue growth;

KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;  
 KW thrombolytic; tumour inhibition; bodily characteristics; fertility;  
 KW behaviour; cancer; proliferative disorder; neurological disorder;  
 KW cardiovascular disease; immune system disorder; organ transplantation;  
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;  
 KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;  
 KW vasotropic; antiproliferative; antidiabetic; cytostatic; neutrotropic;  
 KW neuroprotective; antiparasitism; anticonvulsant; thrombolytic;  
 KW cardiant; hypotensive; antihypertoid; antinflammatory; immunomodulator;  
 KW dermatologic; analgesic; virucide; antibacterial; fungicide.  
 XX OS Homo sapiens.  
 XX W0200190366-A2.  
 XX PD 29-NOV-2001.  
 XX PF 24-MAY-2001; 2001WO-US17076.  
 XX PR 24-MAY-2000; 2000OUS-206690P.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Leach MD, Shinkets RA;  
 XX DR WPI: 2002-106200/14.  
 XX DR N-PSDB; ABB79103.  
 XX PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 XX PT preventing and treating cardiovascular disease, neurodegenerative,  
 XX PT hyperproliferative disorders and disorders related to organ  
 XX PT transplantation -  
 XX PS Claim 10; Page 2271; 2508pp; English.  
 XX  
 XX Sequences ABB31028-ABB35561 represent 4534 novel human proteins  
 CC designated ORF (open reading frame) 1-4534, and sequences ABB75054-  
 CC ABB79587 represent cDNAs encoding them. The invention also encompasses  
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively  
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to  
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX  
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies  
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and  
 CC polypeptides, methods of screening for modulators of ORFX expression or  
 CC activity, and methods of screening individuals for a predisposition to an  
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide  
 CC range of biological activities, such as cytokine, cell proliferation,  
 CC cell differentiation, immune modulation, haematopoiesis regulation,  
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/  
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,  
 CC receptor/ligand, antinflammatory activity, tumour inhibition activity,  
 CC and antineoplastic activity, and may also be involved in the determination  
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,  
 CC nucleic acids and antibodies may be used in the treatment of cancers,  
 CC other proliferative disorders such as psoriasis and benign tumours,  
 CC neurological disorders such as epilepsy and Alzheimer's disease,  
 CC cardiovascular diseases, immune system disorders, disorders related to  
 CC organ transplantation, disorders of tissue growth and regeneration,  
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester  
 CC storage disease, and infectious diseases caused by viral, bacterial,  
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a  
 CC source of primers and probes, in the detection of ORFX genomic sequences  
 CC or transcripts, in the identification and cloning of homologous  
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX  
 CC nucleic acids may additionally be used to produce transgenic animals  
 CC which may be useful for studying the function and/or activity of ORFX  
 CC protein, and in drug screening. The ORFX proteins may also be used as  
 CC immunogens to generate specific antibodies, which are useful in the  
 CC diagnosis, treatment and monitoring of ORFX-associated diseases.  
 XX SQ Sequence 103 AA;  
 XX  
 XX Query Match 28.3%; Score 62.5; DB 23; Length 103;

Best Local Similarity 37.88; Pred. No. 2.8;  
 Matches 14; Conservative 7; Mismatches 15; Indels 1; Gaps 1;  
 QY 4 CIVHKKKEVMPISQSLDALVKEKKLOGKPGGPPPK 40  
 | : | | : : | : | | | | | | |  
 Db 39 CLGAKHKAQSL-QLSLADSPFLKRSKSGKPGNPRPK 74

Search completed: April 11, 2003, 16:11:11  
 Job time : 12.7847 secs





GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:11:18 ; Search time 4.17945 Seconds  
(without alignments)  
614.367 Million cell updates/sec

Title: US-09-821-726a-13\_COPY\_78\_119

Perfect score: 221  
Sequence: 1 KKTCTVHKMKKEVMPSTQSL.....LVKREKLLKGKGGCGPPPKGL 42

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*

2: /cgn2\_6/ptodata/2/pubppaa/PCIT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubppaa/PCITUS\_PUBCOMB.pep:\*

8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep:\*

10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep:\*

12: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*

13: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*

14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	216	97.7	182	9	US-10-050-704-212
2	216	97.7	185	9	US-09-992-598-211
3	216	97.7	185	9	US-09-992-598-211
4	216	97.7	185	9	US-09-992-598-211
5	216	97.7	185	9	US-09-992-598-211
6	216	97.7	185	9	US-09-992-598-211
7	216	97.7	185	9	US-09-992-598-211
8	216	97.7	185	9	US-09-992-598-211
9	216	97.7	185	9	US-09-992-598-211
10	216	97.7	185	9	US-09-992-598-211
11	216	97.7	185	9	US-09-992-598-211
12	216	97.7	185	9	US-09-992-598-211
13	216	97.7	185	9	US-09-992-598-211
14	216	97.7	185	9	US-09-992-598-211
15	216	97.7	185	9	US-09-992-598-211
16	216	97.7	185	9	US-09-992-598-211
17	216	97.7	185	9	US-09-992-598-211
18	216	97.7	185	9	US-09-992-598-211
19	216	97.7	185	9	US-09-992-598-211

20	216	97.7	185	9	US-10-230-163-148	Sequence 148, App
21	216	97.7	185	9	US-09-989-726-211	Sequence 211, App
22	216	97.7	185	9	US-09-746-763-146	Sequence 146, App
23	216	97.7	185	9	US-09-990-437-211	Sequence 211, App
24	216	97.7	185	9	US-09-998-156-211	Sequence 211, App
25	216	97.7	185	9	US-10-218-631-148	Sequence 148, App
26	216	97.7	185	9	US-10-230-338-148	Sequence 148, App
27	216	97.7	185	9	US-09-991-157-211	Sequence 211, App
28	216	97.7	185	9	US-09-991-172-211	Sequence 211, App
29	216	97.7	185	9	US-09-997-514-211	Sequence 211, App
30	216	97.7	185	9	US-09-997-573-211	Sequence 211, App
31	216	97.7	185	9	US-10-050-704-105	Sequence 105, App
32	216	97.7	185	9	US-10-230-414-148	Sequence 148, App
33	216	97.7	185	9	US-09-990-443-211	Sequence 211, App
34	216	97.7	185	9	US-09-990-726-211	Sequence 211, App
35	216	97.7	185	9	US-09-997-559-211	Sequence 211, App
36	216	97.7	185	9	US-09-997-601-211	Sequence 211, App
37	216	97.7	185	9	US-09-989-729A-211	Sequence 211, App
38	216	97.7	185	9	US-09-990-440-211	Sequence 211, App
39	216	97.7	185	9	US-09-991-854-211	Sequence 211, App
40	216	97.7	185	9	US-09-997-349-211	Sequence 211, App
41	216	97.7	185	9	US-09-997-440-211	Sequence 211, App
42	216	97.7	185	9	US-09-997-628-211	Sequence 211, App
43	216	97.7	185	9	US-09-997-683-211	Sequence 211, App
44	216	97.7	185	10	US-09-989-722-211	Sequence 211, App
45	216	97.7	185	10	US-09-989-723-211	Sequence 211, App

## ALIGNMENTS

RESULT 1

US-10-050-704-212

Sequence 212, Application US/10050704

Publication No. US20030050442A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 62 Human secreted proteins

FILE REFERENCE: P2039P1

CURRENT APPLICATION NUMBER: US/10/050,704

CURRENT FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: 09/684,524

PRIOR FILING DATE: 2000-10-10

PRIOR APPLICATION NUMBER: PCT/US00/08979

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 60/128,693

PRIOR FILING DATE: 1999-04-09

PRIOR APPLICATION NUMBER: 60/130,991

PRIOR FILING DATE: 1999-04-26

NUMBER OF SEQ ID NOS: 344

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 212

LENGTH: 182

TYPE: PRT

ORGANISM: Homo sapiens

US-10-050-704-212

Query Match

Best Local Similarity 97.7%; Score 216; DB 9; Length 182;

Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLKGKGGCGPPPKGL 42

Db 78 KKTCTVHKMKKEVMPSTQSLDALVKEKKLKGKGGCGPPPKGL 119

RESULT 2

US-09-992-598-211

Sequence 211, Application US/09992598

Patent No. US20020160384A1

GENERAL INFORMATION:

APPLICANT: Ashtkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Baton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730PIC20  
 CURRENT APPLICATION NUMBER: US/09/992,598  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
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Query Match 97.7%; Score 216; DB 9; Length 185;  
Best Local Similarity 97.6%; Pred. No. 2.5e-20;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKTCTVHKMKKEVWPSIQSLDALVKEKKLOGKGPGRPKGL 42  
Db 78 KKTCTVHKMKKEVWPSIQSLDALVKEKKLOGKGPGRPKGL 119

RESULT 3  
US-09-989-293A-211  
Sequence 211, Application US/09989293A  
Patent No. US20020177164A1  
GENERAL INFORMATION:  
APPLICANT: Askenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Maty E.

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301C66  
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;; Publication No. US20020193299A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
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;; APPLICANT: Gurney, Austin L.  
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;; APPLICANT: Pan, James

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 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
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 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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Query Match 97.7%; Score 216; DB 9; Length 185;  
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RESULT 5  
 US-09-980-444-211  
 Sequence 211, Application US/09990444  
 Publication No. US20020193300A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Bolstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerlitsen, Mary E.  
 APPLICANT: Goddard, Audrey J.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
 TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C19  
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Query Match 97.7%; Score 216; DB 9; Length 185;  
Best Local Similarity 97.6%; Pred. No. 2.5e-20;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6  
US-10-001-054-14  
Sequence 14, Application US/10001054  
Publication No. US20020192209A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Baker, Kevin  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin  
APPLICANT: Hebert, Carolyn  
APPLICANT: Henzel, William  
APPLICANT: Kabakoff, Rhona  
APPLICANT: Shelton, David  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING NEOPLASTIC  
FILE REFERENCE: P3034RIPTCT  
CURRENT APPLICATION NUMBER: US/10/001,054  
CURRENT FILING DATE: 2001-11-30  
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PRIOR FILING DATE: 1998-07-09

Query Match 97.7% Score 216; DB 9; Length 185;  
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Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Sequence 211, Application US/09990436  
Publication No. US20020198148A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavrin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C14  
CURRENT APPLICATION NUMBER: US/09/990.436  
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 ;; PRIOR FILING DATE: 1998-07-09

Query Match  
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 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 9

US-09-991-181-211  
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 ; Publication No. US20020197615A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Bostein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Maty E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2730P1C53  
 ; CURRENT APPLICATION NUMBER: US/09/991,181  
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 ; PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;  
Best local similarity 97.6%; Pred. No. 2,35e-20;

Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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; Publication No. US20020198149A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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Query Match 97.7%; Score 216; DB 9; Length 185;  
 Best local Similarity 97.6%; Pred. No. 2.5e-20;  
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEVMPSTIOSIDLAVKEKKLOGKGGPGGPPKGL 42  
 Db 78 KKTCTVHKMKKEVMPSTIOSIDLAVKEKKLOGKGGPGGPPKGL 119

RESULT 11  
 US-09-989-734-211  
 : Sequence 211, Application US/09989734  
 : Publication No. US20030003531A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Ashkenazi, Avi J.  
 : APPLICANT: Baker, Kevin P.  
 : APPLICANT: Botstein, David  
 : APPLICANT: Desnoyers, Luc  
 : APPLICANT: Eaton, Dan L.  
 : APPLICANT: Ferrara, Napoleone  
 : APPLICANT: Fong, Sherman  
 : APPLICANT: Gerber, Hanspeter  
 : APPLICANT: Gottfred, Audrey  
 : APPLICANT: Godowski, Paul J.  
 : APPLICANT: Grimaldi, J. Christopher  
 : APPLICANT: Gurney, Austin L.  
 : APPLICANT: Kljavin, Ivar J.  
 : APPLICANT: Nepier, Mary A.  
 : APPLICANT: Pan, James  
 : APPLICANT: Paoni, Nicholas F.  
 : APPLICANT: Roy, Margaret Ann  
 : APPLICANT: Stewart, Timothy A.  
 : APPLICANT: Tumas, Daniel  
 : APPLICANT: Watanabe, Collin K.  
 : APPLICANT: Williams, P. Mickey  
 : APPLICANT: Wood, William I.  
 : APPLICANT: Zhang, Zemin  
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 : FILE OF INVENTION: Acids Encoding the Same  
 : FILE REFERENCE: P2730P1C64  
 : CURRENT APPLICATION NUMBER: US/09/989,734  
 : CURRENT FILING DATE: 2001-11-19  
 : PRIOR APPLICATION NUMBER: 60/049787  
 : PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;

Best Local Similarity 97.6%; Pred. No. 2.5e-20;

Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKREVMPSISLDAVLEKKLGGKPGGPPKGL 42  
Db 78 KKTCTVHKMKREVMPSISLDAVLEKKLGGKPGGPPKGL 119

RESULT 12  
US-09-997-653-211

; Sequence 211, Application US/09997653

; Publication No. US20030008297A1

; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C38  
CURRENT APPLICATION NUMBER: US/09/997,653  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-05



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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;  
Best Local Similarity 97.6%; Pred. No. 2,5e-20;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KKTCTVHKMKKEVMPSTIOSLDAIVREKRIQGGKPGGPPKGL 42  
DB 78 KKTCTVHKMKKEVMPSTIOSLDAIVREKRIQGGKPGGPPKGL 119

RESULT 13  
US-09-993-667-211  
Sequence 211, Application US/09993667  
Publication No. US20030022187A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Estou, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C4  
CURRENT APPLICATION NUMBER: US/09/993,667  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-23  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24

APPLICANT: 60/090535  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;  
Best Local Similarity 97.6%; Pred. No. 2,5e-20;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTCIVHKKKEVWPSIOSLDALVKEKKLOGKGGPPKGL 42  
DB 78 KTCIVHKKKEVWPSIOSLDALVKEKKLOGKGGPPKGL 119

RESULT 14  
US-09-990-438-211

Sequence 211, Application US/09990438  
Publication No. US20030027754A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C3  
CURRENT APPLICATION NUMBER: US/09/990,438  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-10

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 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;  
 Best Local Similarity 97.6%; Pred. No. 2, 5e-20;  
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEVMPISQSLDALVKEKTKGSGGPPPKGL 42  
 DB 78 KKTCTVHKMKKEVMPISQSLDALVKEKTKGSGGPPPKGL 119

RESULT 15  
 US-09-990-562-211  
 Sequence 211, Application US/09990562  
 Publication No. US20030027985A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerlitsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C18  
CURRENT APPLICATION NUMBER: US/09/990,562  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
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PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690  
PRIOR FILING DATE: 1998-06-25



GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 ; Search time 2.46656 Seconds  
(Without alignments)  
706.250 Million cell updates/sec

Title: US-09-821-726a-13\_COPY\_78\_119  
Perfect score: 221  
Sequence: 1 KKTCTVHKMKREVMPSIQSLDYLVEKKLQGGPGPPPKGL 42

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	216	97.7	199	1	Q9ns71 homo sapien
2	151	68.3	184	1	Q9cr36 mus musculu
3	59.5	26.9	682	1	P05128 bos taurus
4	59.5	26.9	697	1	P05129 homo sapien
5	59.5	26.9	697	1	P05697 mus musculu
6	59.5	26.9	697	1	P10829 oryctolagus
7	59	26.7	759	1	Q61660 caenorhabdi
8	57.5	26.0	634	1	Q67077 aquifex aeo
9	57.5	26.0	2469	1	Q01056 herpesvirus
10	57	25.8	997	1	Q09033 sordaria fi
11	55	24.9	230	1	Q9k998 bacillus ha
12	55	24.9	431	1	O54915 mus musculu
13	55	24.9	431	1	Q9137 ratu
14	54.5	24.7	477	1	P00543 feline sarc
15	54.5	24.7	820	1	P14238 felis silve
16	54	24.4	875	1	P09097 escherichia
17	54	24.4	876	1	P14829 klebsiella
18	53.5	24.2	494	1	P20812 ratu
19	53.5	24.2	542	1	O00294 homo sapien
20	53.5	24.2	2144	1	Q9qyp2 ratu
21	53.5	24.2	2920	1	Q9r0m0 mus musculu
22	53	24.0	233	1	P06341 ratu
23	53	24.0	263	1	P29826 ratu
24	53	24.0	695	1	P51141 mus musculu
25	53	24.0	695	1	O9wvb ratu
26	52.5	23.8	303	1	P32587 schizosacch
27	52.5	23.8	648	1	O15353 homo sapien
28	52.5	23.8	1189	1	P47035 saccharomyc
29	52	23.5	252	1	P06346 mus musculu
30	52	23.5	263	1	P06343 mus musculu
31	52	23.5	263	1	P06345 mus musculu
32	52	23.5	263	1	P06344 mus musculu
33	52	23.5	265	1	P14483 mus musculu

34	52	23.5	265	1	HB2D_MOUSE	P01921 mus musculu
35	52	23.5	265	1	HB2Q_MOUSE	P06342 mus musculu
36	52	23.5	268	1	HB2X_HUMAN	P05538 homo sapien
37	52	23.5	494	1	CPA4_MOUSE	P15392 mus musculu
38	52	23.5	494	1	CPA5_MOUSE	P20852 mus musculu
39	52	23.5	878	1	CPA5_ERWCA	P41513 erwinia car
40	51.5	23.3	434	1	PXR_HUMAN	O75469 homo sapien
41	51.5	23.3	656	1	HS7C_DROME	P29844 drosophila
42	51.5	23.3	928	1	DNL1_CANAL	P52496 candida alb
43	51	23.1	282	1	YHP0_YEAST	P38806 saccharomyc
44	51	23.1	333	1	PTX2_CHICK	O93385 gallus gall
45	51	23.1	379	1	Y671_CHLMO	O9pk02 chlamydia m

## ALIGNMENTS

RESULT 1  
ID CLIP\_HUMAN STANDARD: PRT; 199 AA.

AC Q9NS71:  
15-JUN-2002 (rel. 41, Created)

DT 15-JUN-2002 (rel. 41, Last sequence update)

DE 15-JUN-2002 (rel. 41, Last annotation update)

DE CA11 protein.

GN CA11.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]  
SEQUENCE FROM N.A.

RP TISSUE=Stomach;

RX MEDLINE=20296773; PubMed=10835488;

RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;

RT Isolation of two novel genes, down-regulated in gastric cancer.;

CC Jpn. J. Cancer Res. 91:459-463(2000).

CC TISSUE SPECIFICITY: Expressed in stomach. No expression is

CC detected in cancer tissue or gastric cancer cell lines.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC -----  
DB EMBL; AB039886; BAA92433.1; -

DR MIM; 606402; -

SQ SEQUENCE 199 AA; 21999 MW; C09988B9A138D7A CRC64;

Query Match 97.7%; Score 216; DB 1; Length 199;  
Best Local Similarity 97.6%; Pred. No. 5e-19;  
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKREVMPSIQSLDYLVEKKLQGGPGPPPKGL 42  
DB 92 KKTCTVHKMKREVMPSIQSLDYLVEKKLQGGPGPPPKGL 133  
RESULT 2  
ID CLIP\_MOUSE STANDARD: PRT; 184 AA.  
AC Q9CR36; Q9D7R7; Q9CR25;  
DT 15-JUN-2002 (rel. 41, Created)  
DT 15-JUN-2002 (rel. 41, Last sequence update)  
DT 15-JUN-2002 (rel. 41, Last annotation update)  
DE CA11 protein homolog.  
GN CA11.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana S.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Sadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schiml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoendach C., Seya T., Shibata Y., Storch K.F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlski S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
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 CC -----  
 DR EMBL: AK008990; BAB26010.1; -  
 DR EMBL: AK008622; BAB25784.1; -  
 DR EMBL: AK008641; BAB25801.1; -  
 DR EMBL: AK008647; BAB25805.1; -  
 DR EMBL: AK008722; BAB25856.1; -  
 DR EMBL: AK008745; BAB25872.1; -  
 DR EMBL: AK008933; BAB25975.1; -  
 DR EMBL: AK008956; BAB25988.1; -  
 DR EMBL: AK009145; BAB26103.1; -  
 DR EMBL: AK019050; BAB31525.1; -  
 DR MGD: MGI:193533; 220002K2R1K.  
 FT CONFLICT 113 113 P -> L (IN REF. 1: BAB26103).  
 FT SEQUENCE 184 AA; 20134 MW; 288962F0404FFRAB CRC64;  
 SQ  
 Query Match 68.3%; Score 151; DB 1; Length 184;  
 Best Local Similarity 66.7%; Pred. No. 3e-11;  
 Matches 28; Conservative 6; Mismatches 6; Indels 2; Gaps 1;  
 Oy 1 KKTCTVHKMKKEVPSIQSDATVKEKKLGKGGCGPPPKL 42  
 Db 78 KKCTIVHRMKNDAMPISLQDDPTMYKEOK--GKGPGAPKDL 117  
 KPCG\_BOVIN STANDARD; PRT; 682 AA.  
 AC P05128;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Protein kinase C, gamma type (EC 2.7.1.1-) (PKC-gamma) (Fragment).  
 GN PRCG.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.

MEDLINE=86289426; PubMed=3755548;  
 RA Coussens L., Parker P.J., Rhee L., Yang-Feng T.L., Chen E.,  
 RA Waterfield M.D., Francke U., Ullrich A.;  
 RT "Multiple, distinct forms of bovine and human protein kinase C  
 RT suggest diversity in cellular signaling pathways."  
 RL Science 233:859-866(1986).  
 RN [2]  
 RP REVIEW.  
 RX MEDLINE=88318921; PubMed=3045562;  
 RA Nishizuka Y.;  
 RT "The molecular heterogeneity of protein kinase C and its implications  
 RT for cellular regulation."  
 RL Nature 334:661-665(1988).  
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 CC -----  
 DR EMBL: M13976; AAA30704.1; -  
 DR PIR: C24664; KIROGC.  
 DR HSSP: P05697; ITBN.  
 DR InterPro: IPR000008; C2.  
 DR InterPro: IPR002219; DAG\_PE-bind.  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR000961; Pkinase\_C.  
 DR InterPro: IPR002290; ser\_thr\_Pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00130; DAG\_PE-bind; 2.  
 DR Pfam: PF00168; C2; 1.  
 DR Pfam: PF00433; pkinase\_C; 1.  
 DR ProDom: PD000001; Euk\_Pkinase; 1.  
 DR SMART: SM00109; C1; 2.  
 DR SMART: SM00239; C2; 1.  
 DR SMART: SM00133; S\_TK\_X; 1.  
 DR PROSITE: PS00499; C2\_DOMAIN\_1; 1.  
 DR PROSITE: PS50004; C2\_DOMAIN\_2; 1.  
 DR PROSITE: PS00479; DAG\_PE\_BIND\_DOM\_1; 2.  
 DR PROSITE: PS50081; DAG\_PE\_BIND\_DOM\_2; 2.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Calcium-binding; Repeat; ATP-binding; Transferase;  
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;  
 KW Phosphorylation.  
 FT NON\_TER 1  
 FT DOMAIN 21 70 PHORBOL-ESTER AND DAG BINDING 1.  
 FT DOMAIN 86 135 PHORBOL-ESTER AND DAG BINDING 2.  
 FT DOMAIN 155 245 C2 DOMAIN.  
 FT DOMAIN 336 599 PROTEIN KINASE.  
 FT NP\_BIND 342 350 ATP (BY SIMILARITY).  
 FT BINDING 365 365 ATP (BY SIMILARITY).  
 FT ACT\_SITE 465 465 BY SIMILARITY.  
 FT MOD\_RES 633 633 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 640 640 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT SEQUENCE 682 AA; 77156 MW; 20392D11188C7A1C CRC64;  
 Query Match 26.9%; Score 59.5; DB 1; Length 682;  
 Best Local Similarity 39.4%; Pred. No. 12;





	DR	EMBL:	M55417;	AAA4878.1;	-	
	DR	EMBL:	X67129;	CAA47608.1;	-	
	DR	EMBL:	I28035;	AAA39939.1;	-	
	DR	PIR:	A05105;	KIRTGC.		
	PIR:	S29620;	S29620.			
	DR	PIR:	JN0548;	JN0548.		
	DR	PDB:	ITBN;	29-APR-98.		
	DR	PDB:	LTBO;	29-APR-98.		
	DR	MGD:	GGI:97597;	P-kcc.		
	DR	InterPro:	IPRO000008;	C2.		
	DR	InterPro:	IPRO002219;	DAG_pe-bind.		
	DR	InterPro:	IPRO007719;	Euk_pkinase.		
	DR	InterPro:	IPRO009611;	pkinase_C.		
	DR	InterPro:	IPRO002290;	Ser_thr_pkinase.		
	DR	pfam:	PF00069;	pkinase; 1.		
	DR	pfam:	PF00130;	DAG-pe-bind; 2.		
	DR	pfam:	PF00168;	C2_1.		
	DR	pfam:	PF00433;	pkinase-C; 1.		
	DR	PRINTS:	PR00360;	C2DOMAIN.		
	DR	PRINTS:	PRO00008;	DAGEPDOMAIN.		
	DR	ProDom:	PD000001;	Euk_pkinase; 1.		
	DR	SMART:	SMO0109;	C1; 2.		
	DR	SMART:	SMO0239;	C2; 1.		
	DR	SMART:	SMO0133;	S_TK_X; 1.		
	DR	SMART:	SMO0220;	S_TKC; 1.		
	DR	PROSITE:	PS00499;	C2_DOMAIN_1; 1.		
	- DR	PROSITE:	PS00004;	C2_DOMAIN_2; 1.		
	DR	PROSITE:	PS00479;	DAG_PE_BIND_DOM_1; 2.		
	DR	PROSITE:	PS50081;	DAG_PE_BIND_DOM_2; 2.		
	DR	PROSITE:	PS00107;	PROTEIN_KINASE_ATP; 1.		
	DK	PROSITE:	PS50011;	PROTEIN_KINASE_ATP; 1.		
	DR	PROSITE:	PS00108;	PROTEIN_KINASE_STY; 1.		
	KW	Calcium-binding; Repeat; ATP-binding; Transferase;				
	KM	Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;				
	KN	Phosphorylation; 3d-structure.				
	FT	DOMAIN	36	85		
	ET	DOMAIN	101	150		
	ET	DOMAIN	170	260		
	FT	NP_BIND	351	614		
	FT	BINDING	357	365		
	FT	ACT_SITE	380	380		
	FT	MOD_RES	480	480		
	FT	MOD_RES	648	648		
	FT	MOD_RES	655	655		
	SO	SEQUENCE	697 AA;	78357 MW;	E6E2F7A3B93042FF CRC64;	
Oy		Query Match		26.9%;	Score 59.5;	DB 1; Length 697;
		Best Local Similarity		39.4%;	Pred. No. 12;	
		Matches 13,	Conservative 7;	Mismatches 10;	Indels 3;	Gaps 1
Db		9 MKKEYMPISQSDALVKEKK---LOGKGGGGPP 38 :: :: :: :: :: :: :: :: :: :: :: ::  382 LKKDIIVODDDVDCTLVKERVLALCGRGGRP 414				
		RESULT 6				
		KPCG_RABIT				
AC		ID KPCG_RABIT STANDARD:	PRT;	697 AA.		
DT		01-JUL-1989 (Rel. 11, Created)				
DT		01-JUL-1989 (Rel. 11, Last sequence update)				
DE		15-JUN-2002 (Rel. 41, Last annotation update)				
DE		Protein Kinase C, gamma type (EC 2.7.1.1-) (PKC-gamma) (PKC-delta).				
GN		KRCOG.				
OS		Oryctolagus cuniculus (Rabbit).				
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC		Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX		NCBII TaxID=9986;				
RN		[1]				
RP		SEQUENCE FROM N.A.				
RX		MEDLINE=88241036; PubMed=2837282;				
RA		Ohno S., Kawasaki H., Konno Y., Inagaki M., Hidaka H., Suzuki K.;				
TA		"A fourth type of rabbit protein kinase C."				

RL Biochemistry 27:2083-2087(1988).  
 CC -1- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,  
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.  
 CC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN  
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS  
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.  
 CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG  
 CC BINDING DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC PKC SUBFAMILY.  
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 CC -----  
 CC EMBL: M19338; AAA31449.1; -  
 DR PIR: A28708; KIRBGC.  
 DR HSSP: P05697; ITBN.  
 DR InterPro: IPR000008; C2.  
 DR InterPro: IPR002219; DAG\_PE-bind.  
 DR InterPro: IPR000719; Euk.pkinase.  
 DR InterPro: IPR000961; Pkinase\_C.  
 DR InterPro: IPR002290; Ser\_Thr\_pkinase.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR Pfam: PF00130; DAG\_PE-bind; 2.  
 DR Pfam: PF00168; C2; 1.  
 DR Pfam: PF00433; Pkinase\_C; 1.  
 DR PRINTS: PRO00360; C2DOMAIN.  
 DR PRINTS: PRO00008; DAGPEDOMAIN.  
 DR ProDom: PD000001; Euk.pkinase; 1.  
 DR SMART: SM00109; C1; 2.  
 DR SMART: SM00239; C2; 1.  
 DR SMART: SM00133; S\_TK\_X; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR PROSITE: PS00499; C2.DOMAIN.1; 1.  
 DR PROSITE: PS50004; C2.DOMAIN.2; 1.  
 DR PROSITE: PS00479; DAG\_PE\_BIND\_DOM.1; 2.  
 DR PROSITE: PS50081; DAG\_PE\_BIND\_DOM.2; 2.  
 DR PROSITE: PS50017; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR Calcium-binding; Repeat: ATP-binding; Transferase;  
 KW Calcium-binding; Repeat: ATP-binding; Transferase;  
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;  
 KW Phosphorylation.  
 FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.  
 FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.  
 FT DOMAIN 170 260 C2 DOMAIN.  
 FT DOMAIN 351 614 PROTEIN KINASE.  
 FT NP\_BIND 357 365 ATP (BY SIMILARITY).  
 FT BINDING 380 380 ATP (BY SIMILARITY).  
 FT ACT\_SITE 480 480 BY SIMILARITY.  
 FT MOD\_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 SQ SEQUENCE 697 AA; 78371 MW; 925D22221F7855BF C6C64;  
 Query Match 26.9%; Score 59.5; DB 1; Length 697;  
 Best Local Similarity 39.4%; Pred. No. 12;  
 Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1;  
 Oy 9 MKKEVMPSTOSLDALVKEK---LOGKGFPGPP 38  
 Db 382 LKKDVIWQDDVDVCTLVERKVALGGGPGGRP 414  
 RESULT 7  
 TOP3\_CAEEL STANDARD; PRT; 759 AA.  
 ID TOP3\_CAEEL  
 AC 061660; Q9U223;

DT 30-MAY-2000 (rel. 39, Created)  
 DT 30-MAY-2000 (rel. 39, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE DNA topoisomerase III (EC 5.99.1.2).  
 GN TOP-3 OR Y56A3A.27.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RC SPRAIN-Bristol N2;  
 RA Kim Y.-C., Koo H.-S.;  
 RT "cDNA cloning and overexpression of Caenorhabditis elegans DNA  
 RL topoisomerase III.";  
 RL submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.  
 RN 121  
 RP SEQUENCE FROM N.A.  
 RC SPRAIN-Bristol N2;  
 RA Matthews L.;  
 RL submitted (Jan-1999) to the EMBL/GenBank/DBJ databases.  
 RA [3]  
 RN REVISIONS.  
 RA Durbin R.;  
 RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded  
 CC DNA, followed by passage and rejoining.  
 CC -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE  
 CC FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AF057032; AAC13567.1; -  
 DR EMBL: AL132860; CAB60518.2; -  
 DR WormBep: Y56A3A.27; CE28138.  
 DR InterPro: IPR002936; DNAPrim\_toprim.  
 DR InterPro: IPR003601; DNATopI\_ATP\_bind.  
 DR InterPro: IPR003602; DNATopI\_DNA\_bind.  
 DR InterPro: IPR000380; ProK\_topoisomerase.  
 DR Pfam: PF01131; Topoisom\_bac; 1.  
 DR Pfam: PF01751; Toprim; 1.  
 DR PRINTS: PRO00417; PRTPISMRASE1.  
 DR SMART: SM00437; TOP1AC; 1.  
 DR SMART: SM00436; TOP1BC; 1.  
 DR SMART: SM00493; TOP1B; 1.  
 DR PROSITE: PS00396; TOPOISOMERASE\_I\_PROK; 1.  
 KW Isomerase; Topoisomerase; DNA-binding.  
 FT ACT\_SITE 334 334 DNA CLEAVAGE (BY SIMILARITY).  
 SQ SEQUENCE 759 AA; 85438 MW; 3D862412D72946BD C6C64;  
 Query Match 26.7%; Score 59; DB 1; Length 759;  
 Best Local Similarity 26.2%; Pred. No. 15;  
 Matches 17; Conservative 7; Mismatches 17; Indels 24; Gaps 2;  
 Oy 1 KKTCTVHKMKKEVMPSTOSLDALVKEKLOGKGFPGPP----- 37  
 Db 566 KEICDGRKQKQEVLDQIGKYRAIFVESERRKIGVLSQSLQRYLDKNNQAGGPGGPGGG 625  
 Oy 38 -PPKG 41  
 Db 626 GPPKG 630  
 RESULT 8  
 FTSH\_AOUAE STANDARD; PRT; 634 AA.  
 ID FTSH\_AOUAE  
 AC 067077;

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DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Probable large tegument protein.
GN 64 OR EERP2.
OS Herpesvirus saimiri (strain 11).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10383;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333688; PubMed=1321287;
RA Albrecht J.-C., Nicolas J., Biller D., Cameron K.R., Biesinger B.,
RA Newman C., Wiltmann S., Craxton M.A., Coleman H., Fleckenstein B.,
RA Honess R.W.;
RT "Primary structure of the herpesvirus saimiri genome.";
RT J. Virol. 66:5047-5058(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92230228; PubMed=1314457;
RA Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;
RT "Analysis of nucleotide sequence of the rightmost 43 kbp of
RT herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
RT organization between HVS and Epstein-Barr virus.";
RT Virology 188:296-310(1992).
CC CC
CC -1- FUNCTION: TEGUMENT PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
CC -1- UL37, UL38, UL39, UL40, UL41, UL42, UL43, UL44, UL45,
CC -1- UL46, UL47, UL48, UL49, UL50, UL51, UL52, UL53, UL54,
CC -1- UL55, UL56, UL57, UL58, UL59, UL60, UL61, UL62, UL63, UL64,
CC -1- UL65, UL66, UL67, UL68, UL69, UL70, UL71, UL72, UL73, UL74,
CC -1- UL75, UL76, UL77, UL78, UL79, UL80, UL81, UL82, UL83, UL84,
CC -1- UL85, UL86, UL87, UL88, UL89, UL90, UL91, UL92, UL93, UL94,
CC -1- UL95, UL96, UL97, UL98, UL99, UL100, UL101, UL102, UL103, UL104,
CC -1- UL105, UL106, UL107, UL108, UL109, UL110, UL111, UL112, UL113,
CC -1- UL114, UL115, UL116, UL117, UL118, UL119, UL120, UL121, UL122,
CC -1- UL123, UL124, UL125, UL126, UL127, UL128, UL129, UL130, UL131,
CC -1- UL132, UL133, UL134, UL135, UL136, UL137, UL138, UL139, UL140,
CC -1- UL141, UL142, UL143, UL144, UL145, UL146, UL147, UL148, UL149,
CC -1- UL150, UL151, UL152, UL153, UL154, UL155, UL156, UL157, UL158,
CC -1- UL159, UL160, UL161, UL162, UL163, UL164, UL165, UL166, UL167,
CC -1- UL168, UL169, UL170, UL171, UL172, UL173, UL174, UL175, UL176,
CC -1- UL177, UL178, UL179, UL180, UL181, UL182, UL183, UL184, UL185,
CC -1- UL186, UL187, UL188, UL189, UL190, UL191, UL192, UL193, UL194,
CC -1- UL195, UL196, UL197, UL198, UL199, UL200, UL201, UL202, UL203,
CC -1- UL204, UL205, UL206, UL207, UL208, UL209, UL210, UL211, UL212,
CC -1- UL213, UL214, UL215, UL216, UL217, UL218, UL219, UL220, UL221,
CC -1- UL222, UL223, UL224, UL225, UL226, UL227, UL228, UL229, UL230,
CC -1- UL231, UL232, UL233, UL234, UL235, UL236, UL237, UL238, UL239,
CC -1- UL240, UL241, UL242, UL243, UL244, UL245, UL246, UL247, UL248,
CC -1- UL249, UL250, UL251, UL252, UL253, UL254, UL255, UL256, UL257,
CC -1- UL258, UL259, UL260, UL261, UL262, UL263, UL264, UL265, UL266,
CC -1- UL267, UL268, UL269, UL270, UL271, UL272, UL273, UL274, UL275,
CC -1- UL276, UL277, UL278, UL279, UL280, UL281, UL282, UL283, UL284,
CC -1- UL285, UL286, UL287, UL288, UL289, UL290, UL291, UL292, UL293,
CC -1- UL294, UL295, UL296, UL297, UL298, UL299, UL300, UL301, UL302,
CC -1- UL303, UL304, UL305, UL306, UL307, UL308, UL309, UL310, UL311,
CC -1- UL312, UL313, UL314, UL315, UL316, UL317, UL318, UL319, UL320,
CC -1- UL321, UL322, UL323, UL324, UL325, UL326, UL327, UL328, UL329,
CC -1- UL330, UL331, UL332, UL333, UL334, UL335, UL336, UL337, UL338,
CC -1- UL339, UL340, UL341, UL342, UL343, UL344, UL345, UL346, UL347,
CC -1- UL348, UL349, UL350, UL351, UL352, UL353, UL354, UL355, UL356,
CC -1- UL357, UL358, UL359, UL360, UL361, UL362, UL363, UL364, UL365,
CC -1- UL366, UL367, UL368, UL369, UL370, UL371, UL372, UL373, UL374,
CC -1- UL375, UL376, UL377, UL378, UL379, UL380, UL381, UL382, UL383,
CC -1- UL384, UL385, UL386, UL387, UL388, UL389, UL390, UL391, UL392,
CC -1- UL393, UL394, UL395, UL396, UL397, UL398, UL399, UL400, UL401,
CC -1- UL402, UL403, UL404, UL405, UL406, UL407, UL408, UL409, UL410,
CC -1- UL411, UL412, UL413, UL414, UL415, UL416, UL417, UL418, UL419,
CC -1- UL420, UL421, UL422, UL423, UL424, UL425, UL426, UL427, UL428,
CC -1- UL429, UL430, UL431, UL432, UL433, UL434, UL435, UL436, UL437,
CC -1- UL438, UL439, UL440, UL441, UL442, UL443, UL444, UL445, UL446,
CC -1- UL447, UL448, UL449, UL450, UL451, UL452, UL453, UL454, UL455,
CC -1- UL456, UL457, UL458, UL459, UL460, UL461, UL462, UL463, UL464,
CC -1- UL465, UL466, UL467, UL468, UL469, UL470, UL471, UL472, UL473,
CC -1- UL474, UL475, UL476, UL477, UL478, UL479, UL480, UL481, UL482,
CC -1- UL483, UL484, UL485, UL486, UL487, UL488, UL489, UL490, UL491,
CC -1- UL492, UL493, UL494, UL495, UL496, UL497, UL498, UL499, UL500,
CC -1- UL501, UL502, UL503, UL504, UL505, UL506, UL507, UL508, UL509,
CC -1- UL510, UL511, UL512, UL513, UL514, UL515, UL516, UL517, UL518,
CC -1- UL519, UL520, UL521, UL522, UL523, UL524, UL525, UL526, UL527,
CC -1- UL528, UL529, UL530, UL531, UL532, UL533, UL534, UL535, UL536,
CC -1- UL537, UL538, UL539, UL540, UL541, UL542, UL543, UL544, UL545,
CC -1- UL546, UL547, UL548, UL549, UL550, UL551, UL552, UL553, UL554,
CC -1- UL555, UL556, UL557, UL558, UL559, UL560, UL561, UL562, UL563,
CC -1- UL564, UL565, UL566, UL567, UL568, UL569, UL570, UL571, UL572,
CC -1- UL573, UL574, UL575, UL576, UL577, UL578, UL579, UL580, UL581,
CC -1- UL582, UL583, UL584, UL585, UL586, UL587, UL588, UL589, UL590,
CC -1- UL591, UL592, UL593, UL594, UL595, UL596, UL597, UL598, UL599,
CC -1- UL600, UL601, UL602, UL603, UL604, UL605, UL606, UL607, UL608,
CC -1- UL609, UL610, UL611, UL612, UL613, UL614, UL615, UL616, UL617,
CC -1- UL618, UL619, UL620, UL621, UL622, UL623, UL624, UL625, UL626,
CC -1- UL627, UL628, UL629, UL630, UL631, UL632, UL633, UL634, UL635,
CC -1- UL636, UL637, UL638, UL639, UL640, UL641, UL642, UL643, UL644,
CC -1- UL645, UL646, UL647, UL648, UL649, UL650, UL651, UL652, UL653,
CC -1- UL654, UL655, UL656, UL657, UL658, UL659, UL660, UL661, UL662,
CC -1- UL663, UL664, UL665, UL666, UL667, UL668, UL669, UL670, UL671,
CC -1- UL672, UL673, UL674, UL675, UL676, UL677, UL678, UL679, UL680,
CC -1- UL681, UL682, UL683, UL684, UL685, UL686, UL687, UL688, UL689,
CC -1- UL690, UL691, UL692, UL693, UL694, UL695, UL696, UL697, UL698,
CC -1- UL699, UL700, UL701, UL702, UL703, UL704, UL705, UL706, UL707,
CC -1- UL708, UL709, UL710, UL7
```

CC LENGTH, AND TEMPERATURE COMPENSATION. BEHAVES AS A NEGATIVE  
CC ELEMENT IN CIRCADIAN TRANSCRIPTIONAL LOOP.  
CC - SIMILARITY: BELONGS TO THE PRO FAMILY.  
CC -----  
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CC -----  
DR EMBL: L14467; AAA20825.1; -  
KW Biological rhythms; Transcription regulation; Nuclear protein.  
FT DOMAIN 250 256 POLY-SER.  
FT DOMAIN 569 573 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT DOMAIN 868 894 ASP/GLU-RICH (ACIDIC).  
SQ SEQUENCE 997 AA; 109056 MW; 2581DD2C62DFF93 CRC64;  
Query Match 25.8%; Score 57; DB 1; Length 997;  
Best Local Similarity 32.1%; Pred. No. 34;  
Matches 17; Conservative 10; Mismatches 12; Indels 14; Gaps 3;  
QY 1 KKTCTIVHKKMK-----EVMPSIOSLD-ALYKEKKLGKGGCGPPPKG 41  
Db 320 KKKLVARLEQLFTGKISGRNMORIPSPMDALVSEGTIM--APRPEPEG 370  
RESULT 11  
DCTR\_BACHD STANDARD; PRT; 230 AA.  
AC Q9K998;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Probable C4-dicarboxylate response regulator dctr.  
GN DCTR OR BH2751.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RA MEDLINE=20512582; Pubmed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis."  
RL Nucleic Acids Res. 28:4317-4331(2000).  
CC - FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.  
CC - ESSENTIAL FOR EXPRESSION OF DCTR (BY SIMILARITY).  
CC - SUBCELLULAR LOCATION: Cytoplasmic (potential).  
CC - PTM: PHOSPHORYLATED BY DCTS (BY SIMILARITY).  
CC - SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.  
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CC -----  
DR EMBL: AP001516; BAB06470.1; -  
DR HSSP: P10957; IRL.  
DR InterPro: IPR001789; Response\_reg.  
DR Pfam: PF00072; response\_reg.1.  
DR ProDom: PD000039; Response\_reg.1.  
DR SMART: SM00448; REC.1.  
DR PROSITE: PS00110; RESPONSE\_REGULATORY.1.  
KW Sensory transduction; Transcription regulation; DNA-binding;  
KW Activator; Phosphorylation; Complete proteome.

FT DOMAIN 8 124 RESPONSE REGULATORY.  
FT MOD\_RES 59 59 PHOSPHORYLATION (BY SIMILARITY).  
FT DNA\_BIND 183 209 H-T-H MOTIF (POTENTIAL).  
SQ SEQUENCE 230 AA; 26376 MW; 06F65F46F57D40 CRC64;  
Query Match 24.9%; Score 55; DB 1; Length 230;  
Best Local Similarity 42.9%; Pred. No. 13;  
Matches 15; Conservative 5; Mismatches 13; Indels 2; Gaps 1;  
QY 8 KMKKEVMSIOSLDALYKEKKLGKGGCGPPKGL 42  
Db 129 KMKKEAEISQDSLDLMEIKOKAQAN--MDLPLKGL 161  
RESULT 12  
PKR\_MOUSE STANDARD; PRT; 431 AA.  
AC O54915;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Orphan nuclear receptor PKR (Pregnane X receptor).  
GN NR112 OR PKR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE=Liver;  
RA MEDLINE=98149345; Pubmed=9489701;  
RA Klierer S.A., Moore J.T., Wade L., Staudinger J.L., Watson M.A.,  
RA Jones S.A., McKee D.D., Oliver B.B., Willson T.M., Zetterstrom R.H.,  
RA Perlman T., Lehmann J.M.;  
RT "An orphan nuclear receptor activated by pregnanes defines a novel  
RT steroid signaling pathway."  
RL Cell 92:73-82(1998).  
CC - FUNCTION: ORPHAN RECEPTOR. ITS NATURAL LIGAND IS PROBABLY  
CC PREGNANE. BINDS TO A RESPONSE ELEMENT IN CYP3A GENES PROMOTER.  
CC - SUBUNIT: FORMS A HETERODIMER WITH PKR.  
CC - SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1/PKR.1 (SHOWN HERE) AND  
CC 2/PKR.2; ARE PRODUCED BY NATURALLY OCCURRING STEROIDS SUCH AS  
CC PREGNENOLONE AND PROGESTERONE, SYNTHETIC GLUCOCORTICOIDS AND  
CC ANTIGLUCOCORTICOIDS AND 16-ALPHA-CAROTRILE (PCN).  
CC - SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
CC - NRI SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL: AF031814; AAC39964.1; -  
DR HSSP: O75469; IILG.  
DR TRANSFAC: T04618; -  
DR TRANSFAC: T04619; -  
DR MGD: MGI:1337040; Nr112.  
DR InterPro: IPR000536; Hormone\_rec\_11g.  
DR InterPro: IPR001723; Scdhnmu\_receptor.  
DR InterPro: IPR001628; ZnF\_C4steroid.  
DR Pfam: PF00104; hormone\_rec.1.  
DR Pfam: PF00105; zf-C4; 1.  
DR PRINTS: PR00047; STRODHOMNER.  
DR PRINTS: PR00047; STRODIFINGER.  
DR ProDom: PD000035; ZnF\_C4steroid.1.  
DR SMART: SM00430; HOL1.1.  
DR SMART: SM00399; ZnF\_C4; 1.  
DR PROSITE: PS00031; NUCLEAR\_RECEPTOR.1.

KW Receptor: Transcription regulation; DNA-binding; Nuclear protein;  
 FT Zinc-finger; Alternative splicing.  
 FT DNA\_BIND 38 104 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_FING 38 58 C4-TYPE.  
 FT ZN\_FING 74 99 C4-TYPE.  
 FT DOMAIN 105 201 HINGE.  
 FT DOMAIN 202 431 LIGAND-BINDING.  
 FT VARSPLIC 171 211 MISSING (IN ISOFORM 2).  
 SQ SEQUENCE 431 AA: 49567 MW: F592AF91F689329E CRC64;

Query Match 24.9%; Score 55; DB 1; Length 431;  
 Best Local Similarity 34.1%; Pred. No. 25;  
 Matches 14; Conservative 9; Mismatches 12; Indels 6; Gaps 2;

OY 2 KTCIVHKKKEVWPS--IQSLDALYKER--KLOGKGP 36  
 Db 97 KCLGSGMKKEMIMSDAAYQORALLIKRKREKIEAPP 137

## RESULT 13

ID PKR\_RAT STANDARD; PRT; 431 AA.

AC 09RIAT;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Orphan nuclear receptor PKR (Pregnane X receptor).  
 GN NR112 OR PKR.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=99345883; PubMed=10415106;  
 RA Zhang H., Lecuylse E., Liu L., Hu M., Matoney L., Zhu W., Yan B.;  
 RT "Rat pregnane X receptor: molecular cloning, tissue distribution, and  
 xenobiotic regulation.";  
 RT Arch. Biochem. Biophys. 368:14-22(1999).  
 CC -1- FUNCTION: ORPHAN RECEPTOR. ITS NATURAL LIGAND IS PROBABLY  
 PREGNANE. BINDS TO A RESPONSE ELEMENT IN CYP3A GENES PROMOTER (BY  
 SIMILARITY).  
 CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 CC NRI SUBFAMILY.

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 CC -----  
 DR EMBL: AF151377; AAD47214.1; -;  
 DR HSSP: 075469; IILG.  
 DR TRANSFAC: T04629; -;  
 DR InterPro: IPR000536; Hormone\_rec.1lg.  
 DR InterPro: IPR001723; Stbhrm\_receptor.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF00104; hormone\_rec.1.  
 DR Pfam: PF00105; zt-C4.1.  
 DR PRINTS: PR00398; STRDHOMNER.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR ProDom: PD000035; Znf\_C4steroid.1.  
 DR SMART: SM00430; HOL1.1.  
 DR SMART: SM00399; ZNF\_C4.1.  
 DR PROSITE: PS00031; NUCLEAR\_RECEPTOR.1.  
 KW Receptor: Transcription regulation; DNA-binding; Nuclear protein;  
 FT Zinc-finger.  
 FT DNA\_BIND 38 104 NUCLEAR RECEPTOR-TYPE.

FT ZN\_FING 38 58 C4-TYPE.  
 FT ZN\_FING 74 99 C4-TYPE.  
 FT DOMAIN 105 201 HINGE.  
 FT DOMAIN 202 431 LIGAND-BINDING.  
 SQ SEQUENCE 431 AA: 49660 MW: 4B545F21F9439697 CRC64;

Query Match 24.9%; Score 55; DB 1; Length 431;  
 Best Local Similarity 34.1%; Pred. No. 25;  
 Matches 14; Conservative 9; Mismatches 12; Indels 6; Gaps 2;

OY 2 KTCIVHKKKEVWPS--IQSLDALYKER--KLOGKGP 36  
 Db 97 KCLGSGMKKEMIMSDAAYQORALLIKRKREKIEAPP 137

## RESULT 14

ID FES\_FSVST STANDARD; PRT; 477 AA.

AC P00543;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase transforming protein FES (EC 2.7.1.112).  
 GN V-FES.  
 OS Feline sarcoma virus (strain Snyder-Theilen).  
 OC Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.  
 OX NCBI\_TaxID=11780;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=83050963; PubMed=6183005;  
 RA Hampe A., Laprevote I., Galibert F., Fedele L.A., Sherr C.J.;  
 RT "Nucleotide sequences of feline retroviral oncogenes (v-fes) provide  
 RT evidence for a family of tyrosine-specific protein kinase genes.";  
 RT Cell 30:775-785(1982).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 tyrosine phosphate.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FES  
 POLYPEPTIDE.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FES/FPS  
 SUBFAMILY.

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 CC -----  
 DR EMBL: J02088; AAA43046.2; -;  
 DR PIR: A00652; TVAVCS.  
 DR HSSP: P11362; IFGK.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00017; SH2.1.  
 DR Pfam: PF00069; pkinase.1.  
 DR PRINTS: PR00401; SH2DOMAIN.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase.1.  
 DR ProDom: PD000093; SH2.1.  
 DR SMART: SM00252; SH2.1.  
 DR SMART: SM00219; TYRK.1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP.1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR.1.  
 DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM.1.  
 DR PROSITE: PS00001; SH2.1.  
 KW Polyprotein; Tyrosine-protein kinase; Oncogene; Transferase;  
 FT ATP-binding; Phosphorylation; SH2 domain.  
 FT DOMAIN 115 204 PROTEIN KINASE.  
 FT DOMAIN 216 477 SH2.  
 FT NP\_BIND 222 230 ATP (BY SIMILARITY).

FT BINDING 245 245 ATP (BY SIMILARITY).  
 FT ACT\_SITE 338 338 BY SIMILARITY.  
 FT MOD\_RES 368 368 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 SO SEQUENCE 477 AA: 53756 MW: 887EDBAE7A3BE5 CRC64;  
 Query Match 24.7%; Score 54.5; DB 1; Length 477;  
 Best Local Similarity 37.2%; Pred. No. 32;  
 Matches 16; Conservative 7; Mismatches 7; Indels 13; Gaps 3;  
 QY 10 KKEVM-PSIOSLD-ALVKEKKLQK-----GGGPPP 39  
 Db 11 KKVLOBALQALVLCQAQKLAQRELLQAKLEQLGPGPPP 53  
 RESULT 15  
 FES\_FELCA STANDARD: PRT; 820 AA.  
 ID FES\_FELCA  
 AC P14238:  
 DT 01-JAN-1990 (rel. 13, Created)  
 DT 01-FEB-1996 (rel. 33, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112) (C-FES).  
 GN FES OR FPS.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxId=9685;  
 RN [1]  
 RM SEQUENCE FROM N.A.  
 RX MEDLINE=87198954; PubMed=3553615;  
 RA Roebroek A.J.M., Schaiken J.A., Onnekink C., Bloemers H.P.J.,  
 RA van de Ven W.J.M.,  
 RT "Structure of the feline c-fes/fps proto-oncogene: genesis of a  
 RT retroviral oncogene."  
 RL J. Virol. 61:2009-2016(1987).  
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FES/FPS  
 CC SUBFAMILY.  
 CC -1 SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 FCH DOMAIN.  
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 CC -----  
 DR EMBL: M16705: AAA30808.1;  
 DR EMBL: M16666: AAA30808.1; JOINED.  
 DR EMBL: M16667: AAA30808.1; JOINED.  
 DR EMBL: M16668: AAA30808.1; JOINED.  
 DR EMBL: M16669: AAA30808.1; JOINED.  
 DR EMBL: M16670: AAA30808.1; JOINED.  
 DR EMBL: M16671: AAA30808.1; JOINED.  
 DR EMBL: M16706: AAA30808.1; JOINED.  
 DR EMBL: M16672: AAA30808.1; JOINED.  
 DR EMBL: M16673: AAA30808.1; JOINED.  
 DR EMBL: M16674: AAA30808.1; JOINED.  
 DR EMBL: M16698: AAA30808.1; JOINED.  
 DR EMBL: M16700: AAA30808.1; JOINED.  
 DR EMBL: M16701: AAA30808.1; JOINED.  
 DR EMBL: M16702: AAA30808.1; JOINED.  
 DR EMBL: M16704: AAA30808.1; JOINED.  
 DR PIR: A27824: TYCTPF.  
 DR HSSP: P11362: IFCK.  
 DR InterPro: IPR001060; Cdc15\_Fes\_CIP4.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR01245; Tyr\_pkinase.  
 DR Pfam: PF00017; SH2; 1.

DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00611; FCH; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR ProDom: PD000093; SH2; 1.  
 DR SMART: SM00055; FCH; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00219; TYRKC; 1.  
 DR PROSITE: PS01073; FCH; 1.  
 DR PROSITE: PS0107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50001; SH2; 1.  
 KW Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;  
 KW Phosphorylation; SH2 domain.  
 FT DOMAIN 1 94 FCH.  
 FT DOMAIN 558 820 SH2.  
 FT DOMAIN 559 820 SH2.  
 FT ND\_BIND 565 573 ATP (BY SIMILARITY).  
 FT BINDING 588 588 ATP (BY SIMILARITY).  
 FT ACT\_SITE 681 681 BY SIMILARITY.  
 FT MOD\_RES 711 711 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 SO SEQUENCE 820 AA: 92974 MW: F3A52B750236834E CRC64;  
 Query Match 24.7%; Score 54.5; DB 1; Length 820;  
 Best Local Similarity 37.2%; Pred. No. 56;  
 Matches 16; Conservative 7; Mismatches 7; Indels 13; Gaps 3;  
 QY 10 KKEVM-PSIOSLD-ALVKEKKLQK-----GGGPPP 39  
 Db 354 KKVLOBALQALVLCQAQKLAQRELLQAKLEQLGPGPPP 396

Search completed: April 11, 2003, 16:11:57  
 Job time: 4.63322 secs





Mon Apr 14 14:01:23 2003

us-09-821-726a-13.rsp

Page 1

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 : Search time 10.8646 Seconds  
(without alignments)  
706.250 Million cell updates/sec

US-09-821-726a-13

Title: 994  
Perfect score: 1 MKPTTFVAGLGVFLAPALA.....YTTSLVIMIVDISFCGDTVEN 185  
Sequence:

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	984	99.0	199	1 CLIP_HUMAN	Q9ns71 homo sapien
2	629	63.3	184	1 CLIP_MOUSE	O9crl6 mus muscula
3	95.5	9.6	719	1 NRPI_YEAST	P32770 saccharomyc
4	91	9.2	623	1 PNT1_DROME	P51022 drosophila
5	91	9.2	718	1 PNT2_DROME	P51023 drosophila
6	84.5	8.5	189	1 YHCN_BACSU	P54598 bacillus su
7	82.5	8.3	858	1 CYAG_DICDI	Q03101 dictyosteli
8	82	8.2	220	1 NUOB_ECOLI	P33598 escherichia
9	81	8.1	666	1 MRKC_YEAST	P40002 saccharomyc
10	81	8.1	828	1 YEAT_KLEPN	P21647 klebsiella
11	80	8.0	695	1 DVL1_MOUSE	P51141 mus musculu
12	80	8.0	749	1 DVL1_RAT	P40957 rattus norv
13	80	8.0	954	1 MADI_YEAST	P29126 schizosacch
14	80	8.0	954	1 XNNA_MOUSE	O9pqr7 felis silve
15	79.5	8.0	535	1 ARSB_FELCA	P17442 saccharomyc
16	79	7.9	1178	1 PH81_YEAST	P27502 rice tungro
17	77.5	7.8	1341	1 Y178_YEAST	O910m0 mus musculu
18	77.5	7.8	1675	1 POL_RTBYP	P55152 macaca mula
19	77	7.7	2920	1 CLR2_MOUSE	O46192 clostridium
20	76.5	7.6	191	1 PSFC_MOUSE	P24164 saccharomyc
21	75.5	7.6	296	1 DPSD_CLOPA	Q52657 rickettsia
22	75.5	7.6	731	1 BAP1_YEAST	P18160 dictyosteli
23	75.5	7.6	2021	1 OMPA_RICCN	P47116 ureaplasma
24	75.5	7.6	1584	1 KYK1_DICDI	P36168 saccharomyc
25	75	7.5	457	1 Y162_UREPA	P22335 lycopersico
26	74.5	7.5	1195	1 PK76_YEAST	O04956 plasmodium
27	74.5	7.5	301	1 HSF2_LTCPE	P15848 homo sapien
28	74.5	7.4	1956	1 ATX1_PLAFA	P04931 plasmodium
29	74	7.4	533	1 ARSB_HUMAN	Q03825 saccharomyc
30	73.5	7.4	537	1 ARP_PLAFA	
31	73.5	7.4	758	1 YM38_YEAST	
32	73.5				
33	73.5				

RESULT 1	CLIP_HUMAN	STANDARD:	PRT:	199 AA.	ALIGNMENTS
AC	Q9NS71:				
DT	15-JUN-2002 (Rel. 41, Created)				
DT	15-JUN-2002 (Rel. 41, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	CALL protein.				
GN	CALL.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Stomach;				
RX	MEDLINE=20296773; PubMed=10835488;				
RA	Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;				
RT	Jpn. J. Cancer Res. 91:459-463(2000).				
RL	Jpn. J. Cancer Res. 91:459-463(2000).				
CC	-I- TISSUE SPECIFICITY: Expressed in stomach. No expression is				
CC	detected in cancer tissue or gastric cancer cell lines.				
CC	-I- This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
DR	EMBL; AB039886; BAA92433.1; -				
DR	MIM; 606402; -				
SO	SEQUENCE 199 AA; 21999 MW; C09988B9A1338D7A CRC64;				

Query Match	99.0%	Score 984:	DB 1:	Length 199:
Best Local Similarity	98.9%	Pred. No. 5.8e-84:		
Matches 183; Conservative		Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MKPTTFVAGLGVFLAPALANYNDVNDNNAGSGGQSVSYNNHNVANVNDNNNDMSW	60	
DB	15	MKPTTFVAGLGVFLAPALANYNDVNDNNAGSGGQSVSYNNHNVANVNDNNNDMSW	74	
QY	61	NSIMDYGNGFAATRLFOKKTCTYHKKKKKEMPSIOSLDAVYEKKIKLOGGPGGPKKLM	120	
DB	75	NSIMDYGNGFAATRLFOKKTCTYHKKKKKEMPSIOSLDAVYEKKIKLOGGPGGPKKLM	134	
QY	121	YVANNKXKDDLSKGGKNANNCRCIPTVMAEEMOBSLFFSYSTCTVTSVLMIVDISFCG	180	
DB	135	YVANNKXKDDLSKGGKNANNCRCIPTVMAEEMOBSLFFSYSTCTVTSVLMIVDISFCG	194	
QY	181	DTVEN 185		
DB	195	DTVEN 199		

## RESULT 2

C1IP\_MOUSE

ID C1IP\_MOUSE STANDARD: PRT: 184 AA.

AC 09CR36; 09D7K7; 09CT25;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE CAIL protein homolog.

GN CAIL

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN NCBI\_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;

RA MEDLINE=21085660; PubMed=11217851;

RA Kawai J Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,

RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schramm L.M., Stuhl F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.F.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmink U.,

RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

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CC EMBL: AK008990; BAB26010.1; -

CC EMBL: AK008622; BAB25784.1; -

CC EMBL: AK008641; BAB25801.1; -

CC EMBL: AK008647; BAB25801.1; -

CC EMBL: AK008722; BAB25856.1; -

CC EMBL: AK008745; BAB25872.1; -

CC EMBL: AK008933; BAB25975.1; -

CC EMBL: AK008956; BAB25988.1; -

CC EMBL: AK009145; BAB26103.1; -

CC EMBL: AK019050; BAB31525.1; -

CC MGD: MGI:191353; 220002K21Rik.

CC CONFLICT 113 113

CC SEQUENCE 184 AA; 20134 MW; 288982P040FFA8B CRC64;

SO Query Match

Best Local Similarity 63.3%; Score 629; DB 1; Length 184;

Matches 116; Conservative 25; Mismatches 40; Indels 4; Gaps 3;

Db 118 MVSVPNTRVEDNTRFPGKAGMCRGIPYVAEEIPGPNQIPLYSKKTATIDILTRNSFC 177

QY 180 GDTVE 184

Db 178 GTSVE 182

## RESULT 3

NRPI\_YEAST

ID NRPI\_YEAST STANDARD: PRT: 719 AA.

AC P32770; 012228;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Asparagine-rich protein (ARP protein).

GN NRPI OR ARP OR YDL167C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OX Saccharomycetales; Saccharomycetaceae; Saccharomyces.

RN NCBI\_TaxID=4932;

[1]

SEQUENCE FROM N.A.

RC STRAIN=AH22;

RA MEDLINE=93247548; PubMed=8483449;

RA Weiner E.P., Rao E., Brendel M.,

RA "Molecular structure and genetic regulation of SFA, a gene

RA responsible for resistance to formaldehyde in Saccharomyces

RA cerevisiae, and characterization of its protein product."

RT Mol. Genet. 237:351-358(1993).

RL

RP SEQUENCE FROM N.A.

RC STRAIN=5288c;

RA Pohl T.M.;

RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS.

CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).

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CC EMBL: X68020; CAA48159.1; -

CC EMBL: Z67750; CAA91579.1; -

CC EMBL: Z74215; CAA98741.1; -

CC PIR: S31139; S31139.

CC SCD: S0002326; NRPI.

CC InterPro: IPR000504; RNA\_rec\_mot.

CC InterPro: IPR001876; Znf\_RandBP.

CC Pfam: PF00064; znf\_RandBP. 2.

CC SMART: SM00360; RRM. 1.

CC SMART: SM00547; ZNF\_NBD. 2.

CC PROSITE: PS0102; RRM. 1.

CC PROSITE: PS0030; RRM\_RNP\_1; FALSE\_NBD.

CC PROSITE: PS01358; ZF\_RANBP2. 1; 2.

CC PROSITE: PS50199; ZF\_RANBP2. 2.

KW Nuclear protein; zinc-finger; RNA-binding; Repeat.

FT ZN\_FING 226 322 RNA-BINDING (RRM).

FT ZN\_FING 355 384 RANBP2-TYPE 1.

FT ZN\_FING 581 610 RANBP2-TYPE 2.

FT DOMAIN 480 564 ASN-RICH.

FT CONFLICT 493 493 I -&gt; N (IN REF. 1).

SO SEQUENCE 719 AA; 79299 MW; ADA9BC09FD562669 CRC64;

Query Match

Best Local Similarity 9.6%; Score 95.5; DB 1; Length 719;

Matches 40; Conservative 18; Mismatches 62; Indels 37; Gaps 5;



RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrell J.F., Aguayo A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.V., Benos P.V., Berman B.P., Bhanderi D., Bolshakov S.,  
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Genter A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Foster C., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Pollard D.R., Pacleb J.M., Reese M.G.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard D.R., Pacleb J.M., Reese M.G.,  
 RA Reineert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spieding A.C., Stapleton M., Strong R., Sun E.,  
 RA Strydom R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-T., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RT Science 287:2185-2195(2000).  
 RL [3]  
 RN SPROUCE OF 551-708 FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL  
 RP SPAGE.  
 RC STRAIN-Canton-S; TISSUE=Larva;  
 RX MEDLINE=92249640; PubMed=1577186;  
 RA Chen T., Bunting M., Karim F.D., Thummel C.S.;  
 RT "Isolation and characterization of five *Drosophila* genes that encode  
 RT an ets-related DNA binding domain.";  
 RT Dev. Biol. 151:176-191(1992).  
 RL -1- FUNCTION: REQUIRED FOR GLIAL-NEURONAL CELL INTERACTIONS AT THE  
 CC VENTRAL MIDLINE WHICH ARE NECESSARY FOR THE PROPER ELABORATION OF  
 CC COMMISSURES IN THE EMBRYONIC CNS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: P1 (AC P91022) AND P2 (SHOWN  
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A COMPLEX DYNAMIC PATTERN IN  
 CC EARLY EMBRYOS, INCLUDING THE MIDLINE AND MIDLINE GLIAL CELLS.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH LOWER  
 CC LEVELS DURING LARVAL DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: X69167; CA448917.1;  
 DR EMBL: AE003742; AAF56125.1;  
 DR EMBL: M88472; AAC34200.1;  
 DR HSSP: P14921; 2STT.  
 DR FlyBase: FBgn0003118; pnt.  
 DR InterPro: IPR000418; Ets.

DR InterPro: IPR002341; HSF-ETS.  
 DR InterPro: IPR003118; SAM\_PNT.  
 DR Pfam: PF00178; Ets; 1.  
 DR Pfam: PF02198; SAM\_PNT; 1.  
 DR PRINTS: PR00454; SAM\_PNT; 1.  
 DR SMART: SM00413; ETS; 1.  
 DR SMART: SM00251; SAM\_PNT; 1.  
 DR PROSITE: PS00345; ETS\_DOMAIN\_1; 1.  
 DR PROSITE: PS00346; ETS\_DOMAIN\_2; 1.  
 DR PROSITE: PS0061; ETS\_DOMAIN\_3; 1.  
 DR DNA-binding; Nuclear protein; Developmental protein;  
 KW Alternative splicing.  
 FT DOMAIN 166 250  
 FT 347  
 FT 359 362  
 FT 389 392  
 FT 405 415  
 FT 418 421  
 FT 481 484  
 FT 610 690  
 FT 133  
 FT 718 AA; 77683 MW; FDCAFDF0F4BCD69C5 CRC64;  
 SQ SEQUENCE  
 Query Match 9.2%; Score 91; DB 1; Length 718;  
 Best local Similarity 27.1%; Pred. No. 0.9;  
 Matches 38; Conservative 21; Mismatches 37; Indels 44; Gaps 8;

OY 15 LAPALANYINDVDDNNNGSGQSVYNNH-----NNAVNNNGGWSNIMDYGNCF 70  
 DB 365 LPPAVQOSN---NENNNTSSSTNNSSNNNNNGSSNNSSNNNNNNNNI-----NFM 417  
 OY 71 AATRIFFOKTCIVHKKKEVMTSISDLAYEKRLGKGGPGPKGLMYSVNPKYDD 130  
 DB 418 AAAATFQ-----HHLKE--PGTON-----GNIGYGGG-----SNSQNDPTD 453  
 OY 131 LSKFGKNINMCGIPTYMA 150  
 DB 454 LSSY-----GLPAHLA 464

RESULT 6  
 YHGN\_BACSU STANDARD; PRT; 189 AA.  
 AC P54598;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical lipoprotein yhcn precursor.  
 GN YHGN.  
 OS *Bacillus subtilis*.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=97124185; PubMed=8969498;  
 RA Noback M.A., Terpstra P., Holtsappell S., Venema G., Bron S.;  
 RT "A 22 kb DNA sequence in the *cspB-glpFKD* region at 75 degrees on the  
 RL *Bacillus subtilis* chromosome.";  
 RL Microbiology 142:3021-3026(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertoletti M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Borriello R., Boursier L., Brans A., Braun M., Brigelli S.C., Bron S.,  
 RA Broillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani U.J., Conerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Ertan K.D., Erington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Gallen N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,



```

RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Rodison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli k-12." ;
RL Electrophoresis 18:1259-1313(1997).
CC -I FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. DOES COUPLE THE REDOX REACTION TO PROTON
CC TRANSLLOCATION AND THUS CONSERVES THE REDOX ENERGY IN A PROTON
CC GRADIENT.
CC -I CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+ ) + ubiquinol.
CC CC -I COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
CC CC -SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS.
CC CC -SIMILARITY: BELONGS TO THE COMPLEX I 20 kDa SUBUNIT FAMILY.
CC CC -CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMEShift IN POSITION 89.
-----
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-----
DR EMBL, X68301; CAAB48361.1; .
DR EMBL; AE000318; AAC75347.1; .
DR EMBL; D90860; BAA16122.1; ALT_FRAME.
DR EMBL; D90860; BAA16121.1; ALT_FRAME.
DR EMBL; AE005461; BAB57416.1; .
DR EMBL; AP002561; BAB56594.1; .
DR PIR; S37059; S37059.
DR PIR; S38311; S38311.
DR SWISS-2DPAGE; P33598; COLI.
DR EcogGene; EG12083; nuob.
DR InterPro: IPRO002096; cplx1_20kda.
DR Pfam; PF01058; oxidored_gq_1.
DR ProSITE; PS01150; COMPLEX1_20K; 1.
KW Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; 4Fe-4S;
Complete proteome.
FT METAL 63 63 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 64 64 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 129 129 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 158 158 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT CONFILCT 71 71 S > L (IN REF. 1 ).
SQ SEQUENCE 220 AA; 25056 MW; BBED6268505938B0 CRC64;

Query Match      8.2%; Score 82; DB 1; Length 220;
Best Local Similarity 18.4%; Pred. No. 1.5;
Matches   33; Conservative    25; Mismatches   47; Indels   74; Gaps       7;

QY     24 IDVDDNNAGSGGQSIV-----SYNNEHHVANVDNNNGDSNSIMDGNGFAATRLF 76
DY          :|:::         |:::        |||||         |: 
Db      8 IDPMNKVPYLQKEITVDLEQEVENKNVMGKLMDVNMGRKSNIMPYNFGLSG---- 63
QY     77 QKTGTCHAKMKKKEMPSIQSIDALVKRKLLKGKPGCGPPRGGLMYSVNPKNVDDLSEFKG 136
DY          |            |:::         |:::         |:::| 
Db      64 -----CYVSPTA-----EAWTSFTA-----VHDVARFG- 82
QY     137 NIAMNCRCIPTMYAEEMGEASLFEGSGTCYTTSV-----LTWIDISFCDDT 182
DY          |::|           ::|:||:|         |:::|         |::: 
Db      83 --AVFLRASP-----ROADLMVVAGIGCFPKMAPIVIQRLLYDQMLEDPRKVVISMGACANS 132


RESULT 9
YEAST_YEAST STANDARD; PRt; 666 AA.
AC PA0002;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 72.5 kDa protein in GCN4-WBP1 intergenic region. YEL007M.
```

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-----
CC      EMBL: M55912; AAA25095.1; -.
DR      PIR: D39142; D39142
DR      InterPro: IPR000015; FimB_usher.
DR      Pfam: PF00577; Usher_1.
DR      PROSITE: PS01151; FIMBRIAL_USHER_1.
DR      Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT      SIGNAL          1      18      POTENTIAL.
FT      CHAIN           19      828      OUTER MEMBRANE USHER PROTEIN MKKC.
FT      DISULFID        813      827      POTENTIAL.
SQ      SEQUENCE       828 AA; 91049 MW; B30EDF5798249FC9 CRC64;

Query Match              8.1%, Score 81; DB 1; Length 828;
Best Local Similarity    24.3%, Pred. No. 9;
Matches   35; Conservative 18; Mismatches 69; Indels 22; Gaps 6;

OY      20 ANYNIDVN---DDNNACSG-QQSVSYVNHENVA-NVDNNGNDMSNSIWDYGNGFAATR 74
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      596 ASSQIGVNCSDISENNLNVGVSTTATGQHDAVLNCGSYRTPWTLNCSOEGYRSG 655
         :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      75 LFQKTCIVHKMKKEVMPISIQSLDALVKKKIKLG-KGPCGP-----PKGLMYS 122
         :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      656 VCASGTFLHGHGVFPSPETGPTMALIEAKDAGVMLPSPGTRIDSNGYALLPYLRPFR 715
         :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      123 VNPKNYD-----DLSEFGKNIAM 141
         :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      716 INSVETDPKGSNDVAFGSTVAQV 739
         :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11
DVLL_MOUSE
ID      DVLL_MOUSE      STANDARD;      PRT;      695 AA.
AC      P51141; O60868;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
DE      (DSH homolog 1).
GN      DVL1 OR DVL.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=Brain;
RX      MEDLINE=95046919; PubMed=7958461;
RX      Susman D.J., Klingensmith J., Salinas P., Adams P.S., Nusse R.,
RA      Persimon N.;
RA      "Isolation and characterization of a mouse homolog of the Drosophila
RT      segment polarity gene dishevelled.";
RL      Dev. Biol. 166:73-86(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RX      MEDLINE=96232916; PubMed=9132266;
RX      Lijam N., Susman D.J.;
RA      "Organization and promoter analysis of the mouse dishevelled-1 gene.";
RL      Genome Res. 5:116-124(1995).
RN      [3]
RP      KNOCK-OUT.
RX      MEDLINE=97442352; PubMed=9298901;
RX      Lijam N., Paylor R., McDonald M.P., Crawley J.N., Deng C.-X.,
RA      Herrup K., Stevens K.E., Maccefferri G., McBain C.J., Susman D.J.,
RA      Wynshaw-Boris A.;
RT      "Social interaction and sensorimotor gating abnormalities in mice
RT      lacking Dvl1.";
RL      Cell 90:893-905(1997).
-i-     FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
CC      MEDIATED BY MULTIPLE WNT GENES. DVL1 DEFICIENT MICE DISPLAY
CC      ABNORMALITIES IN SOCIAL BEHAVIORS AND SENSORIMOTOR GATING.
CC      -i- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

```

CC -1- TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE BRAIN, TESTIS AND  
 CC KIDNEY, LOWER LEVELS IN THE OVARY, BREAST, MUSCLE, LIVER AND SMALL  
 CC INTESTINE, AND VERY LOW LEVELS ARE SEEN IN THE SPLEEN AND THYMUS.  
 CC A MODERATE LEVEL EXPRESSION IS SEEN IN THE HEART.  
 CC -1- DEVELOPMENTAL STAGE: IS EXPRESSED THROUGHOUT THE EMBRYONIC CENTRAL  
 CC NERVOUS SYSTEM FROM PRESOMITE STAGES AND IN NEURON-RICH AREAS OF  
 CC THE BRAIN THROUGHOUT POSTNATAL DEVELOPMENT, AS WELL AS IN MANY  
 CC OTHER TISSUES.  
 CC -1- SIMILARITY: CONTAINS 1 DEP DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U10115; AAA82175.1; -;  
 CC EMBL: U28138; AAA74049.1; -;  
 CC HSP: Q12923; 3PDZ.  
 CC MGD: MGI:94941; DVL.  
 CC InterPro: IPR000591; DEP.  
 CC InterPro: IPR001158; DIX.  
 CC InterPro: IPR003351; Dishevelled.  
 CC InterPro: IPR001478; PDZ.  
 CC Pfam: PF00595; PDZ; 1.  
 CC Pfam: PF00610; DEP; 1.  
 CC Pfam: PF00778; DIX; 1.  
 CC Pfam: PF02377; Dishevelled; 1.  
 CC ProDom: PD003639; DIX; 1.  
 CC SMART: SM00021; DAX; 1.  
 CC SMART: SM00049; DEP; 1.  
 CC SMART: SM00228; PDZ; 1.  
 CC PROSITE: PS50186; DEP; 1.  
 CC PROSITE: PS50106; PDZ; 1.  
 CC KMW Developmental protein.  
 CC FT DOMAIN 251 323  
 CC FT DOMAIN 425 499  
 CC FT DOMAIN 390 393  
 CC FT CONFLICT 122 125  
 CC FT CONFLICT 211 211  
 CC FT CONFLICT 211 211  
 CC SO SEQUENCE 695 AA; 75350 MW; A9FA449F59C75F2 CRC64;  
 CC  
 CC Query Match 8.0%; Score 80; DB 1; Length 695;  
 CC Best Local Similarity 25.7%; Pred. No. 9;  
 CC Matches 28; Conservative 14; Mismatches 49; Indels 18; Gaps 5;  
 CC  
 CC QY 34 GSGQSVSVNHNHVAVDNNNGMDSWNSIMDYGNFATRLFOKKTCTVHKMKKEVMP 93  
 CC DB 598 GSGSES-----DHTVPSGSGSTG-----WER-----PVSQLSRSGS--PRSQAASAVAG 640  
 CC QY 94 IQSLDALVKEKKLQGGKPGPPKGLMTSVNPKVVDLSKFGKNANMC 142  
 CC DB 641 LPPHLPLTKAAYAVGPGPPVRELA-AVPELITGSRQSFQKAMGNPC 688  
 CC  
 CC RESULT 12  
 CC DVL1\_RAT  
 CC ID DVL1\_RAT STANDARD; PRT; 695 AA.  
 CC AC Q9WVB9; Q9WVB8; Q9UG5;  
 CC DT 30-MAY-2000 (Rel. 39, Created)  
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)  
 CC DE (DSH homolog 1).  
 CC GN DVL1.  
 CC OS Rattus norvegicus (Rat).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_TaxID=10116;

CC [1]  
 CC SEQUENCE FROM N.A.  
 CC RP STRAIN=Mistar Kyoto;  
 CC RC MEDLINE=21254118; PubMed=11354832;  
 CC RA de Lange R.P.-J., Burr K., Clark J.S., Negrin C.D., Brosnan M.J.,  
 CC St Clair D.M., Lomniczak A.F., Shaw D.J.;  
 CC "Mapping and sequencing rat dishevelled-1: a candidate gene for  
 CC cerebral ischaemic insult in a rat model of stroke."  
 CC Neurogenetics 3:99-106(2001)  
 CC RL  
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY  
 CC MEDIATED BY MULTIPLE WNT GENES.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 DEP DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: AF143545; AAD33896.2; -;  
 CC EMBL: AF143546; AAD33897.2; -;  
 CC EMBL: AF143547; AAD41492.2; -;  
 CC EMBL: AF143548; AAD41492.2; JOINED.  
 CC EMBL: AF143549; AAD41493.1; -;  
 CC EMBL: AF143550; AAD41493.1; JOINED.  
 CC InterPro: IPR000591; DEP.  
 CC InterPro: IPR001158; DIX.  
 CC InterPro: IPR003351; Dishevelled.  
 CC InterPro: IPR001478; PDZ.  
 CC Pfam: PF00595; PDZ; 1.  
 CC Pfam: PF00610; DEP; 1.  
 CC Pfam: PF00778; DIX; 1.  
 CC Pfam: PF02377; Dishevelled; 1.  
 CC ProDom: PD003639; DIX; 1.  
 CC SMART: SM00021; DAX; 1.  
 CC SMART: SM00049; DEP; 1.  
 CC PROSITE: PS50186; DEP; 1.  
 CC PROSITE: PS50106; PDZ; PARTIAL.  
 CC KMW Developmental protein.  
 CC FT DOMAIN 251 323  
 CC FT DOMAIN 425 499  
 CC FT CONFLICT 122 125  
 CC FT CONFLICT 211 211  
 CC SO SEQUENCE 695 AA; 75447 MW; EEC4AA99A117D22A CRC64;  
 CC  
 CC Query Match 8.0%; Score 80; DB 1; Length 695;  
 CC Best Local Similarity 25.7%; Pred. No. 9;  
 CC Matches 28; Conservative 14; Mismatches 49; Indels 18; Gaps 5;  
 CC  
 CC QY 34 GSGQSVSVNHNHVAVDNNNGMDSWNSIMDYGNFATRLFOKKTCTVHKMKKEVMP 93  
 CC DB 598 GSGSES-----DHTVPSGSGSTG-----WER-----PVSQLSRSGS--PRSQAASAVAG 640  
 CC QY 94 IQSLDALVKEKKLQGGKPGPPKGLMTSVNPKVVDLSKFGKNANMC 142  
 CC DB 641 LPPHLPLTKAAYAVGPGPPVRELA-AVPELITGSRQSFQKAMGNPC 688  
 CC  
 CC RESULT 13  
 CC MAD1\_YEAST  
 CC ID MAD1\_YEAST STANDARD; PRT; 749 AA.  
 CC AC P40957;  
 CC DT 01-FEB-1995 (Rel. 31, Created)  
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE Spindle assembly checkpoint component MAD1 (Mitotic MAD1 protein).  
 CC DE MAD1 OR YG1086M.  
 CC GN MAD1 OR YG1086M.  
 CC OS Saccharomyces cerevisiae (Baker's yeast).  
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomyces;



ID	XYNA_RUMFL	STANDARD:	PRT:	954 AA.
AC	P29126:			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Bifunctional endo-1,4-beta-xylanase Xyla precursor (EC 3.2.1.8).			
GN	XyA.			
OS	Ruminococcus flavofaciens			
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;			
OC	Ruminococcus			
OX	NBL_TextID=1265;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-17;			
RA	MEDLINE=92261318; PubMed=1584021;			
RA	Zhang J.-X., Flint H.J.;			
RT	* A bifunctional xylanase encoded by the xyA gene of the rumen			
RT	cellulolytic bacterium Ruminococcus flavofaciens 17 comprises two			
RL	dissimilar domains linked by an asparagine/glutamine-rich sequence.*;			
ML	Mol. Microbiol. 6:1013-1023(1992).			
CC	- FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XULO-OLIGOSACCHARIDES			
CC	AND DOMAIN 2 MORE XYLLOSE.			
CC	- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic			
CC	linkages in xylans.			
CC	- PATHWAY: xylan degradation.			
CC	- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY			
CC	G (FAMILY 11 OF GLYCOSTYL HYDROLASES).			
CC	- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY			
CC	F (FAMILY 10 OF GLYCOSTYL HYDROLASES).			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL: Z11127; CAAT7476.1; -			
DR	PIR: S18043; S18043.			
DR	PIR: S20907; S20907.			
DR	HSSP: P48793; LXND.			
DR	InterPro: IPR001137; GH_11.			
DR	InterPro: IPR001000; glyco_hydro_10.			
DR	Pfam: PF00331; glyco_hydro_10; 1.			
DR	Pfam: PF00457; glyco_hydro_11; 1.			
DR	PRINTS: PR00134; GLYHDLASE10.			
DR	PRINTS: PR00011; GLYHDLASE11.			
DR	PROSITE: PS00591; GLYCOSTYL_HYDROL_F10; 1.			
DR	PROSITE: PS00776; GLYCOSTYL_HYDROL_F11; 1.			
DR	PROSITE: PS00777; GLYCOSTYL_HYDROL_F11_2; 1.			
KW	xylan degradation; Hydrolase; Glycosidase; Multifunctional enzyme;			
KW	Repeat; Signal.			
FT	SIGNAL	1	27	
FT	CHAIN	28	954	OR 28, OR 29 (POTENTIAL).
FT	DOMAIN	28	244	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XyLA.
FT	DOMAIN	245	622	XYLANASE DOMAIN 1.
FT	DOMAIN	623	954	ASN/GIN/TRP-RICH (LINKER).
FT	ACT_SITE	122	122	XYLANASE DOMAIN 2
FT	ACT_SITE	223	223	NGCLEOPHILE (BY SIMILARITY).
FT	ACT_SITE	774	774	PROTON DONOR (BY SIMILARITY).
FT	ACT_SITE	884	884	PROTON DONOR (BY SIMILARITY).
SO	SEQUENCE	954 AA;	111362 MM;	NCLEOPHILE (BY SIMILARITY). 1033567D4B526EBD CRC64;
Query Match	Best Local Similarity	8.0%;	Score 80; DB 1; Length 954;	
Matches	20; Conservative	4;	Mismatches	18; Indels 16; Gaps 3.
OY	23 NIDVDDNNNGSGQGSQSVNNEHVAN-VNNNNGDSM-----NSTWDYGN 68			
Db	453 NNDNMNNNTWTDMNN 506			

RESULT 15  
 CWMF\_SCHPO STANDARD: PRT: 834 AA.  
 ID 096R9: 074321:  
 AC 15-JUN-2002 (rel. 41, Created)  
 DT 15-JUN-2002 (rel. 41, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Cell cycle control protein cwf22.  
 OS CWF22 OR SPBC15D4.16 OR SPBC13E7.01.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 NCBI\_TaxID=4896;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401: PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Voiclaert G., Aert R., Robben J., Grymonprez B.,  
 RA Welter J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Leinrich H., Reinhardt K., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Drenth S., Gloux S., Lelaure V., Mottier S.,  
 RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RA "The genome sequence of Schizosaccharomyces pombe.";  
 RA Nature 415:871-880(2002).  
 RL [2]  
 RN IDENTIFICATION:  
 RP MEDLINE=21881936; PubMed=11884590;  
 RA Ohi M.D., Link A.J., Ren L., Jennings J.L., McDonald W.H., Gould K.L.;  
 RT "Proteomics analysis reveals stable multiprotein complexes in both  
 RT fission and budding yeasts containing Myb-related Cdc5p/Cef1p, novel  
 RT pre-mRNA splicing factors, and snRNAs.";  
 RT Mol. Cell. Biol. 22:2011-2024(2002).  
 RL -1- FUNCTION: Involved in mRNA splicing where it associates with cdc5  
 CC and other cwf proteins as part of the spliceosome.  
 CC -1- SUBUNIT: Interacts with cdc5.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC  
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 CC  
 CC EMBL: AL031349; CA30491.1: -;  
 CC EMBL: AL354632; CAB89876.1: -;  
 CC InterPro: IPR003890; IF\_eIF4G.  
 CC InterPro: IPR003891; IF\_eIF4G\_MA3.  
 CC Pfam: PF02847; MA3; 1.  
 CC Pfam: PF02854; MIF4G; 1.  
 CC Nuclear protein: mRNA processing; mRNA splicing.  
 CC NUCLEOTIDE SEQUENCE: 834 AA; 96378 MW; 25EDA85E19F3FB3 CRC64;  
 CC SEQUENCE

Query Match 8.0%; Score 79.5; DB 1; Length 834;  
 Best local similarity 24.0%; Pred No. 12;  
 Matches 44; Conservative 16; Mismatches 54; Indels 69; Gaps 8;  
 OY 24 IDVNDNNAGSGOOSVSYNNEHNANVDNNGDSWNSIWDYGNGFATRLQKKTCIV 83  
 DB 13 LDYNRNPPES-SGHSKVAIVIRKQTEQENNLSWEDRHVTPD-----L 54  
 OY 84 HKKKKEVMP-----SIQSIALYKKEKKLQGGKPGG---PPPK----- 117  
 DB 55 HKSNIKITPTSLADEKSSHNEIDPKAOKIKLMTETRSQGYIIPAKKLAKLQALTDVNTPE 114  
 OY 118 -----GLMYSVNPKNVDL--SKRGKNI-----AMNCRIPIYMAEEMQAS 157  
 DB 115 YQRMQEALKKSINGLINVKNKSNIRDIPELFQENIRGRALVCRSI-----MKAQAS 169  
 OY 158 LFF 160  
 DB 170 LPF 172

Search completed: April 11, 2003, 16:11:55  
 Job time: 14.0313 secs

Mon Apr 14 14:01:18 2003

us-09-821-726a-13.rapb

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:11:18 : Search time 18.4095 Seconds  
(without alignments)  
614.367 Million cell updates/sec

Title: US-09-821-726a-13  
Perfect score: 994  
Sequence: 1 MKFTVFAGLGVFLAPALA.....YTSVLMIYDIFSCDPTVEN 185

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 248812 seqs, 61136040 residues  
Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCR\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

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5	984	99.0	185	US-10-001-054-14	Sequence 14, Appl
6	984	99.0	185	US-09-989-730-211	Sequence 211, App
7	984	99.0	185	US-09-990-436-211	Sequence 211, App
8	984	99.0	185	US-09-991-181-211	Sequence 211, App
9	984	99.0	185	US-09-989-734-211	Sequence 211, App
10	984	99.0	185	US-09-997-653-211	Sequence 211, App
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15	984	99.0	185	US-10-227-884-148	Sequence 148, App
16	984	99.0	185	US-09-990-711-211	Sequence 211, App
17	984	99.0	185	US-10-230-163-148	Sequence 148, App
18	984	99.0	185	US-10-230-163-148	Sequence 148, App
19	984	99.0	185	US-10-230-163-148	Sequence 148, App

20	984	99.0	185	US-09-989-726-211	Sequence 211, App
21	984	99.0	185	US-09-746-783-146	Sequence 146, App
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## ALIGNMENTS

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Patient No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertelsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paonli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC20  
CURRENT APPLICATION NUMBER: US/09/992,598  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Eaton, Dan L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
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PRIOR APPLICATION NUMBER: 60/091633  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;  
Best Local Similarity 98.9%; Pred. No. 1, 4e-95;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 3  
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Sequence 211, Application US//09989735  
Publication No. US20020193299A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC61

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48	PRIOR APPLICATION NUMBER: 60/090435
49	PRIOR FILING DATE: 1998-06-24
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51	PRIOR FILING DATE: 1998-06-24
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53	PRIOR FILING DATE: 1998-06-24
54	PRIOR APPLICATION NUMBER: 60/090543
55	PRIOR FILING DATE: 1998-06-24
56	PRIOR APPLICATION NUMBER: 60/090542
57	PRIOR FILING DATE: 1998-06-24
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61	PRIOR FILING DATE: 1998-06-25
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65	PRIOR FILING DATE: 1998-06-25
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68	PRIOR APPLICATION NUMBER: 60/090695
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70	PRIOR APPLICATION NUMBER: 60/090695

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;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;  
Best Local Similarity 98.9%; Pred. No. 1.4e-95;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKETIFAGLIGVFLALANYNINDVNDNNAGSGOOSVSNNEHNANVNDNNNGMSW 60  
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Db 61 NSIWDYNGNGFAATRLFKQKTCIVHKMKKEVWPSIQSLDALYKERRKLGKGGPPKGLM 120  
QY 121 YSVNPKKVDLSFKGKRIAMNGCIPTYMAEMGEASLFFYSGTCYTTSLMIVDISFCG 180  
Db 121 YSVNPKKVDLSFKGKRIAMNGCIPTYMAEMGEASLFFYSGTCYTTSLMIVDISFCG 180  
QY 181 DYVEN 185  
Db 181 DYVEN 185

RESULT 4  
US-09-990-444-211  
; Sequence 211, Application US/09990444  
; Publication No. US20020193300A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paonni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey

;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2730P1C19  
;; CURRENT APPLICATION NUMBER: US/09/990,444  
;; PRIOR FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Query Match

Best Local Similarity 99.0%; Score 984; DB 9; Length 185;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 121 YSVNPNKVDLSKFGKNIANNMCRGIPTYMAEEMOEASLFFSGTCYTSVLMIYDISFCG 180  
Db 121 YSVNPNKVDLSKFGKNIANNMCRGIPTYMAEEMOEASLFFSGTCYTSVLMIYDISFCG 180  
Qy 181 DTVEN 185  
Db 181 DTVEN 185

## RESULT 5

US-10-001-054-14  
Sequence 14, Application US/10001054  
Publication No. US20020192209A1

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
APPLICANT: Baker, Kevin  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin  
APPLICANT: Hebert, Carolyn  
APPLICANT: Henzel, William  
APPLICANT: Kabakoff, Rhona  
APPLICANT: Shelton, David  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
FILE REFERENCE: P3034R1PCT  
CURRENT APPLICATION NUMBER: US/10/001,054  
CURRENT FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17  
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;; PRIOR FILING DATE: 2001-06-01  
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;; PRIOR APPLICATION NUMBER: PCT/US01/21735  
;; PRIOR FILING DATE: 2001-07-09  
;; PRIOR APPLICATION NUMBER: PCT/US01/27099  
;; PRIOR FILING DATE: 2001-08-29  
;; NUMBER OF SEQ ID NOS: 91  
;; SEQ ID NO 14  
;; LENGTH: 185  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-001-054-14

Query Match 99.0%; Score 984; DB 9; Length 185;  
Best Local Similarity 98.9%; Pred. No. 1.4e-95;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKETIVPAGLGLVFLAPALANYINDNDNNAGSGQGSVSNNEHNVANVNDNNQWDSM 60  
DB 1 MKETIVPAGLGLVFLAPALANYINDNDNNAGSGQGSVSNNEHNVANVNDNNQWDSM 60  
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QY 121 YSVNENKVDLSKFGSKNIANNMCRGIPTYMAEEMQASLFFYSGTCYTSVLMIVDISFCG 180  
DB 121 YSVNENKVDLSKFGSKNIANNMCRGIPTYMAEEMQASLFFYSGTCYTSVLMIVDISFCG 180  
QY 181 DTVEN 185  
DB 181 DTVEN 185

RESULT 6  
US-09-989-730-211

;; Sequence 211, Application US/09989730  
;; Publication No. US20020197674A1

;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kijavits, Ivar J.  
;; APPLICANT: Napier, Mary A.

;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC69  
;; CURRENT FILING DATE: 2001-11-20  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
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Query Match 99.0%; Score 984; DB 9; Length 185;  
Best Local Similarity 98.9%; Pred. No. 1,4e-95;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 61 NSTWDYGNFPAATRLFOKKTCTVHKMKKEYMPSIOSDALVKEKKLGKGPGPPKGLM 120

QY 121 YSVNPKKVDLSTFKGNINAMKRGIPTYMAEMQEASLFFYSGTCYTSVLMIVDISFCG 180  
DB 121 YSVNPKKVDLSTFKGNINAMKRGIPTYMAEMQEASLFFYSGTCYTSVLMIVDISFCG 180

QY 181 DYVEN 185  
DB 181 DYVEN 185

RESULT 7  
US-09-990-436-211  
; Sequence 211, Application US/09990436  
; General Information:  
; PUBLIC INFORMATION:  
; APPLICATION: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijaviri, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C14  
CURRENT APPLICATION NUMBER: US/09/990,436  
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PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR FILING DATE: 1998-07-09
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Query Match 99.0%; Score 984; DB 9; Length 185;  
Best Local Similarity 98.9%; Pred. No. 1.4e-95;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 61 NSIMVYGNFATRLFLQKKTCTIVHKMKKEVMPISQISDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPKYVDLSKFGKNINMRCGIPTYAAEEOEASLEFYSGTCYTVSLVIYDISFCG 180
DB 121 YSVNPKYVDLSKFGKNINMRCGIPTYAAEEOEASLEFYSGTCYTVSLVIYDISFCG 180
QY 181 DTVEN 185
DB 181 DTVEN 185
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RESULT 8  
US-09-991-181-211

Sequence 211, Application US/09991181  
Publication No. US20020197615A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Botnays, Luc

APPLICANT: Eaton, Dan L.

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;; APPLICANT: Ferrara, Napoleone
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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C53
;; CURRENT APPLICATION NUMBER: US/09/991,181
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB %; Length 185;  
Best Local Similarity 98.9%; Pred. No. 1.4e-95;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFTTVEFAGLGVFLAPLANYNIDVNDNNAGSGQSVSYNNHNVANYDNNNGWSW 60  
Db 1 MKFTTVEFAGLGVFLAPLANYNINVDNNAGSGQSVSYNNHNVANYDNNNGWSW 60  
Qy 61 NSIDYNGCFATRLFOKKTCTIVHKMKKEVMPSTOSLDALVKEKKLOGKGGPPKGLM 120  
Db 61 NSIDYNGCFATRLFOKKTCTIVHKMKKEVMPSTOSLDALVKEKKLOGKGGPPKGLM 120  
Qy 121 YSVNPNKVDLSKFGKNIANNCRCIPTVMAEEMQASLFFYSGTCYTTSVLMIYDISFCG 180  
Db 121 YSVNPNKVDLSKFGKNIANNCRCIPTVMAEEMQASLFFYSGTCYTTSVLMIYDISFCG 180  
Qy 181 DTVEN 185  
Db 181 DTVEN 185

RESULT 9  
US-09-993-687-211  
; Sequence 211, Application US/09993687  
; Publication No. US20020198149A1  
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Klavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC11  
CURRENT APPLICATION NUMBER: US/09/993,687  
CURRENT FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR FILING DATE: 1998-06-04

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PRIOR APPLICATION NUMBER: 60/090429  
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PRIOR APPLICATION NUMBER: 60/090431



;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;  
Best Local Similarity 98.9%; Pred. No. 1,4e-95;  
Matches 185; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLGVFLAPALANYNDVNDNNAGSGOOSVSVNNEHNVANVNDNNNGWDSW 60  
DB 1 MKFTIVFAGLGVFLAPALANYNDVNDNNAGSGOOSVSVNNEHNVANVNDNNNGWDSW 60  
QY 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPSTIOSIDLALVKKKLOGKCGPGPKKGLM 120  
DB 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPSTIOSIDLALVKKKLOGKCGPGPKKGLM 120  
QY 121 YSVNPNKVVDDLSKFGKNANNCRCGIPYMAFEKMOEASLFFTSCTTYSVLMIYDISFCG 180  
DB 121 YSVNPNKVVDDLSKFGKNANNCRCGIPYMAFEKMOEASLFFTSCTTYSVLMIYDISFCG 180  
QY 181 DTVEN 185  
DB 181 DTVEN 185

RESULT 10  
US-09-989-734-211  
Sequence 211, Application US/09989734  
Publication No. US20030003531A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
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APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C64  
CURRENT APPLICATION NUMBER: US/09/989,734  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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;; PRIOR FILING DATE: 1998-06-23  
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;; PRIOR APPLICATION NUMBER: 60/091626  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;  
Best Local Similarity 98.9%; Pred. No. 1,4e-95;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRETFEAGLLGFLAPALANYNIDVNDNNNGSGOOSVSVNNEHNAVAVDNNNGDSW 60  
DB 1 MRETFEAGLLGFLAPALANYNINNDNNNGSGOOSVSVNNEHNAVAVDNNNGDSW 60  
QY 61 NSIWDYGNFPAATRLRFQKKTCTIVHKMKKEVPSIQSIDALVKEKKLOGKGPGRPGKGLM 120  
DB 61 NSIWDYGNFPAATRLRFQKKTCTIVHKMKKEVPSIQSIDALVKEKKLOGKGPGRPGKGLM 120  
QY 121 YSVNPKKVDLSKFGKNIANMCKGIFTYMAEEMOESLFTSYSGTCYTSVLTWIDISFCG 180  
DB 121 YSVNPKKVDLSKFGKNIANMCKGIFTYMAEEMOESLFTSYSGTCYTSVLTWIDISFCG 180

QY 181 DTVEN 185  
11111  
DB 181 DTVEN 185

RESULT 11  
US-09-997-653-211

; Sequence 211, Application US/09997653  
; Publication No. US20030008297A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bolstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertsens, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kjaivin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C38  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US/09/997,653  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;  
Best Local Similarity 98.9%; Pred. No. 1.4e-95;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MKFTIVAGLIGVFLAPALANYNINVDNNDNNAGSGQGSVSVNNHNVANVDNNGWDSW 60  
QY 61 NSIMDVGNCFATRLFOKKTIVHKMKKEVMPSTOSLDALVKEKKLQCKGPGGPPPKGLM 120  
DB 61 NSIMDVGNCFATRLFOKKTIVHKMKKEVMPSTOSLDALVKEKKLQCKGPGGPPPKGLM 120

QY 121 YSVNPNKVDLDSKFGKNIAMNCRGIPYMAEMQEASLFFYSGTCYTTSVLMIVDISPCG 180  
DB 121 YSVNPNKVDLDSKFGKNIAMNCRGIPYMAEMQEASLFFYSGTCYTTSVLMIVDISPCG 180  
QY 181 DTVEN 185  
DB 181 DTVEN 185

RESULT 12

;; Sequence 211, Application US/09993667  
;; Publication No. US2003002187A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerlitsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kjaavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C4  
;; CURRENT APPLICATION NUMBER: US/09/993,667  
;; PRIOR FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
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;; PRIOR APPLICATION NUMBER: 60/088021

[illegible]

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20	PRIOR FILING DATE: 1998-06-24
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64	PRIOR FILING DATE: 1998-07-07
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66	PRIOR FILING DATE: 1998-07-07
67	PRIOR APPLICATION NUMBER: 60/092183.83
68	PRIOR FILING DATE: 1998-07-09
69	PRIOR APPLICATION NUMBER: 60/092183.83
70	PRIOR FILING DATE: 1998-07-09

Query Match	99.0%	Score 984	DB 9	Length 185
Best Local Similarity	98.9%	Pred. No. 1.4e-95		
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Db 1 MKETIVFAGILGVFLAPALANYNINVDNNAGSGGOOSVSVNNEHNANVDNNGWDSW 60  
QY 61 NSIWDGNGEFAATRLFOKKTCTIVHKMKKEVWPSIQSLDALVKEKKLGKGGPPKGLM 120  
Db 61 NSIWDGNGEFAATRLFOKKTCTIVHKMKKEVWPSIQSLDALVKEKKLGKGGPPKGLM 120  
QY 121 YSVNPKWVDLSEFKGNIANMRCGIPYMAEEMQESLFFYSCTCYTTSVLMIYDISFCG 180  
Db 121 YSVNPKWVDLSEFKGNIANMRCGIPYMAEEMQESLFFYSCTCYTTSVLMIYDISFCG 180  
QY 181 DTVEN 185  
Db 181 DTVEN 185  
RESULT 13  
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Sequence 211, Application US/09990438  
Publication No. US20030027754A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C3  
CURRENT APPLICATION NUMBER: US/09/990,438  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091992  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;

Best Local Similarity 98.9%; Pred. No. 1, 4e-95;  
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKFTVFAGLGVFLPALANIVYDNDNNNAAGSQOQSVYVNEHNVANVANDNNNGMDSW 60  
 Db 1 MKFTVFAGLGVFLPALANIVYDNDNNNAAGSQOQSVYVNEHNVANVANDNNNGMDSW 60  
 QY 61 NSIWDYNGFPAATRLFOKKTCTVHKMKKEVMPISQSLDLVYKXKLOGGPGGPPKGLM 120  
 Db 61 NSIWDYNGFPAATRLFOKKTCTVHKMKKEVMPISQSLDLVYKXKLOGGPGGPPKGLM 120  
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RESULT 14  
 US-09-990-562-211  
 ; Sequence 211, Application US/09990562  
 ; Publication No. US20030027985A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Bolstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730P1C18  
 ; CURRENT APPLICATION NUMBER: US/09/990, 562  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/065311  
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 ; PRIOR FILING DATE: 1998-02-25  
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 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/084600  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/087106

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69	PRIOR FILING DATE: 1998-06-17
70	PRIOR APPLICATION NUMBER: 60/089600
71	PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982



;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/052182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;  
Best Local Similarity 98.9%; Pred. No. 1,4e-95;  
Matches 185; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MKETIVAGLIGVFLALALANYNDVNDNNAGSGOOSVSVNNEHNANVNDNNNGMSW 60  
QY 61 NSIMDWYNGAARTRLFQKKTCTVHKMKKEVWPSIQSLDALVKEKKLOGKGGPPKGLM 120  
DB 61 NSIMDWYNGAARTRLFQKKTCTVHKMKKEVWPSIQSLDALVKEKKLOGKGGPPKGLM 120  
QY 121 YSVNPNKVDLSKFGKNIAMNCRGIPYMAEEMQESLFFSGTCYTSVNIIVDISCG 180  
DB 121 YSVNPNKVDLSKFGKNIAMNCRGIPYMAEEMQESLFFSGTCYTSVNIIVDISCG 180  
QY 181 DTVEN 185  
DB 181 DTVEN 185

RESULT 15  
US-09-997-428-211  
; Sequence 211, Application US/09997428  
; Publication No. US20030027162A1  
; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Bolstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gertlisen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kijavini, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P27301P1C44  
;; CURRENT APPLICATION NUMBER: US/09/997,428  
;; PRIOR FILING DATE: 2001-11-15  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 99.08; Score 984; DB 9; Length 185;  
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QY 181 DTVEN 185  
DB 181 DTVEN 185

Search completed: April 11, 2003, 16:17:43  
Job time : 19.4095 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2003, 16:06:33 ; Search time 51.9086 Seconds  
(without alignments)  
474.899 Million cell updates/sec

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Perfect score: 994  
Sequence: 1 MKETIVFAGLGVFLAPALA.....YTSVLMIVDISFGDIYEN 185

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A.Geneseq\_101002:\*

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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: \*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	984	99.0	185	21	AAW99667
4	984	99.0	185	21	AAW99667
5	984	99.0	185	22	AAW99667
6	984	99.0	185	22	AAW99667
7	984	99.0	185	23	AAW99667
8	984	99.0	185	23	AAW99667
9	984	99.0	185	23	AAW99667
10	984	99.0	186	21	AAW99667

11	984	99.0	194	19	AAW99674
12	984	99.0	194	20	AAW99674
13	602	60.6	184	23	AAW99674
14	189	19.0	184	21	AAW99674
15	189	19.0	184	22	AAW99674
16	188	18.9	184	22	AAW99674
17	188	18.9	184	22	AAW99674
18	188	18.9	184	22	AAW99674
19	188	18.9	184	22	AAW99674
20	188	18.9	184	22	AAW99674
21	178	17.9	176	22	AAW99674
22	154.5	15.5	147	22	AAW99674
23	95.5	9.6	719	22	AAW99674
24	93	9.4	764	21	AAW99674
25	93	9.4	1176	21	AAW99674
26	91	9.2	718	22	AAW99674
27	90	9.1	1245	21	AAW99674
28	88	8.9	286	22	AAW99674
29	84.5	8.5	2188	22	AAW99674
30	84	8.5	1817	21	AAW99674
31	83.5	8.4	1979	21	AAW99674
32	81.5	8.2	537	7	AAW99674
33	80.5	8.1	447	17	AAW99674
34	80.5	8.1	652	18	AAW99674
35	80	8.0	280	21	AAW99674
36	80	8.0	695	22	AAW99674
37	80	8.0	954	22	AAW99674
38	79.5	8.0	943	22	AAW99674
39	78	7.8	540	21	AAW99674
40	78	7.8	2539	21	AAW99674
41	77.5	7.8	1341	23	AAW99674
42	77.5	7.8	1714	21	AAW99674
43	77	7.7	1316	21	AAW99674
44	77	7.7	1337	21	AAW99674
45	77	7.7	2010	21	AAW99674

#### ALIGNMENTS

RESULT 1	AAW99667	standard; Protein; 185 AA.
ID	AAW99667	
XX	AAW99667	
AC	AAW99667	
XX	07-JUN-1999	(first entry)
DT	07-JUN-1999	(first entry)
XX	Human secreted protein clone e90_5 protein.	
DE	Human; secreted protein; nutritional; cytokine; cell proliferation;	
XX	tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;	
KW	anti-inflammatory; cadherin; tumour invasion suppressor;	
KW	tumour inhibition; gene therapy.	
XX	Homo sapiens.	
OS	Homo sapiens.	
PN	W09907840-A1.	
XX	18-FEB-1999.	
PD	18-FEB-1999.	
XX	06-AUG-1998;	98WO-US16318.
PF	06-AUG-1998;	98US-0130189.
XX	06-AUG-1997;	97US-0906708.
PR	06-AUG-1997;	97US-0906708.
XX	(GENY ) GENETICS INST INC.	
PA	Agostino MJ, Evans C, Jacobs K, Lavalie ER, McCoy JM;	
PI	Meiberg D, Racie LA, Steininger RJ, Treacy M;	
XX	WPI: 1999-167419/14.	

Cancer associated  
Human ovarian tumo  
Human ORF protein  
Membrane-bound pro  
Human PRO813 (UNQ4  
Human EST encoded  
Human gene 14 enco  
Human gene 14 enco  
Human albumin fusi  
Human PRO polypept  
Human gene 14 enco  
S cerevisiae apopt  
Plasmodium falcipla  
Plasmodium falcipla  
Drosophila melanog  
Plasmodium falcipla  
Dictyostelium disc  
Drosophila melanog  
Plasmodium falcipla  
Plasmodium falcipla  
Sequence of the As  
Oyster pearl prote  
Plasmodium falcipla  
Gene 21 human secr  
Mouse Dishevelled-  
Rhinococcus flave  
Drosophila melanog  
Plasmodium falcipla  
Plasmodium falcipla  
Fungal ZBC protein  
Plasmodium falcipla  
A calcium-dependen  
Plasmodium falcipla

DR N-PSDB; AAX19493.  
 XX  
 PT New polynucleotides encoding secreted human proteins - derived from  
 PT fetal kidney, adult testes, adult brain, adult heart, adult placenta  
 PT or adult retina cDNA libraries  
 XX  
 PS Claim 34; Page 98-99; 107pp; English.  
 CC The present sequence represents a human secreted protein. The secreted  
 CC protein can have activities such as: nutritional activity, cytokine and  
 CC cell proliferation/differentiation activity, immune stimulating (e.g. as  
 CC vaccines) or suppressing activity, haematopoiesis regulating activity,  
 CC tissue growth activity, activin/inhibin activity, chemotactic/  
 CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/  
 CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion  
 CC suppressor activity, and tumour inhibition activity. The secreted  
 CC protein polynucleotides and proteins are predicted to have biological  
 CC activities which would make them suitable for treating, preventing or  
 CC ameliorating medical conditions in humans and animals. The  
 CC polynucleotides are also stated to be useful for gene therapy.  
 CC  
 XX  
 SQ Sequence 185 AA;

Query Match 99.0%; Score 984; DB 20; Length 185;  
 Best Local Similarity 98.9%; Pred. No. 3.2e-93;  
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTTIFAGLLGVFLAPALANYINVDNDNNAGSGQGSVYNNENHNAVNDNNMGDSW 60  
 DB 1 MKFTTIFAGLLGVFLAPALANYINVDNDNNAGSGQGSVYNNENHNAVNDNNMGDSW 60  
 QY 61 NSIMWDGNFAATRLFOKKTCTVHKMKKEVMPISLOSLDLVYEKKLOGGPGPPKGLM 120  
 DB 61 NSIMWDGNFAATRLFOKKTCTVHKMKKEVMPISLOSLDLVYEKKLOGGPGPPKGLM 120  
 QY 121 YSVNPNKYVDLSKFKGNINAMCGIPTVYAEEMQASLFFYSGTCYTTSVLWIVDISFCG 180  
 DB 121 YSVNPNKYVDLSKFKGNINAMCGIPTVYAEEMQASLFFYSGTCYTTSVLWIVDISFCG 180  
 QY 181 DTVEN 185  
 DB 181 DTVEN 185

RESULT 2  
 AAB24067  
 ID AAB24067 standard; Protein; 185 AA.  
 AC AAB24067;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human PRO1005 protein sequence SEQ ID NO:34.  
 XX  
 KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
 KW neuroprotective; antiinflammatory; immunosuppressive;  
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
 KW neuronal disorder; gliad disorder; astrocytal disorder; angiogenic;  
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;  
 KW epithelial disorder; stromal disorder; blastocoealic disorder;  
 KW inflammatory disorder; immunologic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053755-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 06-JAN-2000; 2000WO-US00376.  
 XX  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 XX

PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
 PI Watanabe CK, Wood WI;  
 PI WPI: 2000-572270/53.  
 XX  
 DR N-PSDB; AAC58377.  
 XX  
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 PT treatment, diagnosis and prevention of cancer -  
 XX  
 PS Claim 61; Fig 22; 286pp; English.

CC The present invention describes an isolated antibody that binds to  
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,  
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
 CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,  
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
 CC growth. The PRO polypeptides and nucleotides are useful in the  
 CC treatment, diagnosis and prevention of cancer. The antibodies and other  
 CC anti-tumour compounds may be used to treat various conditions, including  
 CC those characterized by overexpression and/or activation of the amplified  
 CC PRO genes. Exemplary conditions or disorders to be treated with such  
 CC antibodies and other compounds include benign or malignant tumours  
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
 CC leukaemias, sarcomas, glioblastomas, and various head and neck tumours),  
 CC gliad, astrocytal, hypothalamic and other glandular, macrophagal,  
 CC epithelial, stromal and blastocoealic disorders, and inflammatory,  
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
 CC primers and hybridisation probes used in the isolation of the human PRO  
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
 CC PRO polynucleotide and protein sequences given in the exemplification of  
 CC the present invention.  
 XX  
 SQ Sequence 185 AA;

Query Match 99.0%; Score 984; DB 21; Length 185;  
 Best Local Similarity 98.9%; Pred. No. 3.2e-93;  
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTTIFAGLLGVFLAPALANYINVDNDNNAGSGQGSVYNNENHNAVNDNNMGDSW 60  
 DB 1 MKFTTIFAGLLGVFLAPALANYINVDNDNNAGSGQGSVYNNENHNAVNDNNMGDSW 60  
 QY 61 NSIMWDGNFAATRLFOKKTCTVHKMKKEVMPISLOSLDLVYEKKLOGGPGPPKGLM 120  
 DB 61 NSIMWDGNFAATRLFOKKTCTVHKMKKEVMPISLOSLDLVYEKKLOGGPGPPKGLM 120  
 QY 121 YSVNPNKYVDLSKFKGNINAMCGIPTVYAEEMQASLFFYSGTCYTTSVLWIVDISFCG 180  
 DB 121 YSVNPNKYVDLSKFKGNINAMCGIPTVYAEEMQASLFFYSGTCYTTSVLWIVDISFCG 180  
 QY 181 DTVEN 185  
 DB 181 DTVEN 185

RESULT 3  
 AAY87272  
 ID AAY87272 standard; Protein; 185 AA.  
 AC AAY87272;  
 XX

DT 11-MAY-2000 (first entry)  
XX  
DE Human signal peptide containing protein HSP-49 SFQ ID NO:49.  
XX  
KW Human: signal peptide-containing protein; HSP; diagnosis; cancer;  
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
KW antimicrobial; neuroprotective; cardiovascular; hepatotropic;  
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;  
KW reproductive disorder; developmental disorder; arteriosclerosis;  
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
KW Parkinson's disease; Huntington's diseases; ovulatory defect;  
KW muscular dystrophy.  
XX  
OS Homo sapiens.  
XX  
PN W0200000610-A2.  
XX  
PD 06-JAN-2000.  
XX  
PE 25-JUN-1999; 99WO-US14484.  
XX  
PR 26-JUN-1998; 98US-0090762.  
PR 31-JUL-1998; 98US-0094983.  
PR 01-OCT-1998; 98US-0102686.  
PR 11-DEC-1998; 98US-0112129.  
XX  
PA (INCYT-) INCYTE PHARM INC.  
XX  
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
PI Akerbloom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
PI Bandman O;  
XX  
DR WPI: 2000-160673/14.  
DR N-PSDB: AAZ98157.  
XX  
PT New human signal peptide-containing proteins useful in treatment,  
PT prevention and diagnosis of e.g. cancer, inflammation and  
PT cardiovascular disease  
XX  
PS Claim 1; Page 193-194; 327pp; English.  
XX  
CC AA298109 to AA298242 encode AAY87357 which represent the  
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,  
CC neuroprotective, cardiovascular and antiasthmatic activities, and can  
CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
CC associated with decreased activity or function of HSP. Antagonists of  
CC HSP are used to treat or prevent disorders associated with increased  
CC activity or function of HSP. Such diseases include cell proliferation  
CC (including cancer), inflammation, cardiovascular, neurological,  
CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
CC asthma, Crohn's disease, microbial or other infections, congestive or  
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
CC nucleic acids can be used for the recombinant production of HSP, for  
CC detecting HSP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring), in gene therapy, as antisense,  
CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
CC or genetic variations, and for chromosomal mapping. HSP are also used to  
CC raise specific antibodies (Ab) and to screen for agonists and  
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic  
CC antagonists, in competitive drug screens, and for purification of HSP  
CC from natural sources.  
XX  
SQ Sequence 185 AA;  
Query Match 99.0%; Score 984; DB 21; Length 185;  
Best Local Similarity 98.9%; Pred. No. 3,2e-93;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKETIVFAGLLGFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVNDNNMGWDSW 60  
DB 1 MKETIVFAGLLGFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVNDNNMGWDSW 60  
QY 61 NSIWDYGNCFATRLFPKKTCTVHKMKKEVMPSTSLDALVEKKLOGKPGPPPKGLM 120  
DB 61 NSIWDYGNCFATRLFPKKTCTVHKMKKEVMPSTSLDALVEKKLOGKPGPPPKGLM 120  
QY 121 YSVNPKYDDLSKPKKNLANMCRGIPTYMAEEMOEASLFFYSGTCYTVSLMTVDISFCG 180  
DB 121 YSVNPKYDDLSKPKKNLANMCRGIPTYMAEEMOEASLFFYSGTCYTVSLMTVDISFCG 180  
QY 181 DTVEN 185  
DB 181 DTVEN 185  
RESULT 4  
AAY66686  
ID AAY66686 standard; protein: 185 AA.  
XX  
AC AAY66686;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO1005.  
XX  
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
OS Homo sapiens.  
XX  
PN W09963088-A2.  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US12252.  
XX  
PR 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0088900.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.

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PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089603.
PR 18-JUN-1998; 98US-0089601.
PR 18-JUN-1998; 98US-0089607.
PR 18-JUN-1998; 98US-0089608.
PR 19-JUN-1998; 98US-0089647.
PR 19-JUN-1998; 98US-0089648.
PR 19-JUN-1998; 98US-0089649.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090353.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 25-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090680.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 07-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.

PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097261.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097976.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.

XX (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK.
PI Wood WL, Yuan J;
XX
XX WPL: 2000-072883/06.
DR N-PSDB; AAZ65023.
XX
XX Membrane-bound proteins and related nucleotide sequences -
XX
XX claim 12; Fig 139; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIR
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
XX Sequence 185 AA:
SQ
Query Match 99.0%; Score 984; DB 21; Length 185;
Best Local Similarity 98.9%; Pred. No. 3,2e+93;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLGVFLAPLANYNIDVNDNNAGSGOOSVSVNNEHNVANVNNNGWDSM 60
Db 1 MKFTIVFAGLGVFLAPLANYNINVDNDNNAGSGOOSVSVNNEHNVANVNNNGWDSM 60
QY 61 NSIWDYNGGFAATRLPQKTCIVHKMKREVMPSIQSLDALYKERRIQGKPGGPPPKGLM 120
Db 61 NSIWDYNGGFAATRLPQKTCIVHKMKREVMPSIQSLDALYKERRIQGKPGGPPPKGLM 120
QY 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQASLFFYSGTCTYTTSLMIVDISFCG 180
Db 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQASLFFYSGTCTYTTSLMIVDISFCG 180
QY 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQASLFFYSGTCTYTTSLMIVDISFCG 180
Db 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQASLFFYSGTCTYTTSLMIVDISFCG 180

```

OY 181 DTVEN 185  
 Db 181 DTVEN 185

RESULT 5  
 AAB65209  
 ID AAB65209 standard; Protein: 185 AA.  
 AC AAB65209;  
 XX 02-APR-2001 (first entry)

XX Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.

XX Human: secreted and transmembrane protein; PRO: cytosolic;  
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 XX diagnostic assay.

OS Homo sapiens.

XX MO200073454-A1.

PD 07-DEC-2000.

PF 30-MAR-2000; 2000MO-US08439.

XX 02-JUN-1999; 99MO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 17-AUG-1999; 99US-0149396.

PR 15-SEP-1999; 99MO-US21090.

PR 15-SEP-1999; 99MO-US21547.

PR 08-OCT-1999; 99US-0158663.

PR 30-NOV-1999; 99MO-US28313.

PR 01-DEC-1999; 99MO-US28301.

PR 16-DEC-1999; 99MO-US30095.

PR 20-DEC-1999; 99MO-US30911.

PR 05-JAN-2000; 2000MO-US00219.

PR 06-JAN-2000; 2000MO-US00376.

PR 11-FEB-2000; 2000MO-US03565.

PR 18-FEB-2000; 2000MO-US04341.

PR 22-FEB-2000; 2000MO-US04414.

PR 24-FEB-2000; 2000MO-US04914.

PR 02-MAR-2000; 2000MO-US05004.

PR 15-MAR-2000; 2000MO-US05841.

PR 20-MAR-2000; 2000MO-US06884.

XX (GETH ) GENENTECH INC.

PI Ashtkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gerber H, Gerlitsen ME, Goddard A, Godowski PJ;

PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;

PI Zhang Z;

XX WPI: 2001-032160/04.

DR N-PSDB: AAF44169.

XX PRO polynucleotides used to produce polypeptides used to target

PT bioactive molecules such as toxins, radiolabels or antibodies, to

XX specific cells, to cause targeted cell death -

XX Claim 12: Fig 139; 935pp; English.

CC The present invention describes human secreted and transmembrane PRO

CC proteins. The PRO proteins have cytosolic activity. The PRO proteins

CC can be used for targeted delivery of bioactive molecules, such as

CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 185 AA;

Query Match 99.0%; Score 984; DB 22; Length 185;  
 Best Local Similarity 98.9%; Pred. No. 3.2e-93;  
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKETIFAGILGVELAPALANYNDVNDNNNGSQOQSVSVNNEHVAVVNDNNNGDSW 60  
 Db 1 MKETIFAGILGVELAPALANYNINVDNNNGSQOQSVSVNNEHVAVVNDNNNGDSW 60

OY 61 NSTWYDNGGFAATRLRQKKTCTVHKMKKEVMPSTQSLDALVKKKLLQGGKGGPPPKGLM 120  
 Db 61 NSTWYDNGGFAATRLRQKKTCTVHKMKKEVMPSTQSLDALVKKKLLQGGKGGPPPKGLM 120

OY 121 YSVNPKVKDDLSKFGKININMCRGIPTYMAEEMQEAFLPFSGCTYTSVLWIVDISFCG 180  
 Db 121 YSVNPKVKDDLSKFGKININMCRGIPTYMAEEMQEAFLPFSGCTYTSVLWIVDISFCG 180

OY 181 DTVEN 185  
 Db 181 DTVEN 185

XX 181 DTVEN 185

RESULT 6  
 AAB50957  
 ID AAB50957 standard; Protein: 185 AA.

XX AAB50957;

XX 21-MAR-2001 (first entry)

XX Human PRO1005 protein.

XX Human: PRO: cytosolic; neurotropic; neuroprotective; respiratory general;

KW antiinflammatory; angiogenic; immunosuppressive; immunostimulant;

KW PRO agonist; cancer; inflammatory disorder; immunological disorder.

XX Homo sapiens.

XX MO200073348-A2.

XX 07-DEC-2000.

XX 30-MAY-2000; 2000MO-US14941.

XX 02-JUN-1999; 99MO-US12252.

PR 22-JUN-1999; 99US-0140650.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 01-SEP-1999; 99MO-US20111.

PR 08-SEP-1999; 99MO-US20594.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99MO-US28313.

PR 01-DEC-1999; 99MO-US28634.

PR 16-DEC-1999; 99MO-US30095.

PR 20-DEC-1999; 99MO-US30999.

PR 06-JAN-2000; 2000MO-US00376.

PR 11-FEB-2000; 2000MO-US03565.

PR 18-FEB-2000; 2000MO-US04341.

PR 18-FEB-2000; 2000MO-US04342.

PR 02-MAR-2000: 2000MO-US05841.  
 PR 03-MAR-2000: 2000US-0187202.  
 PR 10-MAR-2000: 2000MO-US06319.  
 PR 15-MAR-2000: 2000MO-US06884.  
 PR 30-MAR-2000: 2000MO-US08439.  
 PR 17-MAY-2000: 2000MO-US13705.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;  
 DR WPI: 2001-016509/02.  
 DR N-PSDB: AAC91559.  
 XX  
 PT Twenty eight nucleic acids encoding PRO polypeptides which are useful  
 PT for treating various tumors, e.g. breast cancer and other  
 PT inflammatory, angiogenic and immunological disorders -  
 PS  
 PS Claim 31: Fig 14: 188bp; English.  
 XX  
 CC The present sequence is one of twenty eight novel PRO polypeptides. The  
 CC PRO polypeptides and their agonists, including antibodies, peptides, and  
 CC small molecule agonists, may be used to treat various tumors, e.g.,  
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal  
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,  
 CC central nervous system cancer, melanoma or leukaemia. They are also  
 CC useful for treating other disorders such as neuronal, glial, astrocytal,  
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and  
 CC blastocoeleic disorders, and inflammatory, angiogenic and immunological  
 CC disorders.  
 CC  
 SQ Sequence 185 AA;  
 XX  
 Query Match 99.0%; Score 984; DB 22; Length 185;  
 Best Local Similarity 98.9%; Pred. No. 3.2e-93;  
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKFTIYFAGLGVFLAPALANYNIDVNDNNAGSGOOSVSNNEHNAVYNDNNMGDSW 60  
 DB 1 MKFTIYFAGLGVFLAPALANYNIDVNDNNAGSGOOSVSNNEHNAVYNDNNMGDSW 60  
 QY 61 NSIWDYNGNGFAATRLFEQKTCIVHKMKREYVPSIQSLDALVKEKKLOGGPGPPKGLM 120  
 DB 61 NSIWDYNGNGFAATRLFEQKTCIVHKMKREYVPSIQSLDALVKEKKLOGGPGPPKGLM 120  
 QY 121 YSYNPNKVDLSTFKGKIANNCRGIPYMAEMQEASLFFSSGCTYTSVLMIYDISFCG 180  
 DB 121 YSYNPNKVDLSTFKGKIANNCRGIPYMAEMQEASLFFSSGCTYTSVLMIYDISFCG 180  
 QY 181 DYVEN 185  
 DB 181 DYVEN 185  
 RESULT 7  
 ABB95492  
 ID ABB95492 standard; Protein: 185 AA.  
 AC ABB95492;  
 XX  
 DT 19-JUL-2002 (first entry)  
 XX  
 DE Human angiogenesis related protein PRO1005 SEQ ID NO: 140.  
 XX  
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiac; cytoskeletal; antiangiogenic; hypotensive; vulneryary;  
 KW antiarteriosclerotic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200206284-A2.

XX  
 PD 31-JAN-2002.  
 XX  
 PF 09-JUL-2001: 2001MO-US21735.  
 XX  
 PR 20-JUL-2000: 2000US-219556P.  
 PR 25-JUL-2000: 2000US-220624P.  
 PR 25-JUL-2000: 2000US-220664P.  
 PR 28-JUL-2000: 2000MO-US20710.  
 PR 02-AUG-2000: 2000US-222695P.  
 PR 17-AUG-2000: 2000US-0643557.  
 PR 23-AUG-2000: 2000MO-US23522.  
 PR 24-AUG-2000: 2000MO-US23328.  
 PR 07-SEP-2000: 2000US-230978P.  
 PR 15-SEP-2000: 2000US-000000P.  
 PR 18-SEP-2000: 2000US-0664610.  
 PR 18-SEP-2000: 2000US-0665350.  
 PR 24-OCT-2000: 2000US-242922P.  
 PR 08-NOV-2000: 2000US-0709238.  
 PR 08-NOV-2000: 2000MO-US30952.  
 PR 10-NOV-2000: 2000MO-US30873.  
 PR 01-DEC-2000: 2000MO-US32678.  
 PR 20-DEC-2000: 2000US-0747259.  
 PR 20-DEC-2000: 2000MO-US34956.  
 PR 22-JAN-2001: 2001US-0767609.  
 PR 28-FEB-2001: 2001US-0796498.  
 PR 28-FEB-2001: 2001MO-US06520.  
 PR 01-MAR-2001: 2001MO-US06666.  
 PR 09-MAR-2001: 2001US-0802706.  
 PR 14-MAR-2001: 2001US-0808689.  
 PR 22-MAR-2001: 2001US-0816744.  
 PR 05-APR-2001: 2001US-0828366.  
 PR 10-MAY-2001: 2001US-0854208.  
 PR 10-MAY-2001: 2001US-0854280.  
 PR 25-MAY-2001: 2001US-0866028.  
 PR 25-MAY-2001: 2001US-0866034.  
 PR 25-MAY-2001: 2001MO-US17092.  
 PR 30-MAY-2001: 2001US-0870574.  
 PR 30-MAY-2001: 2001MO-US17443.  
 PR 01-JUN-2001: 2001MO-US17800.  
 PR 20-JUN-2001: 2001MO-US19692.  
 PR 28-JUN-2001: 2001MO-US00000.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODO/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONTI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 XX  
 PI Baker KP, Ferrera N, Gerber H, Gerritsen ME, Goddard A,  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 DR WPI: 2002-171999/22.  
 DR N-PSDB: ABL95630.  
 XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 PS  
 PS Claim 11: Fig 140: 567bp; English.  
 XX



CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hyper trophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.  
 XX

Sequence 185 AA:

Query Match 99.0%; Score 984; DB 23; Length 185;  
 Best Local Similarity 98.9%; Pred. No. 3.2e-93;  
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKFTVFAGLLGVFLPALANYNDVDDNNNGSGQSVSNNEHNVAVDNNNGDSW 60  
 DB 1 MKFTVFAGLLGVFLPALANYNDVDDNNNGSGQSVSNNEHNVAVDNNNGDSW 60  
 OY 61 NSIMDYGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGGPGPPKGLM 120  
 DB 61 NSIMDYGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGGPGPPKGLM 120  
 OY 121 YSNPNKVDLDSKFGKNIAMKRGIPTYMAEMQEASLFFYSGTCYTTSVLWIVDISFCG 180  
 DB 121 YSNPNKVDLDSKFGKNIAMKRGIPTYMAEMQEASLFFYSGTCYTTSVLWIVDISFCG 180  
 OY 181 DTIVEN 185  
 DB 181 DTIVEN 185

RESULT 8  
 ABB84886  
 ID ABB84886 standard; Protein; 185 AA.

XX ABB84886;

DT 16-MAY-2002 (first entry)

DE Human PRO1005 protein sequence SEQ ID NO:140.

XX Human; angiogenesis; cardiant; cyostatic; antiangiogenic; hypotensive;  
 KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.

XX WO200200690-A2.

PD 03-JAN-2002.

PF 20-JUN-2001; 2001WO-US19692.

XX 23-JUN-2000; 2000US-213637P.  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 28-JUL-2000; 2000US-220664P.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-222695P.  
 PR 23-AUG-2000; 2000US-222695P.  
 PR 24-AUG-2000; 2000US-222695P.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.

PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.

(GETH ) GENENTECH INC.

PI Baker KP, Ferrara N, Gerber H, Gertlsten ME, Goddard A,  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

DR WPI: 2002-090516/12.

XX N-PSDB; ABL8814L.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX Claim 11; Fig 140; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cyostatic,  
 CC antiangiogenic, hypotensive, vulnerability and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC e.g. cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarction, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.

XX Sequence 185 AA:

Query Match 99.0%; Score 984; DB 23; Length 185;  
 Best Local Similarity 98.9%; Pred. No. 3.2e-93;  
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKFTVFAGLLGVFLPALANYNDVDDNNNGSGQSVSNNEHNVAVDNNNGDSW 60  
 DB 1 MKFTVFAGLLGVFLPALANYNDVDDNNNGSGQSVSNNEHNVAVDNNNGDSW 60  
 OY 61 NSIMDYGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGGPGPPKGLM 120  
 DB 61 NSIMDYGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGGPGPPKGLM 120  
 OY 121 YSNPNKVDLDSKFGKNIAMKRGIPTYMAEMQEASLFFYSGTCYTTSVLWIVDISFCG 180  
 DB 121 YSNPNKVDLDSKFGKNIAMKRGIPTYMAEMQEASLFFYSGTCYTTSVLWIVDISFCG 180  
 OY 181 DTIVEN 185  
 DB 181 DTIVEN 185

RESULT 9  
AAU83665  
ID AAU83665 standard; protein; 185 AA.  
XX  
AC AAU83665;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Human PRO protein, seq ID No 148.  
XX  
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha.  
XX  
OS Homo sapiens.  
XX  
PN WO200208288-A2.  
XX  
PD 31-JAN-2002.  
XX  
PE 29-JUN-2001; 2001MO-US21066.  
XX  
XX 20-JUL-2000; 2000US-219556P.  
XX 25-JUL-2000; 2000US-220385P.  
XX 25-JUL-2000; 2000US-220605P.  
XX 25-JUL-2000; 2000US-220607P.  
XX 25-JUL-2000; 2000US-220624P.  
XX 25-JUL-2000; 2000US-220638P.  
XX 25-JUL-2000; 2000US-220664P.  
XX 25-JUL-2000; 2000US-220666P.  
XX 26-JUL-2000; 2000US-220893P.  
XX 28-JUL-2000; 2000US-220710P.  
XX 23-AUG-2000; 2000MO-US23322.  
XX 24-AUG-2000; 2000MO-US23328.  
XX 15-SEP-2000; 2000US-000000P.  
XX 10-NOV-2000; 2000MO-US30873.  
XX 28-NOV-2000; 2000US-253646P.  
XX 01-DEC-2000; 2000MO-US32678.  
XX 20-DEC-2000; 2000US-0747259.  
XX 20-DEC-2000; 2000MO-US34956.  
XX 28-FEB-2001; 2001MO-US06520.  
XX 10-MAY-2001; 2001US-0854280.  
XX 25-MAY-2001; 2001MO-US17092.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Matanabe CK, Wood WI;  
XX  
XX WPI: 2002-172001/22.  
XX  
XX N-PSDB; ABK33609.  
XX  
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumours  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
PT tumour or liver tumour -  
XX  
XX Claim 11; Figure 148; 359pp; English.  
XX  
XX The invention relates to one hundred and twenty two nucleic acids  
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,  
XX agonists and antagonists are useful for treating a PRO related disorder.  
XX The PRO polypeptides are useful for diagnosing tumours, especially lung  
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
XX liver tumour. The PRO polypeptides are useful for stimulating the  
XX proliferation of, or gene expression, in pericyte cells, for stimulating  
XX the proliferation of, or differentiation of chondrocyte cells, for  
XX stimulating the release of tumour necrosis factor-alpha from human blood,  
XX for stimulating or inhibiting the proliferation of normal human dermal

CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO  
CC protein sequences of the invention.  
XX  
SQ Sequence 185 AA;  
XX  
Query Match 99.0%; Score 984; DB 23; Length 185;  
Best Local Similarity 98.9%; Pred. No. 3.2e-93;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1 MKFTTFAGILGVFLAPALANTYNDVDDNNAGSGQSVSVNNEHVAVNDNNNGDSW 60  
DB 1 MKFTTFAGILGVFLAPALANTYNDVDDNNAGSGQSVSVNNEHVAVNDNNNGDSW 60  
QY 61 NSIMWYGNFPAATRLFOKTCIVHKMKKEVMPSTIOSIDALYKEKKLOGKPGGPPRGLM 120  
DB 61 NSIMWYGNFPAATRLFOKTCIVHKMKKEVMPSTIOSIDALYKEKKLOGKPGGPPRGLM 120  
QY 121 YSVNPKKVDLSKFGKNIAMNRCGIPYMAEMQEASLFFYSGTCYTSVLIVDISFCG 180  
DB 121 YSVNPKKVDLSKFGKNIAMNRCGIPYMAEMQEASLFFYSGTCYTSVLIVDISFCG 180  
QY 181 DIVEN 185  
DB 181 DIVEN 185  
XX  
RESULT 10  
AAB38329  
ID AAB38329 standard; protein; 186 AA.  
XX  
XX AAB38329;  
XX  
XX 31-JAN-2001 (first entry)  
XX  
XX Human secreted protein encoded by gene 9 clone HNSAD53.  
XX  
XX Immunosuppressive; antiarthritic; antitumour; antiproliferative;  
KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;  
KW nootropic; antibacterial; virucide; fungicide; ophthalmological; human;  
XX  
XX vulnerable; gene therapy; infection; secreted protein.  
XX  
XX Homo sapiens.  
XX  
XX WO200061623-A1.  
XX  
XX 19-OCT-2000.  
XX  
XX 06-APR-2000; 2000MO-US08979.  
XX  
XX 09-APR-1999; 99US-0128693.  
XX  
XX 26-APR-1999; 99US-0130991.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;  
PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;  
PI Young PE;  
XX  
XX WPI: 2000-647418/62.  
XX  
XX New nucleic acid molecules encoding 62 human secreted proteins for  
XX diagnosing, preventing, treating or ameliorating medical conditions and  
XX used as food additives or preservatives -  
XX  
XX Claim 11; Page 598; 716pp; English.  
XX  
XX Sequences AAB38321-B38396 represent the amino acid sequences of 62  
XX human secreted proteins encoded by the genes AAC69512-C69587. The genes  
XX and proteins are useful for preventing, ameliorating or treating medical  
XX conditions, e.g. by protein or gene therapy. The genes are isolated from

CC a range of human tissues disclosed in the specification. The nucleic  
CC acids, proteins, antibodies and (any)agonists are useful in the  
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.  
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms  
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac  
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)  
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)  
CC infections caused by bacteria, viruses and fungi; and (h) ocular  
CC disorders e.g. corneal infection. The polypeptides can also be used to  
CC aid wound healing and epithelial cell proliferation, to prevent skin  
CC aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis.

XX Sequence 186 AA;

Query Match 99.0%; Score 984; DB 21; Length 186;  
Best Local Similarity 98.9%; Pred. No. 3.2e-93;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLGVFLAPALANYNIDVNDNNAGSGQSVSVNNEHNVANVNDNNGMDSW 60  
DB 1 MKFTIVFAGLGVFLAPALANYNIDVNDNNAGSGQSVSVNNEHNVANVNDNNGMDSW 60  
QY 61 NSIMDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTIOSLDALVKEKKLOGKGGCGPPPKGLM 120  
DB 61 NSIMDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTIOSLDALVKEKKLOGKGGCGPPPKGLM 120  
QY 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQESLFFYSCTCTTSLVIMIVDISFCG 180  
DB 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQESLFFYSCTCTTSLVIMIVDISFCG 180  
QY 181 DTVEN 185  
DB 181 DTVEN 185

RESULT 11

ID AAM69974  
AAW69974 standard; Protein; 194 AA.

XX AC AAW69974;  
XX AC AAW69974;  
XX DT 16-NOV-1998 (first entry)  
XX DE Cancer associated protein.  
XX KW Cancer; PCR: Northern blotting; ribonuclease protection assay;  
XX KW diagnosis; metastatic cancer.  
XX OS Synthetic.  
XX OS Synthetic.  
XX PN WO9837187-A1.  
XX PD 27-AUG-1998.  
XX PF 18-FEB-1998; 98WO-JP00667.  
XX PR 21-FEB-1997; 97JP-0052508.  
XX PA (TAKI) TAKARA SHUZO CO LTD.  
XX PI Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;  
XX DR WPI: 1998-467552/40.  
XX PT Detection of cancer cells in tissue samples - by changes in mRNA  
XX PT expression compared to normal tissue of specific cancer-associated  
XX PS gene sequences  
XX PS Claim 14; Page 64-65; 92pp; Japanese.  
XX CC The cancer associated proteins AAW69974-W69976 where used in the method

CC of the invention to detect cancer cells in tissue samples or biological  
CC fluids. They are detected by monitoring the change in mRNA expression  
CC as compared to normal tissue of one or more cancer-associated genes  
CC whose cDNA stringently hybridises to cancer associated gene nucleic acid  
CC fragments. The change in expression may be an increase or a decrease  
CC compared to normal tissue. The mRNA expression may be determined by  
CC PCR, Northern blotting or ribonuclease protection assay, or by  
CC determining the change in the amount of protein encoded by the gene(s) as  
CC compared to normal tissue, for example by using a labelled antibody  
CC recognising the protein. Detection of cancer cells for cancer diagnosis,  
CC including detection of metastatic cancer cells in tissues other than the  
CC primary tumour site.

XX Sequence 194 AA;

Query Match 99.0%; Score 984; DB 19; Length 194;  
Best Local Similarity 98.9%; Pred. No. 3.4e-93;  
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLGVFLAPALANYNIDVNDNNAGSGQSVSVNNEHNVANVNDNNGMDSW 60  
DB 10 MKFTIVFAGLGVFLAPALANYNIDVNDNNAGSGQSVSVNNEHNVANVNDNNGMDSW 69  
QY 61 NSIMDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTIOSLDALVKEKKLOGKGGCGPPPKGLM 120  
DB 70 NSIMDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTIOSLDALVKEKKLOGKGGCGPPPKGLM 129  
QY 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQESLFFYSCTCTTSLVIMIVDISFCG 180  
DB 130 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQESLFFYSCTCTTSLVIMIVDISFCG 189  
QY 181 DTVEN 185  
DB 190 DTVEN 194

RESULT 12

ID AAY76591  
AAV76591 standard; Protein; 194 AA.

XX AC AAY76591;  
XX AC AAY76591;  
XX DT 10-APR-2000 (first entry)  
XX DE Human ovarian tumor EST fragment encoded protein 87.  
XX KW Expressed sequence tag; EST; human; ovarian tumor; anticancer;  
XX KW gene therapy; treatment.  
XX OS Homo sapiens.  
XX OS Homo sapiens.  
XX PN DE19817557-A1.  
XX PD 21-OCT-1999.  
XX PF 09-APR-1998; 98DE-1017557.  
XX PR 09-APR-1998; 98DE-1017557.  
XX PA (METRA-) METAGEN GES GENOMFORSCHUNG MBH.  
XX PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;  
XX DR WPI: 1999-591920/51.  
XX DR N-PSDB; AAZ77487.  
XX PT New nucleic acid sequences expressed in ovarian, and some other, cancer  
XX PT tissues, and derived polypeptides, for treatment of ovarian cancer and  
XX PT identification of therapeutic agents  
XX PS Claim 25; Page 279; 310pp; German.  
XX CC This invention describes novel nucleic acid (cDNA) sequences (A) which

CC have anticancer activity and are highly expressed in ovarian tumor  
 CC tissue (and some also in testis and breast cancer tissue). The products  
 CC of the invention can be used for gene therapy. (A) are used (i) for  
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete  
 CC genes. (B) are used (i) to identify agents suitable for treatment of  
 CC ovarian cancer; (ii) directly for treating this form of cancer  
 CC (including expression from gene therapy vectors) and (iii) for generation  
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed  
 CC sequence tags) from a particular tissue type before comparison of  
 CC expression patterns. This allows a significantly longer fragment of the  
 CC gene to be revealed, so should reduce the number of failures associated  
 CC with the fact that ESTs from different libraries may represent different  
 CC parts of the same unknown gene, distorting the estimated frequency of  
 CC occurrence in a particular tissue. AAY6505-Y/6638 represent protein  
 CC fragments encoded by the human ovarian tumor CDNA library derived EST  
 CC fragments represented in AAZ77450-277572.

XX Sequence 194 AA;

Query Match 99.0%; Score 984; DB 20; Length 194;  
 Best Local Similarity 98.9%; Pred. No. 3.4e-93;  
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLPALANYNIDVNDNNAGSGQGSVSNNEHNVANVDNNNGWDSW 60  
 Db 10 MKFTIVFAGLLGVFLPALANYNINVDNNAGSGQGSVSNNEHNVANVDNNNGWDSW 69

QY 61 NSIMWDYNGEFAATRLFOKKTICIVHKMKKEVMPISLDALVKEKKLOGKGGPPPKGLM 120  
 Db 70 NSIMWDYNGEFAATRLFOKKTICIVHKMKKEVMPISLDALVKEKKLOGKGGPPPKGLM 129

QY 121 YSVNPNKVDLDSKFGKNIANNMCRGIPTYMAEEMQESLFFYSGTCYTSVLMIVDISFCG 180  
 Db 130 YSVNPNKVDLDSKFGKNIANNMCRGIPTYMAEEMQESLFFYSGTCYTSVLMIVDISFCG 189

QY 181 DTVEN 185  
 Db 190 DTVEN 194

RESULT 13  
 AABP09922  
 ID AABP09922 standard; Protein; 184 AA.

AC AABP09922;  
 XX  
 DT 24-JUN-2002 (first entry)  
 XX  
 DE Human ORFX protein sequence SEQ ID NO:19826.  
 XX  
 XX Human: open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
 KW hypertension; hypothyroidism; cholesterol ester storage disease;  
 KW immune deficiency; immune disorder; infectious disease;  
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 KW myasthenia gravis.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192523-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 29-MAY-2001; 2001MO-US10836.  
 XX  
 PR 30-MAY-2000; 2000US-206132P.  
 PR 29-AUG-2000; 2000US-228716P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shinkets RA, Leach MD;

XX WPI: 2002-106308/14.  
 DR N-PSDB: ABN25674.  
 XX  
 PR Novel human polypeptides and polynucleotides useful for diagnosing,  
 PR preventing and treating cardiovascular disease, neurodegenerative,  
 PR hyperproliferative disorders and autoimmune disorders  
 PS Disclosure; SEQ ID 19826; 1037pp; English.

XX The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
 CC in the specification)). ABN15762 to ABN27232 encode the human ORFX  
 CC proteins given in AABP00010 to AABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with an ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 184 AA;

Query Match 60.6%; Score 602; DB 23; Length 184;  
 Best Local Similarity 60.5%; Pred. No. 7.3e-54;  
 Matches 112; Conservative 28; Mismatches 41; Indels 4; Gaps 3;

QY 1 MKFTIVFAGLLGVFLPALANYNIDVNDNNAGSGQGSVSNNEHNVANVDNNNGWDS 59  
 Db 1 MKLTFVYVGLGLLAPGFA-YTVNINQNDANVDSGQGSVSNNGHVNANIDNNNGWDS 59

QY 60 WNSIMWDYNGEFAATRLFOKKTICIVHKMKKEVMPISLDALVKEKKLOGKGGPPPKGL 119  
 Db 60 WNSIMWDYNGEFAATRLFOKKTICIVHKMKKEVMPISLDALVKEKKLOGKGGPPPKGL 117

QY 120 YSVNPNKVDLDSKFGKNIANNMCRGIPTYMAEEMQESLFFYSGTCYTSVLMIVDISFC 179  
 Db 118 WNSIMPTREYEDVNTGPKTASMCRGIPTYVAEETIPQNPVLSKKCYTANILILMSFC 177

QY 180 GDYVE 184  
 Db 178 ETSVE 182

RESULT 14  
 AAY66690  
 ID AAY66690 standard; Protein; 184 AA.

AC AAY66690;  
 XX  
 DT 05-APR-2000 (first entry)  
 XX  
 DE Membrane-bound protein PRO813.  
 XX  
 PR Membrane-bound polypeptide: PRO polypeptide: LDL receptor; TIE ligand;  
 KW pharmaceutical; receptor immunoadhesin; gene mapping.  
 XX  
 OS Homo sapiens.

XX	PN	WO963088-A2.	PR	25-JUN-1998;	98US-0090678
XX	XX		PR	25-JUN-1998;	98US-0090688
PD	09-DEC-1999.		PR	25-JUN-1998;	98US-0090699
XX	XX		PR	25-JUN-1998;	98US-0090691
PF	02-JUN-1999;	99WO-US12252.	PR	25-JUN-1998;	98US-0090694
XX	XX		PR	25-JUN-1998;	98US-0090695
XX	XX		PR	25-JUN-1998;	98US-0090696
XX	XX		PR	25-JUN-1998;	98US-0090697
XX	XX		PR	25-JUN-1998;	98US-0090698
XX	XX		PR	25-JUN-1998;	98US-0090699
XX	XX		PR	25-JUN-1998;	98US-0090700
XX	XX		PR	25-JUN-1998;	98US-0090701
XX	XX		PR	25-JUN-1998;	98US-0090702
XX	XX		PR	25-JUN-1998;	98US-0090703
XX	XX		PR	25-JUN-1998;	98US-0090704
XX	XX		PR	25-JUN-1998;	98US-0090705
XX	XX		PR	25-JUN-1998;	98US-0090706
XX	XX		PR	25-JUN-1998;	98US-0090707
XX	XX		PR	25-JUN-1998;	98US-0090708
XX	XX		PR	25-JUN-1998;	98US-0090709
XX	XX		PR	25-JUN-1998;	98US-0090710
XX	XX		PR	25-JUN-1998;	98US-0090711
XX	XX		PR	25-JUN-1998;	98US-0090712
XX	XX		PR	25-JUN-1998;	98US-0090713
XX	XX		PR	25-JUN-1998;	98US-0090714
XX	XX		PR	25-JUN-1998;	98US-0090715
XX	XX		PR	25-JUN-1998;	98US-0090716
XX	XX		PR	25-JUN-1998;	98US-0090717
XX	XX		PR	25-JUN-1998;	98US-0090718
XX	XX		PR	25-JUN-1998;	98US-0090719
XX	XX		PR	25-JUN-1998;	98US-0090720
XX	XX		PR	25-JUN-1998;	98US-0090721
XX	XX		PR	25-JUN-1998;	98US-0090722
XX	XX		PR	25-JUN-1998;	98US-0090723
XX	XX		PR	25-JUN-1998;	98US-0090724
XX	XX		PR	25-JUN-1998;	98US-0090725
XX	XX		PR	25-JUN-1998;	98US-0090726
XX	XX		PR	25-JUN-1998;	98US-0090727
XX	XX		PR	25-JUN-1998;	98US-0090728
XX	XX		PR	25-JUN-1998;	98US-0090729
XX	XX		PR	25-JUN-1998;	98US-0090730
XX	XX		PR	25-JUN-1998;	98US-0090731
XX	XX		PR	25-JUN-1998;	98US-0090732
XX	XX		PR	25-JUN-1998;	98US-0090733
XX	XX		PR	25-JUN-1998;	98US-0090734
XX	XX		PR	25-JUN-1998;	98US-0090735
XX	XX		PR	25-JUN-1998;	98US-0090736
XX	XX		PR	25-JUN-1998;	98US-0090737
XX	XX		PR	25-JUN-1998;	98US-0090738
XX	XX		PR	25-JUN-1998;	98US-0090739
XX	XX		PR	25-JUN-1998;	98US-0090740
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XX	XX		PR	25-JUN-1998;	98US-0090742
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XX	XX		PR	25-JUN-1998;	98US-0090744
XX	XX		PR	25-JUN-1998;	98US-0090745
XX	XX		PR	25-JUN-1998;	98US-0090746
XX	XX		PR	25-JUN-1998;	98US-0090747
XX	XX		PR	25-JUN-1998;	98US-0090748
XX	XX		PR	25-JUN-1998;	98US-0090749
XX	XX		PR	25-JUN-1998;	98US-0090750
XX	XX		PR	25-JUN-1998;	98US-0090751
XX	XX		PR	25-JUN-1998;	98US-0090752
XX	XX		PR	25-JUN-1998;	98US-0090753
XX	XX		PR	25-JUN-1998;	98US-0090754
XX	XX		PR	25-JUN-1998;	98US-0090755
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XX	XX		PR	25-JUN-1998;	98US-0090757
XX	XX		PR	25-JUN-1998;	98US-0090758
XX	XX		PR	25-JUN-1998;	98US-0090759
XX	XX		PR	25-JUN-1998;	98US-0090760
XX	XX		PR	25-JUN-1998;	98US-0090761
XX	XX		PR		

PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
DR WPI: 2000-072883/06.  
DR N-PSDB; AAB65029.  
XX  
PT Membrane-bound proteins and related nucleotide sequences  
XX  
PS claim 12; Fig 149; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 184 AA;  
Query Match 19.0%; Score 189; DB 21; Length 184;  
Best Local Similarity 27.1%; Pred. No. 2.6e-11;  
Matches 52; Conservative 40; Mismatches 78; Indels 22; Gaps 4;  
QY 1 MKFTVFAGLLGVFLAPALANYINDNDNNAGSGQSVSYNNEHNVANVDNNGWDSW 60  
DB 1 MKILVAFVLVLTIFGQSGYEVFNISPSNNGVDETITDNEKNTAIVNHAGSCSS 60  
QY 61 NSIMDYGNGFAATRLFFQKTCIVHKMKKEVMDSTQSLDALVKEKKLOGGPGGPPKGLM 120  
DB 61 TTTFYKHGYIASRYLSRACFLKMDHONIPPLNLMOWIYEKQALDN-----M 110  
QY 121 VS-----VAPKNVDDLK-----FGKNIANMCGRIPTYMAEEMOESLFFYSGTCYTT 169  
DB 111 FSNKYTWKYNPLESLIKQVDFLGSPIEKLCKHILPYKGEVENTHNVAGGCAKAG 169  
QY 170 VLMIVDISFCGD 181  
DB 170 LIGIGISICAD 181  
RESULT 15  
AAB65213  
ID AAB65213 standard; Protein; 184 AA.  
XX  
AC AAB65213;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO813 (UNQ465) protein sequence SEQ ID NO:221.  
XX  
KW Human; secreted and transmembrane protein; PRO; cytosolic;  
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay.  
XX  
OS Homo sapiens.  
XX  
PN WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000WO-US08439.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.

PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146322.  
PR 17-AUG-1999; 99US-0149396.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 08-OCT-1999; 99US-0158663.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03365.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
DR WPI: 2001-032160/04.  
DR N-PSDB: AAF44175.  
XX  
PT PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
XX  
PS Claim 12; Fig 149; 935pp; English.  
XX  
CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 184 AA;  
Query Match 19.0%; Score 189; DB 22; Length 184;  
Best Local Similarity 27.1%; Pred. No. 2.6e-11;  
Matches 52; Conservative 40; Mismatches 78; Indels 22; Gaps 4;  
QY 1 MKFTVFAGLLGVFLAPALANYINDNDNNAGSGQSVSYNNEHNVANVDNNGWDSW 60  
DB 1 MKILVAFVLVLTIFGQSGYEVFNISPSNNGVDETITDNEKNTAIVNHAGSCSS 60  
QY 61 NSIMDYGNGFAATRLFFQKTCIVHKMKKEVMDSTQSLDALVKEKKLOGGPGGPPKGLM 120  
DB 61 TTTFYKHGYIASRYLSRACFLKMDHONIPPLNLMOWIYEKQALDN-----M 110  
QY 121 VS-----VAPKNVDDLK-----FGKNIANMCGRIPTYMAEEMOESLFFYSGTCYTT 169  
DB 111 FSNKYTWKYNPLESLIKQVDFLGSPIEKLCKHILPYKGEVENTHNVAGGCAKAG 169  
QY 170 VLMIVDISFCGD 181

Mon Apr 14 14:01:13 2003

us-09-821-726a-13.rag

Page 13

Db 170 LGLGISICAD 181

Search completed: April 11, 2003, 16:11:10  
Job time : 53.9086 secs





GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2003, 16:06:33 ; Search time 3.92822 Seconds  
(without alignments)  
474.899 Million cell updates/sec

Title:	US-09-821-726A-3
Perfect score:	81
Sequence:	1 KKLQCKGPGGPPK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

Database :

A\_Geneseq\_101002 : \*

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18:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT : *
19:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT : *
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21:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT : *
22:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT : *
23:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	81	100.0	185	20	AA099667	Human secreted pro
2	81	100.0	185	21	AA024067	Human PRO1005 prot
3	81	100.0	185	21	AA087272	Human signal peptid
4	81	100.0	185	21	AA066806	Membrane-bound pro
5	81	100.0	185	22	AA065209	Human PRO1005 (UNG
6	81	100.0	185	22	AA050957	Human PRO1005 prot
7	81	100.0	185	23	AB095492	Human angiogenesisis
8	81	100.0	185	23	AB084886	Human PRO1005 prot
9	81	100.0	185	23	AA083665	Human PRO protein,
10	81	100.0	186	21	AA083529	Human secreted pro

11	81	100.0	194	19	AAW69974
12	81	100.0	194	20	AAV76591
13	52	64.2	103	21	AA841048
14	52	64.2	103	23	ABP35077
15	52	64.2	163	23	AA001151
16	52	64.2	279	22	AAU03592
17	52	64.2	467	22	AA894309
18	51	63.0	108	22	AA004166
19	51	63.0	125	22	AA011472
20	50.5	62.3	140	22	AA008289
21	50	61.7	673	21	AAV58042
22	49.5	61.1	147	21	AA006867
23	49	60.5	84	22	AA013411
24	49	60.5	115	22	AA008183
25	49	60.5	120	22	AA000652
26	49	60.5	855	22	AAU08748
27	49	60.5	855	23	ABR08448
28	48	59.3	127	22	AA005497
29	48	59.3	128	22	AA003368
30	48	59.3	247	20	AAH89037
31	48	59.3	247	22	ABR51188
32	48	59.3	532	21	AB842542
33	48	59.3	774	22	AB864148
34	48	59.3	2061	22	ABR71759
35	47.5	58.6	109	22	AA009868
36	47	58.0	71	22	AAU41527
37	47	58.0	102	22	AA000839
38	47	58.0	1963	22	ABR62819
39	46.5	57.4	127	22	AAU07630
40	46	56.8	99	22	AA011475
41	46	56.8	114	22	AA003173
42	46	56.8	125	22	AA012870
43	46	56.8	135	22	AA002140
44	46	56.8	135	22	AA011562
45	46	56.8	141	22	AA006613

## ALIGNMENTS

XX	RESULT 1
XX	AAW99667
ID	AAW99667 standard; Protein: 185 AA.
XX	
AC	AAW99667;
XX	
DI	07-JUN-1999 (first entry)
XX	
DE	Human secreted protein clone ej90_5 protein.
XX	
KW	Human: secreted protein; nutritional; cytokine; cell proliferation;
KW	differentiation; immune stimulating; vaccine; haematopoiesis; regulation
KW	tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;
KM	anti-inflammatory; cadherin; tumour invasion suppressor;
KW	tumour inhibition; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO9907840-A1.
XX	
PD	18-FEB-1999.
XX	
PF	06-AUG-1998; 98WO-US16318.
XX	
PR	04-AUG-1998; 98US-0130189.
PR	06-AUG-1997; 97US-0906708.
XX	
PA	(GENY ) GENETICS INST INC.
XX	
PI	Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;
PI	Merberg D, Racie LA, Steinsinger RJ, Treacy M;
XX	
DR	WPI; 1999-167419/14.

1-3. rag  
element, considering

DR N-PSDB: AAX19493.  
XX  
XX New polynucleotides encoding secreted human proteins - derived from  
PT fetal kidney, adult testes, adult brain, adult heart, adult placenta  
PT or adult retina cDNA libraries  
XX  
XX  
PS Claim 34; Page 98-99; 107pp; English.  
XX  
XX The present sequence represents a human secreted protein. The secreted  
CC protein can have activities such as: nutritional activity, cytokine and -  
CC cell proliferation/differentiation activity, immune stimulating (e.g. as  
CC vaccines) or suppressing activity, haematopoiesis regulating activity,  
CC tissue growth activity, activin/inhibin activity, chemotactic/  
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/  
CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion  
CC suppressor activity, and tumour inhibition activity. The secreted  
CC protein polynucleotides and proteins are predicted to have biological  
CC activities which would make them suitable for treating, preventing or  
CC ameliorating medical conditions in humans and animals. The  
CC polynucleotides are also stated to be useful for gene therapy.  
XX  
SQ Sequence 185 AA:  
XX  
XX  
XX Query Match 100.0%; Score 81; DB 20; Length 185;  
XX Best Local Similarity 100.0%; Pred. No. 0.0034;  
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KKLQGGPGGPPPK 14  
DB 104 KKLQGGPGGPPPK 117  
XXXXXXXXXXXXXXXXXXXX  
RESULT 2  
AAB24067  
ID AAB24067 standard; Protein: 185 AA.  
XX  
XX AAB24067;  
AC  
XX  
XX 29-JAN-2001 (first entry)  
DT  
DE Human PRO1005 protein sequence SEQ ID NO:14.  
XX  
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
KW neotropic; neuroprotective; antiinflammatory; immunosuppressive;  
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
KW neuronal disorder; glial disorder; astrocyt disorder; angiogenic;  
KW hypothalamic disorder; glandular disorder; macrophage disorder;  
KW epithelial disorder; stromal disorder; blastocoele disorder;  
KW inflammatory disorder; immunologic disorder.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200053755-A2.  
PN  
XX  
XX 14-SEP-2000.  
PD  
XX  
XX 06-JAN-2000; 2000WO-US00376.  
PF  
XX  
XX 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 26-JUL-1999; 99US-0145698.  
PR 30-NOV-1999; 99WO-US28313.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
XX  
XX (GENTH ) GENTECH INC.  
PA  
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
PI Watanabe CK, Wood WI;  
XX

DR WPI: 2000-572270/53.  
DR N-PSDB: AAC58377.  
XX  
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
PT treatment, diagnosis and prevention of cancer -  
XX  
XX  
XX Claim 61; Fig 22; 286pp; English.  
XX  
XX The present invention describes an isolated antibody that binds to  
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,  
CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1133, PRO1182, PRO1184,  
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,  
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
CC growth. The PRO polypeptides and nucleotides are useful in the  
CC treatment, diagnosis and prevention of cancer. The antibodies and other  
CC anti-tumour compounds may be used to treat various conditions, including  
CC those characterised by overexpression and/or activation of the amplified  
CC PRO genes. Exemplary conditions or disorders to be treated with such  
CC antibodies and other compounds include benign or malignant tumours  
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),  
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,  
CC glial, astrocyt, hypothalamic and other glandular, macrophage,  
CC epithelial, stromal and blastocoele disorders, and inflammatory,  
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
CC primers and hybridisation probes used in the isolation of the human PRO  
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
CC PRO polynucleotide and protein sequences given in the exemplification of  
CC the present invention.  
XX  
XX  
SQ Sequence 185 AA:  
XX  
XX  
XX Query Match 100.0%; Score 81; DB 21; Length 185;  
XX Best Local Similarity 100.0%; Pred. No. 0.0034;  
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KKLQGGPGGPPPK 14  
DB 104 KKLQGGPGGPPPK 117  
XXXXXXXXXXXXXXXXXXXX  
RESULT 3  
AAY87272  
ID AAY87272 standard; Protein: 185 AA.  
XX  
XX AAY87272;  
AC  
XX  
XX 11-MAY-2000 (first entry)  
DT  
DE Human signal peptide containing protein HSP-49 SEQ ID NO:49.  
XX  
XX  
XX Human; signal peptide-containing protein; HSP; diagnosis; cancer;  
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
KW antimicrobial; neuroprotective; cardiovascular; hepatotropic;  
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;  
KW reproductive disorder; developmental disorder; arteriosclerosis;  
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
KW Parkinson's disease; Huntington's disease; ovulatory defect;  
KW muscular dystrophy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200000610-A2.  
PN  
XX  
XX 06-JAN-2000.  
PD  
XX  
XX 25-JUN-1999; 99WO-US14484.  
PF  
XX  
XX 26-JUN-1998; 98US-0090762.  
PR 31-JUL-1998; 98US-0094983.  
XX

PR 01-OCT-1998; 98US-0102686.  
PR 11-DEC-1998; 98US-0112129.  
PA (INCY-) INCYTE PHARM INC.  
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
PI Bandman O;  
XX WPI: 2000-160673/14.  
DR N-PSDB: AAZ98157.  
DR  
XX  
PT New human signal peptide-containing proteins useful in treatment,  
PT prevention and diagnosis of e.g. cancer, inflammation and  
PT cardiovascular disease  
XX  
PS Claim 1; Page 193-194; 327pp; English.  
XX  
CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the  
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,  
CC neuroprotective, cardiovascular and antiasthmatic activities, and can  
CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
CC associated with decreased activity or function of HSP. Antagonists of  
CC HSP are used to treat or prevent disorders associated with increased  
CC activity or function of HSP. Such diseases include cell proliferation  
CC (including cancer), inflammation, cardiovascular, neurological,  
CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
CC asthma, Crohn's disease, microbial or other infections, congestive or  
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases), schizophrenia, ovulatory defects, muscular dystrophy). HSP  
CC nucleic acids can be used for the recombinant production of HSP, for  
CC detecting HSP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring) in gene therapy, as antisense,  
CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
CC or genetic variations, and for chromosomal mapping. HSP are also used to  
CC raise specific antibodies (Ab) and to screen for agonists and  
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic  
CC antagonists, in competitive drug screens, and for purification of HSP  
CC from natural sources.  
XX  
SQ Sequence 185 AA;  
XX  
Query Match 100.0%; Score 81; DB 21; Length 185;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KKIQKGGPGPPK 14  
Db 104 KKIQKGGPGPPK 117  
IIIIIIIIIIII  
RESULT 4  
AAV6686  
ID AAV6686 standard; protein; 185 AA.  
XX  
AC AAV6686;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO1005.  
XX  
KM Membrane-bound polypeptide: PRO polypeptide; LDL receptor; TIE ligand;  
KM pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
OS Homo sapiens.  
XX  
PN WO963088-A2.  
XX  
PD 09-DEC-1999.  
XX

PF 02-JUN-1999; 99WO-US12252.  
XX  
PR 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089952.  
PR 19-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 25-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.

PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 02-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095283.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096737.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.  
PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JAN-1999; 99US-0115565.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WJ, Yuan J;  
XX WPI; 2000-072883/06.  
DR N-PSDB; AA265023.  
DR

XX  
PT Membrane-bound proteins and related nucleotide sequences -  
XX  
PS claim 12; Fig 139; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 185 AA;  
OY 1 KKLGGKPGCGPPPK 14  
Db 104 KKLGGKPGCGPPPK 117  
Query Match 100.0%; Score 81; DB 21; Length 185;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
RESULT 5  
AAB65209  
ID AAB65209 standard; Protein; 185 AA.  
XX  
AC AAB65209;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.  
XX  
KW Human; secreted and transmembrane protein; PRO; cytosolic;  
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay.  
XX  
OS Homo sapiens.  
XX  
FN WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000WO-US08439.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 17-AUG-1999; 99US-0149396.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 08-OCT-1999; 99US-0158663.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000MO-US05004.  
 PR 02-MAR-2000; 2000MO-US05841.  
 PR 15-MAR-2000; 2000MO-US06884.  
 PR 20-MAR-2000; 2000MO-US07377.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Ashtkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Geber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX  
 DR WPI: 2001-032160/04.  
 N-PSDB: AAF44169.  
 XX  
 PT PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -  
 XX  
 PS Claim 12; Fig 139; 935pp; English.  
 XX  
 CC The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65114 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SQ Sequence 185 AA:  
 Query Match 100.0%; Score 81; DB 22; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 0.0034;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLQKGKPGGPPK 14  
 ||||||||||||  
 DB 104 KKLQKGKPGGPPK 117  
 RESULT 6  
 AAB50957  
 ID AAB50957 standard; Protein: 185 AA.  
 XX  
 AC AAB50957;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Human PRO1005 protein.  
 XX  
 KM Human; PRO; cytostatic; neuroprotective; respiratory general;  
 KM antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;  
 KM PRO agonist; cancer; inflammatory disorder; immunological disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073348-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 30-MAY-2000; 2000MO-US14941.  
 XX  
 PR 02-JUN-1999; 99MO-US12252.  
 PR 22-JUN-1999; 99US-0140650.  
 PR 23-JUN-1999; 99US-0141037.  
 XX

PR 20-JUL-1999; 99US-0144758.  
 PR 01-SEP-1999; 99MO-US20111.  
 PR 08-SEP-1999; 99MO-US20594.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 01-DEC-1999; 99MO-US28634.  
 PR 02-DEC-1999; 99MO-US28551.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30999.  
 PR 06-JAN-2000; 2000MO-US00376.  
 PR 11-FEB-2000; 2000MO-US03565.  
 PR 18-FEB-2000; 2000MO-US04341.  
 PR 02-MAR-2000; 2000MO-US05841.  
 PR 03-MAR-2000; 2000MO-US06884.  
 PR 10-MAR-2000; 2000MO-US06319.  
 PR 15-MAR-2000; 2000MO-US06884.  
 PR 30-MAR-2000; 2000MO-US08439.  
 PR 17-MAY-2000; 2000MO-US13705.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;  
 PI  
 XX  
 DR WPI: 2001-016509/02.  
 N-PSDB: AAC91559.  
 XX  
 PT Twenty eight nucleic acids encoding PRO polypeptides which are useful  
 PT for treating various tumors, e.g. breast cancer, and other  
 PT inflammatory, angiogenic and immunological disorders -  
 XX  
 PS Claim 31; Fig 14; 188pp; English.  
 XX  
 CC The present sequence is one of twenty eight novel PRO polypeptides. The  
 CC PRO polypeptides and their agonists, including antibodies, peptides, and  
 CC small molecule agonists, may be used to treat various tumors, e.g.,  
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal  
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,  
 CC central nervous system cancer, melanoma or leukemia. They are also  
 CC useful for treating other disorders such as neuronal, glial, astrocytal,  
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and  
 CC blastocoele disorders, and inflammatory, angiogenic and immunological  
 CC disorders.  
 XX  
 SQ Sequence 185 AA:  
 Query Match 100.0%; Score 81; DB 22; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 0.0034;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KKLQKGKPGGPPK 14  
 ||||||||||||  
 DB 104 KKLQKGKPGGPPK 117  
 RESULT 7  
 ABB95492  
 ID ABB95492 standard; Protein: 185 AA.  
 XX  
 AC ABB95492;  
 XX  
 DT 19-JUL-2002 (first entry)  
 XX  
 DE Human angiogenesis related protein PRO1005 SEQ ID NO: 140.  
 XX  
 KM Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KM cardiac; cytostatic; antiangiogenic; hypotensive; vulnerary;  
 KM antiarteriosclerotic.  
 XX  
 OS Homo sapiens.  
 XX

PN WO200208284-A2.  
XX  
XX 31-JAN-2002.  
XX  
PF 09-JUL-2001; 2001WO-US21735.  
XX  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 15-SEP-2000; 2000US-000000P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 01-JUN-2001; 2001WO-US17443.  
PR 20-JUN-2001; 2001WO-US17800.  
PR 28-JUN-2001; 2001WO-US19692.  
XX  
XX (GETH) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANU/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
XX  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
XX MPI: 2002-171999/22.  
XX  
XX N-PSDB: ABL95630.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
XX infarction), endothelial or angiogenic disorders in a mammal -  
XX  
XX Claim 11; Fig 140; 567pp; English.

XX  
XX The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a PRO protein of the invention.  
XX  
SQ Sequence 185 AA;  
Query Match 100.0%; Score 81; DB 23; Length 185;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KRIQKGPGGPPPK 14  
DB 104 KRIQKGPGGPPPK 117  
RESULT 8  
ABR84886  
ID ABR84886 standard; Protein; 185 AA.  
XX  
XX ABR84886;  
AC  
XX  
XX 16 MAY-2002 (first entry)  
DE Human PRO1005 protein sequence SEQ ID NO:140.  
XX  
XX  
XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;  
XX vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
XX age-related macular degeneration; arterial restenosis; angina;  
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
XX lymphangitis; tumor angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping.  
OS Homo sapiens.  
XX  
XX WO200200690-A2.  
XX  
XX 03-JAN-2002.  
XX  
XX 20-JUN-2001; 2001WO-US19692.  
XX  
XX  
XX 23-JUN-2000; 2000US-213637P.  
XX 20-JUL-2000; 2000US-219556P.  
XX 25-JUL-2000; 2000US-220624P.  
XX 25-JUL-2000; 2000US-220664P.  
XX 28-JUL-2000; 2000US-222695P.  
XX 02-AUG-2000; 2000WO-US20710.  
XX 17-AUG-2000; 2000US-222695P.  
XX 23-AUG-2000; 2000US-0643657.  
XX 23-AUG-2000; 2000WO-US23522.  
XX 24-AUG-2000; 2000WO-US23328.  
XX 07-SEP-2000; 2000US-230978P.  
XX 18-SEP-2000; 2000US-0664610.  
XX 18-SEP-2000; 2000US-0665350.  
XX 24-OCT-2000; 2000US-242922P.  
XX 08-NOV-2000; 2000US-0709238.  
XX 10-NOV-2000; 2000WO-US30873.  
XX 01-DEC-2000; 2000WO-US32678.  
XX 20-DEC-2000; 2000US-0747259.  
XX 20-DEC-2000; 2000WO-US34956.  
XX 22-JAN-2001; 2001US-0767609.  
XX 28-FEB-2001; 2001US-0796498.  
XX 28-FEB-2001; 2001WO-US06520.  
XX 01-MAR-2001; 2001WO-US06666.  
XX 09-MAR-2001; 2001US-0802706.  
XX 14-MAR-2001; 2001US-0808689.

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PF      29-JUN-2001: 2001WO-US21066.
XX      20-JUL-2000: 2000US-219556P.
PR      25-JUL-2000: 2000US-220585P.
PR      25-JUL-2000: 2000US-220605P.
PT      25-JUL-2000: 2000US-220607P.
PR      25-JUL-2000: 2000US-220624P.
PR      25-JUL-2000: 2000US-220638P.
PR      25-JUL-2000: 2000US-220664P.
PR      25-JUL-2000: 2000US-220666P.
PR      26-JUL-2000: 2000US-220893P.
PR      28-JUL-2000: 2000WO-US20710.
PR      23-AUG-2000: 2000WO-US23528.
PR      24-AUG-2000: 2000WO-US23528.
PR      15-SEP-2000: 2000US-000000P.
PR      10-NOV-2000: 2000WO-US30873.
PR      28-NOV-2000: 2000WO-US25646P.
PR      01-DEC-2000: 2000WO-US32678.
PR      20-DEC-2000: 2000WO-US47259.
PR      20-DEC-2000: 2000WO-US49456.
PR      28-FEB-2001: 2001WO-US06520.
PR      10-MAY-2001: 2001WO-US854280.
PR      25-MAY-2001: 2001WO-US17092.
XX      (GETH ) GENENTECH INC.
XX      Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ:
PI      Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI:
XX      WPI: 2002-172001/22.
XX      N-PSDB; ABR33609.
XX      One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT      useful for treating a PRO related disorder and for diagnosing tumours
PT      such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT      tumour or liver tumour -
XX      Claim 11; Figure 148; 359pp; English.
XX      The invention relates to one hundred and twenty two nucleic acids
XX      encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX      encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX      agonists and antagonists are useful for treating a PRO related disorder.
XX      The PRO polypeptides are useful for diagnosing tumours, especially lung
XX      cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX      liver tumour. The PRO polypeptides are useful for stimulating the
XX      proliferation of, or gene expression, in pericyte cells, for
XX      the proliferation or differentiation of chondrocyte cells, for
XX      stimulating the release of tumour necrosis factor-alpha from human blood,
XX      for stimulating or inhibiting the proliferation of normal human dermal
XX      fibroblast cells. The PRO polypeptide may also be used as molecular
XX      weight markers and for tissue typing. The PRO nucleic acids have
XX      applications in molecular biology, including use as hybridisation probes,
XX      and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
XX      protein sequences of the invention.
XX      Sequence      185 AA:
XX
XX      Query Match      100.0%:      Score 81:      DB 23:      Length 185:
XX      Best Local Similarity      100.0%:      Pred. No. 0 0034:
XX      Matches      14:      Conservative      0:      Mismatches      0:      Gaps      0:
OY      1      KKLGGKGGPGGPPK      14
DB      104      KKLGGKGGPGGPPK      117

```





PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

DR WPI: 1999-591920/51.

XX N-PSDB: AA277487.

PT New nucleic acid sequences expressed in ovarian, and some other, cancer  
PT tissues, and derived polypeptides, for treatment of ovarian cancer and  
PT identification of therapeutic agents -

PS Claim 25; Page 279; 310pp; German.

XX This invention describes novel nucleic acid (cDNA) sequences (A) which  
XX have anticancer activity and are highly expressed in ovarian tumor  
XX tissue (and some also in testis and breast cancer tissue). The products  
XX of the invention can be used for gene therapy. (A) are used (i) for  
XX recombinant expression of polypeptides (B) and (ii) to isolate complete  
XX genes. (B) are used (i) to identify agents suitable for treatment of  
XX ovarian cancer; (ii) directly for treating this form of cancer  
XX (including expression from gene therapy vectors) and (iii) for generation  
XX of specific antibodies. (A) are identified by assembling ESTs (expressed  
XX sequence tags) from a particular tissue type before comparison of the  
XX expression patterns. This allows a significantly longer fragment of the  
XX gene to be revealed, so should reduce the number of failures associated  
XX with the fact that ESTs from different libraries may represent different  
XX parts of the same unknown gene, distorting the estimated frequency of  
XX occurrence in a particular tissue. AAY76505-Y76638 represent protein  
XX fragments encoded by the human ovarian tumor cDNA library derived EST  
XX

SO Sequence 194 AA;

Query Match 100.0%; Score 81; DB 20; Length 194;

Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLGGKGGGPPPK 14

Db 113 KKLGGKGGGPPPK 126

RESULT 13

ID AAB41048 standard; Protein: 103 AA.

XX AAB41048;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF812 polypeptide sequence SEQ ID NO:1624.

XX Human; open reading frame; ORFX: detection; cytostatic; hepatotropic;  
XX vulnery; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;  
XX anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
XX hypotensive; dermatological; immunosuppressive; antiinflammatory;  
XX antiviral; antibacterial; antifungal; antineuritic; acetylcholin;  
XX antinaemic; gene therapy; cancer; proliferative disorder; hyperextension;  
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;  
XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
XX cholesterol ester storage; systemic lupus erythematosus; infection;  
XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
XX thrombosis; cartilage damage; antiinflammatory disease; coagulation;  
XX

OS Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI: 2000-602362/57.

XX N-PSDB: AAC75257.

PT Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease -

PS Claim 11; Page 1306; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX  
XX sequences have activities such as: cytostatic; hepatotropic; vulnery;  
XX antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;  
XX osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
XX immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
XX antidiabetic; hypotensive; dermatological; immunosuppressive;  
XX antiinflammatory; antibacterial; antiviral; antifungal; antineuritic;  
XX antihypoid; and antinaemic. The sequences can be used for determining  
XX the presence of or predisposition to, or preventing or treating  
XX pathological conditions associated with an ORFX-associated disorder. The  
XX nucleic acids can be used to express ORFX proteins in gene therapy  
XX vectors. The proteins and nucleic acids may be used to treat cancers,  
XX proliferative disorders, neurodegenerative disorders, osteoarthritis,  
XX graft vs host disease, cardiovascular disease, diabetes mellitus,  
XX hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
XX erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
XX bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
XX allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
XX nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
XX coagulation; to inhibit thrombosis; and as a contraceptive.

SO Sequence 103 AA;

Query Match 64.2%; Score 52; DB 21; Length 103;

Best Local Similarity 64.3%; Pred. No. 12;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKLGGKGGGPPPK 14

Db 61 KKLGGKGGGPPPK 74

RESULT 14

ID AAB35077 standard; Protein: 103 AA.

XX AAB35077;

DT 08-JUL-2002 (first entry)

DE Human ORFX050 protein, SEQ ID NO:8100.

XX Human; ORF; open reading frame; ORFX: drug screening; diagnosis;  
XX disease monitoring; cytokine; cell proliferation; cell differentiation;  
XX immune modulation; haematopoiesis regulation; tissue growth;  
XX angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;  
XX thrombolytic; tumour inhibition; bodily characteristics; fertility;  
XX behaviour; cancer; proliferative disorder; neurological disorder;  
XX cardiovascular disease; immune system disorder; organ transplantation;  
XX tissue growth disorder; tissue regeneration disorder; diabetes mellitus;  
XX hypothyroidism; cholesterol ester storage disease; infection; vulnery;  
XX vasotropic; antiproliferative; antidiabetic; cytostatic; neurotrophic;

KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;  
 KW cardiac; hypotensive; antihypertensive; antiinflammatory; immunomodulator;  
 KW dermatological; analgesic; virucide; antibacterial; fungicide.  
 OS Homo sapiens.  
 XX WO200190366-A2.  
 PN 29-NOV-2001.  
 PD 24-MAY-2001; 2001WO-US17076.  
 PF 24-MAY-2000; 2000US-206690P.  
 PR 24-MAY-2000; 2000US-206690P.  
 XX (CURA-) CURAGEN CORP.  
 PA Leach MD, Shimkets RA;  
 PI WPI: 2002-106200/14.  
 DR N-PSDB; ABN79103.  
 XX Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and disorders related to organ  
 PT transplantation -  
 XX Claim 10; Page 2271; 2508pp; English.  
 PS Sequences ABP31028-ABP35561 represent 4534 novel human proteins  
 XX designated ORF (open reading frame) 1-4534, and sequences ABN75054-  
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses  
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively  
 CC referred to as ORF) proteins, polynucleotides at least 85% identical to  
 CC the ORF nucleic acid sequences, vectors and host cells comprising ORF  
 CC polynucleotides, the recombinant production of ORF proteins, antibodies  
 CC specific for ORF proteins, methods of detecting ORF polynucleotides and  
 CC polypeptides, methods of screening individuals for a predisposition to an  
 CC activity, and methods of screening individuals for a predisposition to a wide  
 CC ORF-associated disorder. The ORF proteins of the invention have a wide  
 CC range of biological activities, such as cytokine, cell proliferation,  
 CC cell differentiation, immune modulation, hematopoiesis regulation,  
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/  
 CC chemokinetic activity, haemostatic activity, tumour inhibition activity,  
 CC receptor/ligand, antiinflammatory activity, and may also be involved in the determination  
 CC of bodily characteristics, fertility and behaviour. ORF proteins,  
 CC nucleic acids and antibodies may be used in the treatment of cancers,  
 CC other proliferative disorders such as psoriasis and benign tumours,  
 CC neurological disorders such as epilepsy and Alzheimer's disease,  
 CC cardiovascular diseases, immune system disorders, disorders related to  
 CC organ transplantation, disorders of tissue growth and regeneration, ester  
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol,  
 CC storage disease, and infectious diseases caused by viral, bacterial,  
 CC fungal and other pathogens. ORF nucleic acids may also be used as a  
 CC source of primers and probes, in the detection of ORF genomic sequences  
 CC or transcripts, in the identification and cloning of homologous  
 CC sequences, in genetic diagnosis, and in forensic biology. The ORF  
 CC nucleic acids may additionally be used to produce transgenic animals  
 CC which may be useful for studying the function and/or activity of ORF  
 CC protein, and in drug screening. The ORF proteins may also be used as  
 CC immunogens to generate specific antibodies, which are useful in the  
 CC diagnosis, treatment and monitoring of ORF-associated diseases.

XX Sequence 103 AA;

Query Match 64.2%; Score 52; DB 23; Length 103;  
 Best Local Similarity 64.3%; Pred. No. 12;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKLGGKPGGPPK 14  
 :|||||  
 DB 61 KKSSGKPGNPRK 74

RESULT 15  
 AA001151  
 ID AA001151 standard; Protein; 163 AA.  
 XX  
 AC AA001151;  
 DT 06-NOV-2001 (first entry)  
 DE Human polypeptide SEQ ID NO 15043.  
 XX  
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.  
 XX  
 OS Homo sapiens.  
 OS  
 XX WO200164835-A2.  
 PN 07-SEP-2001.  
 PD 26-FEB-2001; 2001WO-US04927.  
 PF 28-FEB-2000; 2000US-0515126.  
 PR 18-MAY-2000; 2000US-0577409.  
 XX (HYSE-) HYSEQ INC.  
 PA Tang YT, Liu C, Drmanac RT;  
 PI WPI: 2001-514838/56.  
 DR N-PSDB; AA181082.  
 XX

Isolated nucleic acids and polypeptides, useful for preventing  
 PT diagnosing and treating e.g. leukaemia, inflammation and immune  
 PT disorders -  
 XX Claim 20; SEQ ID NO 15043; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and  
 CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, immunomodulatory activity and  
 CC activity, tissue growth factor activity, haemostatic activity and/or  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 163 AA;

Query Match 64.2%; Score 52; DB 22; Length 163;  
 Best Local Similarity 69.2%; Pred. No. 18;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 KKLGGKPGGPPK 13  
 :|||||  
 DB 57 KKGRKGPKNPPK 69

Search completed: April 11, 2003, 16:11:08  
 Job time : 4.92822 secs

GenCore version 5.1.4.P5-4578  
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 ; Search time 10.8059 Seconds

(without alignments)  
706.250 Million cell updates/sec

Title: US-09-821-726a-16

Perfect score: 993

Sequence: 1 MKLTMFVGLGLAAPGFA.....TADILWLMSFCGTSVETV 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	993	100.0	184	1	C1IP_MOUSE
2	640	64.5	199	1	C1IP_HUMAN
3	91	9.2	553	1	FXC1_HUMAN
4	89	9.0	345	1	EFB1_MOUSE
5	86	8.7	538	1	PPCK_SALTY
6	85.5	8.6	335	1	CHM1_BOVIN
7	85.5	8.6	346	1	EFB1_HUMAN
8	85.5	8.6	539	1	PPCK_SALTY
9	85	8.6	345	1	EFB1_HUMAN
10	84.5	8.5	334	1	CHM1_MOUSE
11	84	8.5	752	1	HYSA_PROAC
12	83.5	8.4	347	1	CHM1_CHICK
13	81	8.2	553	1	FXC1_MOUSE
14	80.5	8.1	728	1	KDGI_ARATH
15	80	8.1	555	1	P263_RAT
16	79.5	8.0	539	1	PPCK_YERPE
17	79	8.0	336	1	EFB2_MOUSE
18	77.5	7.8	407	1	CHM1_RAT
19	77.5	7.7	193	1	RPI1_YEAST
20	76.5	7.7	484	1	CSR2_CHICK
21	76.5	7.7	775	1	GUNA_XANCP
22	76	7.7	775	1	CSR2_HUMAN
23	75.5	7.6	193	1	CSR2_COTLA
24	75.5	7.6	421	1	YB1U_ECOLI
25	75	7.6	334	1	CHM1_HUMAN
26	74.5	7.5	404	1	FTR1_YEAST
27	74.5	7.5	747	1	YEM1_YEAST
28	74	7.5	775	1	ECCL_MOUSE
29	74	7.5	775	1	ECCL_RAT
30	73	7.4	465	1	MTR6_HUMAN
31	72.5	7.3	409	1	YG4S_YEAST
32	72	7.3	333	1	CHM1_RABIT
33	72	7.3	333	1	EFB2_HUMAN

RESULT 1	ID	CLIP_MOUSE	STANDARD	PRT	184 AA.
AC	Q9GR36	Q9D7K7	Q9CTZ5		
DT	15-JUN-2002	(Rel. 41)	Created		
DT	15-JUN-2002	(Rel. 41)	Last sequence update		
DT	15-JUN-2002	(Rel. 41)	Last annotation update		
DE	CALL protein homology.				
GN	CALL.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
NCBI	Taxid=10090;				
RP	[1]				
RC	SEQUENCE FROM N.A.				
RA	STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;				
RA	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberti S.,				
RA	Nardone P., Ring B., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,				
RA	Wyszewski H., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
DR	EMBL	AK008990	BAR26010.1	-	P06914 plasmodium
DR	EMBL	AK008622	BAR25784.1	-	P42893 rattus norv
DR	EMBL	AK008641	BAR25801.1	-	P22265 drosophila
DR	EMBL	AK008647	BAR25805.1	-	P22259 escherichia
DR	EMBL	AK008722	BAR25856.1	-	P06841 myxoma vira
DR	EMBL	AK008745	BAR25872.1	-	O08010 bovine rota
DR	EMBL	AK008933	BAR25975.1	-	O16527 homo sapien
DR	EMBL	AK008956	BAR25988.1	-	P08398 escherichia
DR	EMBL	AK009145	BAR26103.1	-	P12929 saccharomyc
DR	EMBL	AK019050	BAR31525.1	-	P21543 penicillium
DR					O27309 bombyx mori

DR MGD: MGI:1913533; 2200002K21R1K.  
 FT CONFLICT 113 113 P -> L (IN REF. 1; BAB26103).  
 SQ SEQUENCE 184 AA: 20134 MW: 288982F0404FFAB8 CRC64;  
 Query Match 100.0%; Score 993; DB 1; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 4, 3e-88;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLTMEVVGILGLIAPGFAYTVNNGNDGVSGQSVSINGVHNVANINDNNNGDSW 60  
 DB 1 MKLTMEVVGILGLIAPGFAYTVNNGNDGVSGQSVSINGVHNVANINDNNNGDSW 60  
 QY 61 NSLMDYENSFATRLFSKSKSCIVHHRNKNKAMPDLSLODLMVKEQKSGAPPKDLMS 120  
 DB 61 NSLMDYENSFATRLFSKSKSCIVHHRNKNKAMPDLSLODLMVKEQKSGAPPKDLMS 120  
 QY 121 VNPTEVEDLNTFGPKIAGCRCGIPYVAEIPGPNOPLYSKRCYADILMLMSFCGTS 180  
 DB 121 VNPTEVEDLNTFGPKIAGCRCGIPYVAEIPGPNOPLYSKRCYADILMLMSFCGTS 180  
 QY 181 VETY 184  
 DB 181 VETY 184

RESULT 2  
 CLIP\_HUMAN STANDARD; PRT; 199 AA.  
 ID CLIP\_HUMAN  
 AC 09NS71:  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE CALL protein.  
 GN CALL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Stomach;  
 RX MEDLINE=20296773; PubMed=10835488;  
 RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;  
 RT Isolation of two novel genes, down-regulated in gastric cancer.";  
 RL Jpn. J. Cancer Res. 91:459-463(2000).  
 CC -1- TISSUE SPECIFICITY: Expressed in stomach. No expression is  
 detected in cancer tissue or gastric cancer cell lines.  
 CC -----  
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 CC -----  
 CC EMBL: AB039886; BAA92433.1; -  
 DR MIR: 606402; -  
 DR SEQUENCE 199 AA: 21999 MW: C099BB89A138D7A CRC64;  
 SQ

Query Match 64.5%; Score 640; DB 1; Length 199;  
 Best Local Similarity 63.8%; Pred. No. 3, 1e-54;  
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMEVVGILGLIAPGFAYTVNNGNDGVSGQSVSINGVHNVANINDNNNGDS 59  
 DB 1 MKLTMEVVGILGLIAPGFAYTVNNGNDGVSGQSVSINGVHNVANINDNNNGDS 59  
 QY 15 MKFTTVPACILGVFLPALANINYNV-DNNNAGSQSQSVSNHNHNANVNDNNGWS 73  
 DB 15 MKFTTVPACILGVFLPALANINYNV-DNNNAGSQSQSVSNHNHNANVNDNNGWS 73  
 QY 60 NSLMDYENSFATRLFSKSKSCIVHHRNKNKAMPDLSLODLMVKEQK--GKPGGAPPKDL 117  
 DB 60 NSLMDYENSFATRLFSKSKSCIVHHRNKNKAMPDLSLODLMVKEQK--GKPGGAPPKDL 117  
 QY 74 NMSIMDYNGGFATRLFEQKTCIVHKMKRKMPSIOGLDALYKEKKLOGKGGGPPPKGL 133  
 DB 74 NMSIMDYNGGFATRLFEQKTCIVHKMKRKMPSIOGLDALYKEKKLOGKGGGPPPKGL 133  
 QY 118 MYSVNPTEVEDLNTFGPKIAGCRCGIPYVAEIPGPNOPLYSKRCYADILMLMSFC 177

DB 134 MYSVNPTEVEDLNTFGPKIAGCRCGIPYVAEIPGPNOPLYSKRCYADILMLMSFC 193  
 QY 178 GTSVE 182  
 DB 194 GDIVE 198

RESULT 3  
 FXCL\_HUMAN STANDARD; PRT; 553 AA.  
 ID FXCL\_HUMAN  
 AC 012948; Q9UP06; Q9NUE5; Q9BYM1; Q9UD00;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Forkhead box protein C1 (Forkhead-related protein FKHL7) (Forkhead-  
 DE related transcription factor 3) (FREC-3).  
 GN FOXO1 OR FKHL7 OR FREAC3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND VARIANTS S-112; M-126 AND L-131.  
 RX MEDLINE=98282091; PubMed=9620769;  
 RA Nishimura D.Y., Swiderski R.E., Alward W.L.M., Searby C.C.,  
 RA Patel S.R., Bennet S.R., Kanis A.B., Gastler J.M., Stone E.M.,  
 RA Sheffield V.C.;  
 RT "The forkhead transcription factor gene FKHL7 is responsible for  
 RT glaucoma phenotypes which map to 6p25.";  
 RL Nat. Genet. 19:140-147(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANTS ARA THR-82 AND MET-87.  
 RX MEDLINE=99011252; PubMed=9792859;  
 RA Meers A.J., Jordan T., Mirzayans F., Dubois S., Kume T., Parlee M.,  
 RA Ritch R., Koop B., Kuo W.-L., Collins C., Marshall J., Gould D.B.,  
 RA Pearce W., Carlsson P., Enerbaeck S., Morrisette J., Bhattacharya S.,  
 RA Hogen B., Raymond V., Walter M.A.;  
 RT "Mutations of the forkhead/winged-helix gene, FKHL7, in patients with  
 RT Axenfeld-Rieger anomaly.";  
 RL Am. J. Hum. Genet. 63:1316-1328(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Patel R.;  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 68-177 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Erythrocytes;  
 RX MEDLINE=93271467; PubMed=8499623;  
 RA Hromas R., Moore J., Johnston T., Socha C., Klemm M.;  
 RT "Prophila forkhead homologues are expressed in a lineage-restricted  
 RT manner in human hematopoietic cells.";  
 RL Blood 81:2854-2859(1993).  
 RN [5]  
 RP SEQUENCE OF 73-178 FROM N.A.  
 RX MEDLINE=95045392; PubMed=7957066;  
 RA Pierrou S., Hellqvist M., Samuelsson L., Enerbaeck S., Carlsson P.;  
 RT "Cloning and characterization of seven human forkhead proteins:  
 RT binding site specificity and DNA bending.";  
 RL EMBL J. 13:5002-5012(1994).  
 CC -1- FUNCTION: BINDING OF FREAC-3 AND FREAC-4 TO THEIR COGNATE SITES  
 CC RESULTS IN BENDING OF THE DNA AT AN ANGLE OF 80-90 DEGREES.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues and cell lines  
 CC examined.  
 CC -1- DISEASE: DEFECTS IN FOXO1 ARE THE CAUSE OF A SPECTRUM OF GLAUCOMA  
 CC PHENOTYPES SUCH AS AXENFELD-RIEGER ANOMALY (ARA), AXENFELD-RIEGER  
 CC SYNDROME (ARS) AND IRIDOGONIOSGENESIS ANOMALY (IGDA). ARS IS AN  
 CC AUTOSOMAL DOMINANT DISORDER PRESENTING WITH ARA-LIKE OCULAR  
 CC FINDINGS IN ADDITION TO ABNORMALITIES OF THE TEETH, JAW AND  
 CC UMBILICUS.  
 CC -1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.

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CC -----
DR EMBL: AF048693; AAC18081.1; -
DR EMBL: AF078096; AAC72915.1; -
DR EMBL: AL034344; CAB81658.1; -
DR EMBL: L12143; AKI3575.1; -
DR HSSP: Q63245; 2HFH.
DR TRANSFAC: T02471; -
DR Genew: HGNC:3800; FOXCL.
DR MIM: 601090; -
DR MIM: 601631; -
DR InterPro: IPR001766; TF_Fork_head.
DR Pfam: PF00250; Fork_head_3.
DR Prodom: PD000425; TF_Fork_head_1.
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS50039; FORK_HEAD_3; 1.
KW DNA-binding; Nuclear protein; Transcription regulation;
KW Disease mutation.
FT DNA_BIND 77 168 FORK-HEAD.
FT DOMAIN 28 33 POLY-ALA.
FT DOMAIN 169 173 POLY-ARG.
FT DOMAIN 194 197 POLY-PRO.
FT DOMAIN 262 272 POLY-SER.
FT DOMAIN 292 297 POLY-PRO.
FT DOMAIN 375 382 POLY-GLY.
FT DOMAIN 438 445 POLY-SER.
FT DOMAIN 447 456 POLY-GLY.
FT DOMAIN 486 495 POLY-ALA.
FT VARIANT 82 82 S->T (IN ARS).
FT VARIANT 87 87 /FTID=VAR_007944.
FT VARIANT 112 112 I->M (IN ARS).
FT VARIANT 126 126 F->S (IN IGDA).
FT VARIANT 131 131 /FTID=VAR_007815.
FT VARIANT 131 131 I->M (IN ARS).
FT VARIANT 131 131 S->L (IN ARS).
FT CONFLICT 70 77 OROPKDMV->RSRPRHG (IN REF. 4).
FT CONFLICT 101 101 L->Q (IN REF. 4).
FT CONFLICT 180 180 V->L (IN REF. 2).
FT CONFLICT 199 202 RQPP->ASPR (IN REF. 2).
FT CONFLICT 426 426 D->N (IN REF. 1).
SQ SEQUENCE 553 AA; 56788 MW; 59C6FB94303ED59A CRC64;
Query Match 9.28; Score 91; DB 1; Length 553;
Best Local Similarity 19.68; Pred. NO. 0.43;
Matches 38; Conservative 21; Mismatches 57; Indels 78; Gaps 9;

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RESULT 4
EPBL_MOUSE
ID EPBL_MOUSE STANDARD: PRT: 345 AA.
AC P52795;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE (LEK-2) (ELK ligand) (ELK-L) (STRA1 protein) (CEK5 receptor ligand)
DE (CEK5-L).
DE EPNB1 OR EPLG2 OR LEK2 OR STRA1 OR EPL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RP STRAIN-129/SV;
RX MEDLINE=95203867; PubMed=7896266;
RA Fletcher F.A., Renshaw B., Hollingsworth T., Baum P., Lyman S.D.,
RA Jenkins N.A., Gilbert D.J., Copeland N.G., Davison B.L.;
RT "Genomic organization and chromosomal localization of mouse Eplg2, a
RT gene encoding a binding protein for the receptor tyrosine kinase
RT elk.";
RL Genomics 24:127-132(1994).
[2]
SEQUENCE FROM N.A.
RP MEDLINE=95377533; PubMed=7649373;
RA Bouillet P., Oulad-Abdelghani M., Violette S., Garnier J.M.,
RA Schaubaur B., Dolle P., Chambon P.;
RT "Efficient cloning of cDNAs of retinoic acid-responsive genes in p19
RT embryonal carcinoma cells and characterization of a novel mouse gene,
RT Stral (mouse LEK-2/Eplg2).";
RL Dev. Biol. 170:420-433(1995).
[3]
SEQUENCE FROM N.A.
RP TISSUE-Brain;
RX MEDLINE=95014510; PubMed=7929389;
RA Shao H., Lou L., Pandey A., Pasquale E.B., Dixit V.M.;
RT "cDNA cloning and characterization of a ligand for the CEK5 receptor
RT protein-tyrosine kinase.";
RL J. Biol. Chem. 269:26606-26609(1994).
[4]
FUNCTION.
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors
RT in the mouse spinal cord: a possible role in constraining the
RT orientation of longitudinally projecting axons.";
RL Development 127:1367-1410(2000).
-i- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL
CC AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE
CC ORIENTATION OF LONGITUDINALLY PROJECTING AXONS.
CC -i- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB1 AND EPHA1.
CC -i- SUBCELLULAR LOCATION: Type I membrane protein.
CC -i- TISSUE SPECIFICITY: EXPRESSED ON LATERAL FLOOR PLATE CELLS.
CC SPECIFICALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROUGH
CC THE FLOOR PLATE. EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL
CC LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISC.
CC -i- DEVELOPMENTAL STAGE: EXPRESSED IN THE FLOOR PLATE THROUGHOUT THE
CC PERIOD OF COMMISSURAL AXON PATHFINDING.
CC -i- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE
CC CYTOPLASMIC DOMAIN.
CC -i- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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CC -----
DR EMBL; U07602; AAC53247.1; JOINED.
DR EMBL; U07598; AAC53247.1; JOINED.
DR EMBL; U07599; AAC53247.1; JOINED.
DR EMBL; U07600; AAC53247.1; JOINED.
DR EMBL; U248781; CA88695.1; -.
DR EMBL; U12983; AAS53231.1; -.
DR MGD; MGI:102708; Efnb1.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin.
DR PRINTS; P01347; Ephrin.
DR PRODOM; PD002533; Ephrin.
DR PROSITE; PS01299; Ephrin.
KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW Signal; Phosphorylation.
FT CHAIN 1 24 POTENTIAL.
FT DOMAIN 25 345 EPHRIN-B1.
FT TRANSMEM 237 257 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 238 345 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 343 345 PDZ RECOGNITION MOTIF (POTENTIAL).
FT CARBOHD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 90 90 S -> T (IN REF. 2).
SO SEQUENCE 345 AA; 37859 MW; 8C96FD3DC5BCA05 CRC64;

Query Match 9.0%; Score 89; DB 1; Length 345;
Best Local Similarity 23.1%; Pred. No. 0.38;
Matches 40; Conservative 26; Mismatches 57; Indels 50; Gaps 10;

OY 16 ABGFATVINGNDGNVDS---GOOSVINGVHNVANIDNNGWSNLSMDYENSFA 71
DB 199 AGG-----RSGQSDGDKHETVNDQEKSGPGAGGSGSDSDFNSKVAL-----FA 241
OY 72 ARRLSKKSCIV-----HRANKAMPISLQDDITVAKKKGKPGGAP 113
DB 242 AV---GAGCVIFLLIIFLTLLLRKKRRHHTQOAAALSLTASPPGGTAGTE 297
OY 114 PKDLMSVNPTRFEDINTFGR---KIAGMCRGIPTYVAEELPGNOP--LYSK 161
DB 298 PDDIIIFLRTTE---NNYCPHEKVSQ-DYGHVYIVQEMP-POSTANITYK 344

RESULT 5
PCKK_SALTY STANDARD; PRT; 538 AA.
AC P41033:
DT 01-FEB-1995 (rel. 31, Created)
DT 15-JUN-2002 (rel. 41, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Phosphoenolpyruvate carboxylase [ATP] (EC 4.1.1.49) (PEP
DE carboxylase) (Phosphoenolpyruvate carboxylase) (PEPCK).
CN PCKA OR PCK OR STM3500.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
ON 111
RP SEQUENCE FROM N.A.
RC STRAIN-LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE-21534948; PubMed-11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Portolillo S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
RP SEQUENCE OF 251-538 FROM N.A.
RC STRAIN-LT2.
RX MEDLINE-89011922; PubMed-2845093;

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RA Listerium P., Laanenen I., Palva E.T.;
RT "Structure and expression of the omp operon, the regulatory locus
RT for the outer membrane porin regulon in Salmonella typhimurium
RT Lt-2."
RL J. Mol. Biol. 201:663-673(1988).
RN [3]
RP IDENTIFICATION.
RX MEDLINE-91072271; PubMed-1701430;
RA Medina V., Pontarollo R., Glaeske D., Tabel H., Goldie H.;
RT "Sequence of the pckA gene of Escherichia coli K-12: relevance to
RT genetic and allosteric regulation and homology of E. coli
RT phosphoenolpyruvate carboxylase with the enzymes from Trypanosoma
RT brucei and Saccharomyces cerevisiae."
RL J. Bacteriol. 172:7151-7156(1990).
CC -1- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
CC + CO(2).
CC -1- ENZYME REGULATION: ALLOSTERICALLY ACTIVATED BY CALCIUM.
CC -1- POSITIVELY REGULATED BY CAMP (BY SIMILARITY).
CC -1- PATHWAY: Rate-limiting gluconeogenic enzyme.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
CC FAMILY.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
CC in position 363, 458 and 530.
CC
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CC
DR EMBL; AE008861; AAL22362.1; -.
DR EMBL; X12374; -. NOT_ANNOTATED_CDS.
DR HSSP; P22259; 1A02.
DR StyGene; SG10497; pck.
DR InterPro; IPR001272; PEPCK_ATP.
DR Pfam; PF01293; PEPCK_ATP.1.
DR TIGRFAMs; TIGR00224; PCKA.1.
DR PROSITE; PS00532; PEPCK_ATP.1.
KW Gluconeogenesis; Lyase; Decarboxylase; ATP-binding; Calcium;
KW Allosteric enzyme; Complete proteome.
FT NP_BIND 247 254 ATP (BY SIMILARITY).
FT SEQUENCE 538 AA; 59576 MW; 8502FF986D22860A CRC64;

Query Match 8.7%; Score 86; DB 1; Length 538;
Best Local Similarity 23.5%; Pred. No. 1.3;
Matches 47; Conservative 32; Mismatches 65; Indels 56; Gaps 11;

OY 1 MKLTMEFV--GGLGLAARFAYTVINGNDGNV-----DGGQOSVINGVHNVANID 52
DB 210 MKKMFVSNVNYLLPLKGTSMHCSANV-GEKGVAAVFFGLSGTKITLSTDPKRLIG-D 267
OY 53 NNNGWSNLSMDYENS-FAATRLFEKSKS--CLVHRANKDAMS----- 93
DB 268 DEHGMD-DGVNFEFGCYAKPTIKLSKEAPEIYHAIRPALLENVTVREDGTVDFDGS 326
OY 94 -----LQDDITVMEKKGKGP-----GGAPKDLMSVNPTRFEDINTF 132
DB 327 KIENRVSPIYIHIDIVAPSKAGHATVIFLTADFGVLPVSRK-TANOTQYHLSGF 365
OY 133 GPKIAGMCRGI---PTYVA 148
DB 386 TAKLAGTERGVTEPPTFSA 405

RESULT 6
CHN1_BOVIN STANDARD; PRT; 335 AA.
ID CHN1_BOVIN
AC P17404; P23590;
DT 01-AUG-1990 (rel. 15, Created)

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GN EFNBI OR EPLG2 OR LERK2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN NCBI\_TaxID=10116;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95022634; PubMed=7936648;  
 RA Fletcher F.A., Carpenter M., Shilling H., Baum P., Ziegler S.,  
 RA Gimel S., Hollingsworth T., Vandenbos T., Davison B.L.,  
 RT "LERK-2, a binding protein for the receptor-tyrosine kinase Elk, is  
 RT evolutionarily conserved and expressed in a developmentally regulated  
 RT pattern.";  
 RL Oncogene 9:3241-3248(1994).  
 CC -i- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL  
 CC AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE  
 CC ORIENTATION OF LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY).  
 CC -i- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB3 (PREFERRED),  
 CC EPHB1 AND EPHB2.  
 CC -i- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).  
 CC -i- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.  
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 CC EMBL: U07560; AAA51092.1; -  
 CC InterPro: IPR001799; Ephrin.  
 CC Pfam: PF00812; Ephrin.  
 CC PRINTS: PR01347; EPHRIN.  
 CC PRODOM: PD002533; Ephrin.  
 CC DR PROSITE: PS01299; EPHRIN: 1.  
 CC KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;  
 CC Signal; Phosphorylation.  
 CC FT SIGNAL 1 24  
 CC FT CHAIN 25  
 CC FT DOMAIN 25 345  
 CC FT TRANSMEM 237 257  
 CC FT DOMAIN 258 345  
 CC FT DOMAIN 343 345  
 CC FT CARBOHYD 139 139  
 CC SEQUENCE 345 AA: 37951 MW: 183045657358F7E CRC64;  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 Query Match 8.6%; Score 85; DB 1; Length 345;  
 Best Local Similarity 23.1%; Pred. No. 0.91;  
 Matches 40; Conservative 24; Mismatches 59; Indels 50; Gaps 10;  
 QY 16 AFGAYVYININDNVDGSGGAGSGSGDIDSPNSVAL-----FA 241  
 DB 195 AFG-----KSGQSDSDCKHETVNOEKSQSGAGSGSGDIDSPNSVAL-----FA 241  
 QY 72 ATRFSKSCVY-----HRMNDAMPISLDDLOTMYKEQKGGPGAP 113  
 DB 242 AV---GAGCVIFLLIFLVLLKLKRKRKHQQAALSLSTLSPKDSGTAGTE 297  
 QY 114 PKDLMSYVNPTRVELNITFGP---KIAGMCGIPTVVAEEIIPGPQP---LYSK 161  
 DB 298 PSDIITPLRTTE---NNYCPHYEKVSG-DYGHVYIVQEMP-PQSPANIYK 344  
 RESULT 10  
 CHM1\_MOUSE  
 ID CHM1\_MOUSE STANDARD; PRT; 334 AA.  
 AC 0921F6; 090XU5; PRT; 334 AA.  
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Chondromodulin-I precursor (Chm-I) (Leukocyte cell-derived chemotaxin  
 DE 1) [Contains: Chondrosurfactant protein (Ch-SP)].  
 GN CHM1 OR LECT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RA Hiraki Y., Shukunami C., Inoue H., Suzuki F.,  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RP [2]  
 RC SEQUENCE FROM N.A.  
 RX SRRAIN=C57BH/6J; TISSUE=Embryonic head;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner T., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuoka Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 CC "Functional annotation of a full-length mouse cDNA collection.";  
 CC Nature 409:685-690(2001).  
 CC -i- FUNCTION: Bifunctional growth regulator that stimulates the growth  
 CC of cultured chondrocytes in the presence of basic fibroblast  
 CC growth factor (FGF) but inhibits the growth of cultured vascular  
 CC endothelial cells. May contribute to the rapid growth of cartilage  
 CC and vascular invasion prior to the replacement of cartilage by  
 CC bone during endochondral bone development (By similarity).  
 CC -i- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the  
 CC inter-territorial matrix of cartilage (By similarity).  
 CC -i- PPM: After cleavage, the post-translationally modified Chm-I is  
 CC secreted as a glycoprotein (By similarity).  
 CC -i- SIMILARITY: BELONGS TO THE CHONDROMODULIN-I FAMILY.  
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 CC EMBL: U43509; AAD00027.1; -  
 CC DR EMBL: AK013975; BAB29095.1; -  
 CC DR MGD: MG1:1341171; Lect1.  
 CC KW Cartilage; Glycoprotein; Transmembrane;  
 CC Cleavage on pair of basic residues.  
 CC FT CHAIN 1 210  
 CC FT PROPEP 211 214  
 CC FT CHAIN 215 334  
 CC FT TRANSMEM 46 66  
 CC FT CARBOHYD 243 243  
 CC FT CONFLICT 108 109  
 CC FT CONFLICT 163 163  
 CC FT CONFLICT 207 207  
 CC SEQUENCE 334 AA: 37252 MW: DAFDEC43C7D745D6 CRC64;  
 CHONDROSURFACTANT PROTEIN  
 (BY SIMILARITY).  
 CHONDROMODULIN-I (BY SIMILARITY).  
 POTENTIAL.  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 AK -> FE (IN REF. 2).  
 V -> A (IN REF. 2).  
 K -> KANFA (IN REF. 2).  
 DAFDEC43C7D745D6 CRC64;



Matches 37; Conservative 27; Mismatches 68; Indels 57; Gaps 7;

QY 4 TMFVGLGLGLAAP-----GFAIVNNG--NGDNVDSGQSVSINGVH 46  
 Db 44 TVLIAGALLLLAAGICAFYWKATEROVYVNVHTMSINGKVOD-----SMEIDAGN 95  
 QY 47 NVANIDNNNGWDSWNSIMDYENSPATRLFSKSCIVHRNKDAMPLOLDITVKEQK 106  
 Db 96 NLETFKTSGSSEBAVEVHDQIGITGRFAGGKCYIKAPKARP--EVDAMTK---- 148  
 QY 107 KGGGAPPPDLMYSVNPREDINT-----FGPRAGMCRGIPYVAEIP 152  
 Db 149 -----ASLSSDLEDEIMVPREDENSLIWAADPEIKHNGFLSPKILELCGLPIFWL----- 200  
 QY 153 GPNQPLYSK 161  
 Db 201 ---RPPYPK 206

RESULT 13  
 EXCL\_MOUSE

ID FXCL\_MOUSE STANDARD: PRT: 553 AA.  
 AC Q61572; Q61582; 088409;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Forkhead box protein C1 (Forkhead-related protein FKHL7) (Forkhead-related transcription factor 3) (FRCAC-3) (Transcription factor FKH-1)  
 DE (Mesoderm/mesenchyme forkhead 1) (Mf-1).  
 GN FOXCI OR FKHL7 OR FRCAC3 OR FKHL1 OR MFL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98297351; PubMed=9635428;  
 RA Kume T., Deng K.Y., Wanfrey V., Gould D.B., Walter M.A., Hogan B.L.M.;  
 RT "The forkhead/winged helix gene Mfl is disrupted in the pleiotropic  
 RT mouse mutation congenital hydrocephalus.";  
 RL Cell 93:985-996(1998).  
 RN [2]  
 RP SEQUENCE OF 69-179 FROM N.A.  
 RC STRAIN=129;  
 RX MEDLINE=93361500; PubMed=7689224;  
 RA Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H.,  
 RA Monaghan A.P., Schuetz G.;  
 RT "Six members of the mouse forkhead gene family are developmentally  
 RT regulated";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).  
 RN [3]  
 RP SEQUENCE OF 71-187 FROM N.A.  
 RX MEDLINE=93387221; PubMed=8375339;  
 RA Sasaki H., Hogan B.L.;  
 RT "Differential expression of multiple fork head related genes during  
 RT gastrulation and axial pattern formation in the mouse embryo.";  
 RL Development 118:47-59(1993).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY EMBRYONIC TISSUES, INCLUDING  
 CC PERICHONDROGENIC MESENCHYME, PERICULAR MESENCHYME, MENINGES,  
 CC ENDOTHELIAL CELLS, AND KIDNEY.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS.  
 CC -1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.

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 CC EMBL: AF045017; AAC24209.1; -

DR EMBL: L10406; AAA03159.1; -  
 DR EMBL: X71939; CAA50741.1; -  
 DR HSSP: Q63243; ZHPH.  
 DR TRANSFAC: T02426; -  
 DR MGI: MGI:1347466; Foxc1.  
 DR InterPro: IPR001766; TF\_Fork\_head.  
 DR Pfam: PF00250; Fork\_head\_1.  
 DR PRINTS: PR00053; FORKHEAD.  
 DR Prodom: PD000425; TF\_Fork\_head\_1.  
 DR SMART: SM00339; FH\_1.  
 DR PROSITE: PS00657; FORK\_HEAD\_1; 1.  
 DR PROSITE: PS00658; FORK\_HEAD\_2; 1.  
 DR PROSITE: PS50039; FORK\_HEAD\_3; 1.  
 KW DNA-binding; Nuclear protein; Transcription regulation.  
 FT DOMAIN 28 33  
 FT DNA\_BIND 77 168  
 FT DOMAIN 169 173  
 FT DOMAIN 194 197  
 FT DOMAIN 264 274  
 FT DOMAIN 375 386  
 FT DOMAIN 444 451  
 FT DOMAIN 453 456  
 FT DOMAIN 466 496  
 FT CONFLICT 180 186  
 SO SEQUENCE 553 AA; 56953 MW; 3CDD12F69CA4F217 CRC64;  
 VKDKRK -> KKEIFI (IN REF. 3).

Query Match  
 Best Local Similarity 8.2%; Score 81; DB 1; Length 553;  
 Matches 38; Conservative 21; Mismatches 61; Indels 72; Gaps 9;

QY 14 LAAPFAIVNNGNDVDSGQSVSINGVHNA-----NIDNNNGW----- 57  
 Db 76 MKPPSYIALIT---MAIONAPDKKITLNGIYOFIMDFPPYRNKQGWQMSIRHNSL 132  
 QY 58 -----DSWNSIMDYENSPATRLFSKSCIVHRNKDAMPLOLDITVKEQK 91  
 Db 133 NECFYKVPDRDKKPPKGSYWTLPDSTNM--FENGSEFLRRRRRKKKDAYDKKEKGR 189  
 QY 92 PSLDLDITVKEQKGGGCGAPPPKDLMSV-----NPTREVDLNTFCPKIKMGCGIPT 146  
 Db 190 ----HLOPPPPQAGROPAPAPPEQAGSAPGPPPPYRIDIKTEN-----GTC----- 235  
 QY 147 VAEIIPGNPL 158  
 Db 236 -----PSPPEPL 242

RESULT 14  
 KDGL\_ARATH STANDARD: PRT: 728 AA.

ID KDGL\_ARATH  
 AC Q39017; Q9SD92;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE diacylglycerol kinase 1 (EC 2.7.1.107) (Diacylglyceride kinase 1)  
 DE (DGK 1) (DAG kinase 1).  
 GN DGK1 OR ATSG07920 OR F13G24.120 OR MXM12.16.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=96189276; PubMed=8605313;  
 RA Katagiri T., Mizoguchi T., Shinzaki K.;  
 RT "Molecular cloning of a cDNA encoding diacylglycerol kinase (DGK) in  
 RL Arabidopsis thaliana.";  
 RL Plant Mol. Biol. 30:647-653(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;

RA MEDLINE-21016721; PubMed-1130714; Kotani H., Kato T., Asamizu E.,  
 RA Tabata S., Kaneko T., Nakamura Y., Hosouchi T., Kawashima K.,  
 RA Miyajima N., Sasamoto S., Kimura T., Muraishi A., Nakayama S.,  
 RA Kohara M., Matsumoto M., Matsuno A., Shino S., Takeuchi C., Wada T.,  
 RA Nakazaki N., Naruo K., Okumura S., Sato S., de la Bastide M.,  
 RA Matanabe A., Yarnada M., Yasuda M., O'Shaughnessy A., Preston R.,  
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Nelson J.,  
 RA Habermann K., Murray J., Johnson D., Kohlberg T., Beckner M.,  
 RA Stoeckert T., Pepin K., Cordes M., Courtney L., Armstrong J., Dante M.,  
 RA Belter E., Cordum H., Cordes M., Courtney L., Armstrong J., Dante M.,  
 RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,  
 RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strommatt C.,  
 RA Wagner-McPherson C., Mollam A., Yookum M., Bell M., Dedina N.,  
 RA Parnell L., Shah R., Rodriguez M., Bauret A., Miller B., Marra M.,  
 RA Kirchhoff K., Toth K., King L., Bauret A., Miller B., Marra M.,  
 RA Martensen R., McCombie W.R., Wilsson R.K., Murphy G., Bancroft I.,  
 RA Volckert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,  
 RA Ertlan K.-D., Terryn N., Hartley N., Bent E., Johnson S.,  
 RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,  
 RA Ramsperger U., Wedler H., Balke K., Wedler E., Peters S.,  
 RA van Staveren M., Dirke G., Rose M., Hauf J., Berner S., Hempel S.,  
 RA Weitzenecker T., Bothe G., Villarroel S., Gielens J., Ardiles W.,  
 RA Feldpausch M., Lamberth S., Villarroel S., Gielens J., Ardiles W.,  
 RA Berts O., Lemcke K., Kolesov G., Mayer K.F.X., Rued S., Schoof H.,  
 RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.,  
 RA "Sequence and analysis of chromosome 5 of the plant Arabidopsis  
 RT thaliana." Nature 408:823-826(2000).  
 RL [3]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-CV. Columbia;  
 RC MEDLINE-97471969; PubMed-9330910;  
 RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,  
 RA Miyajima N., Tabata S.; Arabidopsis thaliana chromosome 5. I. Sequence  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence  
 RT features of the 1.6 Mb regions covered by twenty physically assigned  
 RL DNA Res. 4:215-230(1997).  
 CC -1- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-  
 CC diacylglycerol 3-phosphate.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: DETECTED IN ROOTS, SHOOTS, AND LEAVES.  
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHOSBO-ESTER AND DAG  
 CC BINDING DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL: D63787; BAA09856.1; -  
 CC EMBL: AL133421; CAB62604.1; -  
 CC EMBL: AB005249; BAB09956.1; -  
 CC InterPro: IPR000756; DAGKa.  
 CC InterPro: IPR001206; DAGKc.  
 CC InterPro: IPR002219; DAG-pe-bind.  
 CC InterPro: IPR003622; DAG\_kin\_cat.  
 CC Pfam: PF00609; DAGKa.1.  
 CC Pfam: PF00781; DAGKc.1.  
 CC ProDom: PD002939; DAGKa.1.  
 CC ProDom: PD005043; DAG\_kin\_cat.1.  
 CC SMART: SM00109; C1; 2.  
 CC SMART: SM00045; DAGKa.1.  
 CC SMART: SM00046; DAGKc.1.  
 CC PROSITE: PS00479; DAG-pe-bind-dom-1; FALSE\_NG.  
 CC PROSITE: PS00481; DAG-pe-bind-dom-2; 2.  
 CC TRANSFERase: Kinase; Phospho-ester binding; Transmembrane; Repeat.  
 KW TRANSMEM 27 48 POTENTIAL.

FT DOMAIN 95 137  
 FT DOMAIN 169 212  
 FT DOMAIN 359 490  
 FT DOMAIN 507 664  
 FT CONFLICT 509 509  
 FT SEQUENCE 728 AA; 79983 MW; 9E3190721C0830E9 CRC64;  
 Query Match 8.1%; Score 80.5; DB 1; Length 728;  
 Best Local Similarity 24.1%; Pred. No. 6.2;  
 Matches 34; Conservative 27; Mismatches 7;  
 QY 27 GNDG-NVDSGQSOVS-----SINGVH-----NVANIDNNNGDMSIMDYENSPATR 74  
 DB 275 GNGSNDTESTHADTGPVNGAHAVLENSISVYNGSDSSGSDSKLEKESYKRTG 334  
 QY 75 LPSKSCIVHRMKNKAMPISLODLDT-----WYEGKRGKPGGAPKDMYSNPTRVE 127  
 DB 335 SFGQKE--YHALRSKILYELADLPSPDARPLVFLINKSGAQRGSRLRLHLNPQVVF 392  
 QY 128 DLNTE-GPKIA-GMCRGIPTV 146  
 DB 393 ELSSVQGPVGLFLFRKVPHF 413  
 RESULT 15  
 ID F263\_RAT STANDARD; PRT; 555 AA.  
 AC 035552; 035553; 035554; 035555; 035556; 035557; 090W05; 090W06;  
 AC 035096; 16-0CT-2001 (Rel. 40, Created)  
 DT 16-0CT-2001 (Rel. 40, Last sequence update)  
 DT 16-0CT-2001 (Rel. 40, Last annotation update)  
 DE 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 (6PF-2-K/Fru-  
 DE 2,6-P2KSE brain-type isozyme) (RB2K) [includes: 6-phosphofructo-2-  
 DE kinase (EC 2.7.1.105); Fructose-2,6-bisphosphatase (EC 3.1.3.46)].  
 GN 6PF2K3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC STRAIN-Sprague-Dawley; TISSUE-Brain;  
 RX MEDLINE-97345796; PubMed-9202288;  
 RA Watanabe F., Sakai A., Furuya E.;  
 RT "Novel isoforms of rat brain fructose 6-phosphate 2-kinase/fructose  
 RT 2,6-bisphosphatase are generated by tissue-specific alternative  
 RT splicing." J. Neurochem. 69:1-9(1997).  
 RL [2]  
 RP SEQUENCE OF 61-369 FROM N.A.  
 RC STRAIN-Wistar; TISSUE-Placenta;  
 RA Sakakibara R.;  
 RL submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: SYNTHESIS AND DEGRADATION OF FRUCTOSE 2,6-BISPHOSPHATE.  
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-  
 CC fructose 2,6-bisphosphate.  
 CC -1- CATALYTIC ACTIVITY: D-fructose 2,6-bisphosphate + H(2)O = D-  
 CC fructose 6-phosphate + phosphate.  
 CC -1- ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1/RB2K1 (SHOWN HERE), 2/RB2K2,  
 CC 3/RB2K3, 4/RB2K4, 5/RB2K5, 6/RB2K6, 7/RB2K7 AND 8/RB2K8; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE  
 CC PHOSPHOGUANYLATE MUTASE FAMILY.  
 CC -----  
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 CC -----

DR EMBL; D87240; BAA21749.1; -  
 DR EMBL; D87241; BAA21750.1; -  
 DR EMBL; D87242; BAA21751.1; -  
 DR EMBL; D87243; BAA21752.1; -  
 DR EMBL; D87244; BAA21753.1; -  
 DR EMBL; D87245; BAA21754.1; -  
 DR EMBL; D87246; BAA21755.1; -  
 DR EMBL; D87247; BAA21756.1; -  
 DR EMBL; AB006710; BAA22048.1; -  
 DR InterPro: IPR000546; 6PF2K.  
 DR InterPro: IPR003094; 6PF2K\_kin.  
 DR InterPro: IPR001345; PG/BPGM\_mutase.  
 DR Pfam: PF00300; PGAM; 1.  
 DR Pfam: PF01591; 6PF2K; 1.  
 DR PRINTS: PR00991; 6PF2KCNASE.  
 DR PRODOM: PD002665; 6PF2K; 1.  
 DR PROSITE: PS00175; PG\_MUTASE; 1.  
 KW Multifunctional enzyme; Transferase; Kinase; Hydrolase; ATP-binding;  
 KW Phosphorylation; Multigene family; Alternative splicing.  
 FT DOMAIN 1 245 6-PHOSPHOFRUCTO-2-KINASE.  
 FT NP\_BIND 246 555 FRUCTOSE-2,6-BISPHOSPHATASE.  
 FT BINDING 42 49 ATP (BY SIMILARITY).  
 FT BINDING 99 99 TO FRU-6-P (BY SIMILARITY).  
 FT ACT\_SITE 125 125 POTENTIAL.  
 FT ACT\_SITE 155 155 POTENTIAL.  
 FT ACT\_SITE 254 254 POTENTIAL.  
 FT ACT\_SITE 323 323 FORMS THE PHOSPHOISTIDINE INTERMEDIATE.  
 FT ACT\_SITE 388 388 POTENTIAL.  
 FT VARSPPLIC 448 476 PROTON DONOR (BY SIMILARITY).  
 FT VARSPPLIC 543 555 MISSING (IN ISOFORM 4, ISOFORM 5, ISOFORM 6 AND ISOFORM 8).  
 FT VARSPPLIC 535 555 RTCHIRKESPY -> T (IN ISOFORM 2 AND ISOFORM 5).  
 FT VARSPPLIC 543 555 PLGKACLRVCHIRKESPY -> NMRSPRGAESSQKH (IN ISOFORM 3 AND ISOFORM 6).  
 FT VARSPPLIC 543 555 MISSING (IN ISOFORM 7 AND ISOFORM 8).  
 FT CONFLICT 185 185 D -> H (IN REF. 2).  
 FT CONFLICT 367 367 V -> L (IN REF. 2).  
 SQ SEQUENCE 555 AA; 63675 MW; 45B2D090B44FCDBD CRC64;

Query Match

Best Local Similarity 8.18; Score 80; DB 1; Length 555;  
 Matches 26; Conservative 17; Mismatches 42; Indels 20; Gaps 4;

OY 79 KSCIIVHRMNDAM-----PSLQDLDTM---VKEGKGKPGGAPPKDL---MYS 120  
 Db 437 ESYSTHRESEAVKIQHFASVVRSSSTYELDFLSVESAKODAKKGNPLMRNSVTPLAS 496  
 OY 121 VNFTRVEDLNTFGPKTAGMGRCIPTYVAEEIPG--PNQPLYSKKC 163  
 Db 497 PEPTKKRINSFEHVASTSAALPSCLPPEVPQQLPQPLGKAC 541

Search completed: April 11, 2003, 16:11:59  
 Job time : 12.9725 secs

